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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-5497. The polypeptides sequences are designated SEQ ID NO: 5498-10994. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-5497 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-5497. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-5497 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-5497.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety

of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

5 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath
10 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-5497;
15 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-5497. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing
20 (e.g., SEQ ID NO: 5498-10994); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

25 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-5497; or (b) polynucleotides that hybridize to the complement of the
30 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably

produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a
5 hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium
10 under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use
15 as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample
20 using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

25 The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight
30 markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-5497.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-5497. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an

eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5 The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic
10 elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

15 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino
20 acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that
25 have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

30 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue
35 may be removed from the protein during processing in the cell. The peptide may be produced

synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer
5 attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*,
10 recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

15 Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in
20 the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino
25 acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and
30 glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using
35 recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

10 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 15 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural

or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*,

washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for
5 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse
10 functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less).
15 Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this
20 embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably
25 at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence
30 identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation
35 of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be

disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

10 As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

15 Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

25 The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-5497; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 5498-10994; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 5498-10994. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-5497; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide. comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 5498-10994.

30 Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in

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receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-5497 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-5497 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-5497 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-5497, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most

preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-5497, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-5497 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-5497 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the

polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-5497, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-5497, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 5498-10994 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-5497 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-5497), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-5497). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-5497 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and
5 Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical
10 structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or
15 solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral
20 backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For
25 example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or
30 primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug
35 delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 5498-10994 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-5497 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or the corresponding full length or mature protein; and
5 "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.
10 Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 5498-10994.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.
15 U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where
20 proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

30 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.
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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunoaffinity chromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 5498-10994.

15 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or
20 deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to
35 retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

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4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active
5 portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to
10 the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which
15 the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.
20 The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays
25 to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for
30 appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can
35 subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked
5 in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*,
5 by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and
10 PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard
15 selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to
20 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or
25 protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene
30 under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally
35 occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce
5 autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In
20 addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al.,
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci. U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methycellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al.,
5 Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21,
10 Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

20 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of
25 artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of
30 bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in:
International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent
Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be
5 sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

10 The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et
15 al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune
20 diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production
25 of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine
30 experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means
35 of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected
10 cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

 A polypeptide of the present invention may provide the necessary stimulation signal to T
15 cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain
20 protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as
25 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

 The activity of a protein of the invention may, among other means, be measured by the
30 following methods:

 Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;
35 Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1
10 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,
15 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
20 Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation*
25 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research*
30 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

5 A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

20 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margules, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates
15 and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al. *APMIS* 103:140-146, 1995; Muller et al. *Eur. J. Immunol.* 25:1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153:1762-1768, 1994.

20 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

5 Aminogluthethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate
10 (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., *J. Natl. Can. Inst.*, 52: 921-30
25 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., *Anticancer Res.*, 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., *Intl. J. Dev. Biol.*, 40: 1189-97 (1999) and Li et al., *Clin. Exp. Metastasis*, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,
30 *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the
35 invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
5 recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

 Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28,
15 Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

 By way of example, the polypeptides of the invention may be used as a receptor for a
20 ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the
25 present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent
30 molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

 This invention is particularly useful for screening chemical compounds by using the
35 novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

5 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
10 of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or
15 chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid
20 arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

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4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia,
30 acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- 10 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord
15 infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 20 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the
25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to
30 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
35 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit
5 any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*,
10 choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may
15 be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron
20 conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect
25 neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

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4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing
35 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified
5 nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*,
10 by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model
15 system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, *Science*, 219:56, or by B. Waksman et al., 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant
20 mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and
25 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

35

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

5 The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, 10 lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or 15 complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that 20 therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the 25 relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or 30 simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in 35 combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue

5 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution

10 and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

15 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of

20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include

25 compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in

30 the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell
5 cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred.
10 The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the
15 individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will
20 depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local
25 administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and
30 children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of any of the full length proteins of the invention, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention, *e.g.*, a hydrophilic

region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al, (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

5 Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the
10 recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct
15 bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion
20 preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable
25 host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the
30 CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for
35 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been
10 described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), *momordica charantia* inhibitor, curcin, crotin, *sapaonaria officinalis* inhibitor, gelonin,
15 mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP),
20 iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a
25 ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
30 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

35 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-5497 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-5497 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

5 In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see 10 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA 15 molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

20 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

 In general, methods for detecting a polynucleotide of the invention can comprise 25 contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed 30 polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

 In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a 35 polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

- 5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

- In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

- In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

15

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-5497, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see
5 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into
10 polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the
15 present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid
20 hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-5497. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-5497 can be used as an indicator of the presence of RNA of cell type of such a tissue
25 in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The
30 probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes
35 *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic
10 strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader
15 aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon
20 consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

25 5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The
30 inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid
5 Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from
10 a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-5497 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases
15 (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score
20 greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-5497) of the present invention are incorporated in the attached Sequence Listing. A subset of the predicted polypeptide sequences contain an unknown amino acid; a stop codon; a possible nucleotide deletion; or a possible nucleotide insertion. These sequences have also been
25 shown in their entirety in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-5497. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson,
30 Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers

to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

5 The nearest neighbor results for SEQ ID NO: 1-5497 were obtained by a BLASTX version 2.0al 19MP-WashU search against Genpept release 122 and Geneseq release 200105 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-5497. The nearest neighbor results for SEQ ID NO: 1-5497 are incorporated in the attached Sequence Listing.

10 Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

15 Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by pFam analysis for each polypeptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain
20 within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-5497. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID
25 NO: in USSN 09/770,160.

Table 1

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	81-82 126 136 154-156 175-177 213-215 278-283 346-349 445-446 459 491-492 543 561-562 652-653 709-711 755-757 794-795 822-823 899 924 971-988 995 997-998 1017- 1021 1026-1027 1036-1037 1048 1085 1128 1143 1154 1173 1202-1204 1269-1270 1290- 1291 1300-1301 1320-1321 1353-1355 1357- 1359 1363-1371 1388 1394-1396 1410 1415- 1417 1422-1424 1426 1455-1456 1465-1470 1508-1510 1533-1535 1541-1546 1550 1580- 1581 1585 1588-1589 1592 1603-1608 1648 1655 1663 1674-1682 1685 1709 1719-1721 1723 1727-1734 1746 1753 1755-1756 1773- 1774 1805-1806 1827-1829 1839-1847 1876- 1877 1915-1918 1951 2005 2021-2024 2027- 2034 2042-2043 2054 2057 2072-2074 2092 2096-2097 2118 2144-2145 2177 2188-2190 2193-2195 2208-2210 2214-2215 2251-2252 2281-2283 2288-2291 2294-2299 2331 2344 2382 2417-2420 2422 2430 2437 2439-2441 2446 2456 2483 2496 2499 2510-2513 2552 2656 2686 2741-2743 2746-2747 2774-2778 2783 2786 2842-2843 2857-2860 2865 2873- 2874 2879-2881 2883-2884 2960-2962 2976- 2977 3009 3136-3137 3139-3148 3167-3168 3170-3171 3174 3198 3207 3213-3214 3220- 3222 3230 3240 3257-3259 3276-3277 3280- 3282 3289-3290 3304-3307 3323-3324 3345- 3346 3394-3395 3456 3477-3478 3536-3543 3558-3562 3587 3689 3694-3696 3729-3730 3737-3738 3772 3822-3825 3831-3833 3864- 3865 3891 3963-3965 4001 4055-4056 4060- 4061 4093 4098 4112-4113 4123 4125 4136- 4141 4230-4231 4273-4274 4291-4295 4520 4546-4548 4569-4571 4575-4576 4691-4692 4740-4741 4796-4797 4804-4805 4864-4865 4900 4907-4909 5148-5149 5276-5277 5295- 5296 5298-5302 5464-5466
adult brain	GIBCO	ABD003	1-11 52 64 81-82 123 154-156 175-177 233 248 258-260 278-283 313-315 335 339 354 357-361 365 379-380 388-390 394 459 491- 492 557 561-562 574-577 582 597-598 607 652-653 670-671 677-678 682-684 719-722 743-744 794-795 799-800 814-816 818 822- 823 840-844 863-869 873-875 878 882-886 889-897 909-914 916-920 924 927 930-936 944-960 964-966 969 971-988 993-995 997- 999 1008-1009 1017-1021 1023-1027 1036-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult brain	Clontech	ABR001	3-11 70 137 175-177 478 491-492 597-598 755-757 796 852-854 910-914 964-966 1026-1027 1049 1158-1159 1173 1198-1201 1271 1274 1281-1282 1297 1351 1363-1371 1389 1479 1671-1673 1685 1719-1721 1784-1790 1870-1875 1900-1902 1919-1922 1926-1927 2035 2072-2074 2224-2228 2298-2299 2305-2306 2404 2419-2420 2436 2528-2531 2644 2713-2714 2751 2762 2774-2776 2786 2978 3113 3151-3152 3181-3183 3213-3214 3424-3427 3554-3556 3577-3582 3587 3595-3596 3638-3640 3663 3742-3744 3853 3911-3919 3931 3941-3942 3962 4036-4039 4077-4079 4125 4220-4223 4320 4545 4549 4570-4571 4672-4674 4738-4739 4764-4766 4781 4815 4910 5001-5003 5435-5437 5464-5466
adult brain	Clontech	ABR006	47 126 130 154-156 278-283 395 561-562 583-590 661-662 709-711 855-856 889-897 903-905 909 945 961-962 1063-1067 1069 1088 1095 1154-1155 1235-1236 1281-1282 1349-1350 1360-1362 1394 1418-1420 1580-1584 1626 1634-1637 1671-1673 1688-1689 1694-1698 1715-1716 1728-1734 1763-1764 1770-1771 1773-1774 1839-1844 1903-1911 1913-1914 2027-2030 2035 2054-2056 2076-2077 2121-2124 2145 2163-2168 2188 2197-2199 2214-2215 2445 2591-2592 2598 2650 2686 2737-2738 2745 2774-2778 2857-2860 3323-3324 3328-3330 3342-3344 3354 3396-3398 3498-3501 3536-3543 3658-3660 3856-3857 4300-4308 4379-4380 4410-4412 4451-4452 4481-4489 4549 4624-4626 4660 4824-4826 4832-4834 4967-4970 5050-5052 5278-5279
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult brain	Clontech	ABR011	154-156 388-390 1076 1128 1182-1184 1193 1202-1204 1422-1424 2072-2074 2144 2251- 2252 2549-2550 4062-4064 5298-5302
adult brain	BioChain	ABR012	440-441 602-603 889-897 997-998 1582- 1584 1719-1721 1780-1783 2072-2074 2186- 2187 2223 2377-2379 3394-3395 4291-4295 4581-4582 5123-5124
adult brain	Invitrogen	ABR013	341-344 491-492 1205-1207 1580-1581 1599-1602 1857-1859 1925 2072-2074 2186- 2187 2208-2210 2377-2379 2469 3250-3252 3304-3307 4267-4270 4796-4797
adult brain	Invitrogen	ABT004	12-13 38 52 70 92-95 126 175-177 255-257 291 341-344 346-349 354 478 557 583-590 612-620 675 789-793 796 840-844 871-872 879-884 909 919-920 964-966 997-998 1017- 1021 1026-1027 1042-1043 1051 1070-1071 1076 1088 1108 1151-1153 1160-1164 1193 1217-1218 1228-1229 1269-1270 1281-1282 1320-1321 1349-1350 1385 1427-1431 1467- 1469 1485 1532 1575-1576 1626 1629-1632 1640-1645 1708 1715-1716 1727 1742-1746 1773-1774 1799-1804 1807-1813 1852 1860 1865-1875 1900-1911 1948-1949 1954-1962 1964-1965 1981-1983 1990-1991 2010-2013 2036-2037 2054 2072-2074 2078-2082 2086- 2087 2143-2147 2174-2176 2186-2187 2224- 2228 2231-2232 2255-2257 2264 2284 2310- 2312 2369-2375 2397-2399 2419-2420 2436 2526-2527 2592 2604 2624 2626 2629-2631 2696-2697 2734 2751 2785 2813 2857-2860

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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cultured preadipocytes	Stratagene	ADP001	74-77 134 154-156 175-177 201-205 213-215 278-283 313-315 489-492 520-521 652-653 670-671 680-684 736-740 743-744 784-786 796 814-816 822-823 857-859 885-886 944 950 964-966 994 1028 1042-1043 1052 1069- 1071 1089-1091 1129-1130 1143 1154 1156 1172 1198-1204 1249-1255 1278-1280 1317- 1318 1320-1321 1351 1359 1380 1410 1455- 1456 1473 1507 1532-1535 1547-1548 1553- 1556 1559-1560 1588-1589 1611 1617-1619 1640-1645 1648 1663 1666 1723-1724 1727 1746 1755-1756 1765-1769 1773-1774 1780- 1783 1839-1844 1870-1877 1925 1990-1991 2060-2061 2118 2193-2195 2197-2199 2223 2234-2242 2298-2299 2310 2331 2380-2381 2443 2452-2454 2524-2525 2572-2573 2591- 2592 2594-2595 2604 2672-2674 2709-2711 2734 2739 2819 2843-2847 2861-2862 2899- 2900 2913 2925-2929 2979 2985 3013-3014 3159-3162 3181-3183 3189-3191 3220-3222 3253-3255 3285 3310-3311 3462 3486-3487 3587 3638-3640 3673-3677 3754 3804-3806 3815-3816 3871-3872 3969-3971 4014-4015 4036-4039 4068-4069 4140-4141 4241-4242 4254 4341 4534 4554-4555 4570-4571 4581- 4582 4622-4623 4740-4741 4864-4865 4910 5001-5003 5038-5039 5095-5097 5137-5140
adrenal gland	Clontech	ADR002	1-2 12-13 35 52 62 100-106 121-122 140-142 153-156 191-192 213-215 221 232 301-303 306 313-315 341-344 366-367 394 459 491- 492 513 551-553 583-590 592-595 652-653 670-671 719-722 728-733 743-744 747-750 755-757 772 784-786 814-816 847 849-851 889-897 909-914 916-920 944 946-949 961- 962 993-995 997-999 1049 1070-1071 1078 1089-1091 1117-1119 1128 1151-1153 1160- 1164 1175 1182-1184 1193 1220-1221 1269- 1270 1272-1273 1287 1307 1352 1355 1357- 1359 1407 1415-1417 1422-1423 1480 1485 1498-1499 1505 1507-1510 1526 1541-1546

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult. heart	GIBCO	AHR001	45-46 52 56 100-106 133-134 140-142 154- 156 173 175-177 192 195-196 201-205 212- 218 227-230 235 278-283 286-287 301-303 313-315 323 332-333 341-344 346-352 366- 367 379-380 395 400-404 413-414 436 469 478 491-492 511 520-521 531-532 551-553 557 574-577 583-590 599-601 604 607 612- 620 652-653 675 677-678 680-685 697 707 743-744 784-786 789-796 799-800 814-816 822-823 847 885-886 889-897 915-920 924- 929 931-936 944-945 950 957-960 964-966 969 971-979 992 994-1002 1017-1027 1044- 1050 1052-1054 1056-1057 1063-1067 1070- 1071 1075 1110-1113 1117-1119 1127-1136 1139-1143 1154 1156 1159 1172-1173 1182- 1185 1192-1193 1202-1207 1220-1221 1228

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult kidney	GIBCO	AKD001	32-34 36-37 39-40 42 45-47 74-78 87 100- 106 116-119 136 165 175-177 213-218 220 223-231 235 244 252-253 258-260 278-283 298-300 313-320 324-325 332-333 341-344 346-349 364 366-367 379-380 394 396-398 419 436 440-441 445-446 452 474 491-492 498 519 548-553 557 574-577 583-590 602- 603 607 629-630 652-653 677-678 682-684 707 709-711 719-722 728-733 736-740 778- 786 789-793 799-800 806-808 814-816 822- 823 836-838 840-844 852-854 857-859 871- 875 879-886 889-897 899-905 909-915 919- 920 924-926 931-936 944-962 964-966 969- 974 980-988 994-995 997-998 1000-1009 1017-1021 1026-1027 1036-1040 1042-1043 1049-1050 1052 1063-1071 1075-1076 1078- 1079 1081-1082 1085 1088-1091 1110-1113 1116-1121 1127-1130 1137-1142 1151-1155 1159 1172-1173 1182-1184 1189-1193 1198- 1207 1217-1218 1220-1221 1230-1232 1235- 1236 1249-1260 1269-1271 1278-1280 1287 1294-1297 1300-1301 1307 1315-1321 1328 1334-1335 1349-1350 1352-1354 1357-1362 1374 1385-1389 1397-1399 1403-1407 1410 1414-1420 1422-1423 1425-1426 1435-1436 1438 1440-1441 1444 1451-1462 1465-1466 1470-1472 1475-1477 1479 1481-1485 1488- 1489 1498-1499 1504-1505 1507-1510 1515- 1517 1524 1527-1532 1536-1538 1540-1548 1551-1557 1561-1563 1569-1576 1579-1589 1591 1597 1603-1608 1611-1619 1625-1626 1634-1648 1653-1654 1656 1663-1665 1667- 1682 1685 1688-1692 1694-1698 1701-1704 1707-1708 1710-1716 1719-1721 1723-1724 1727-1739 1743-1746 1753 1755-1758 1763- 1771 1773-1783 1796-1798 1805-1806 1814- 1817 1830-1847 1857-1860 1865-1877 1882- 1885 1903-1911 1913-1922 1925-1927 1948- 1953 1964-1974 1978-1979 1981-1983 1993-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1998 2004-2005 2010-2013 2021-2038 2042- 2043 2045-2047 2055-2061 2068-2083 2086- 2087 2092 2094 2096-2100 2111-2114 2116 2118 2125-2133 2137-2142 2144 2146-2147 2151-2152 2156-2160 2173-2181 2186-2188 2191-2195 2197-2199 2202-2203 2208-2213 2216-2221 2223-2230 2234-2242 2244-2248 2251-2252 2254-2257 2261 2267-2270 2272- 2273 2280-2282 2284 2288-2291 2296-2297 2302 2310 2318-2320 2331 2333-2334 2338- 2340 2368 2377-2382 2386 2388-2392 2403 2405-2415 2422-2424 2427 2430 2440-2441 2446-2447 2451 2467-2472 2475 2483-2485 2488 2490-2491 2496 2499 2510-2513 2521- 2525 2528-2531 2536 2546 2554-2556 2564- 2572 2574-2575 2579-2584 2591-2592 2596 2604 2629-2637 2645-2649 2672-2676 2693 2696-2697 2702-2706 2709-2711 2716-2718 2721 2726 2730 2734 2747-2748 2754-2758 2760-2761 2763 2768-2772 2774-2778 2781 2785 2800-2801 2805-2806 2809 2814 2818 2828 2836-2839 2842-2843 2854-2863 2865 2873-2874 2888 2894-2898 2901-2903 2913 2925-2929 2931-2939 2945-2946 2960-2962 2969-2976 2979 3009 3013-3014 3017-3022 3026-3027 3054 3076-3078 3082 3098-3100 3102-3105 3109 3136-3137 3139-3147 3151- 3162 3167-3168 3170-3174 3189-3191 3195 3204 3215-3216 3218 3224-3230 3234 3240 3242 3256-3267 3276-3277 3280-3282 3285 3288-3290 3292-3293 3296-3299 3313 3323- 3324 3331-3335 3339-3340 3342-3344 3367- 3368 3374-3382 3394-3398 3403-3404 3406- 3407 3409-3410 3428-3429 3438-3441 3443- 3445 3456 3462 3466-3468 3470-3471 3519 3535-3543 3554-3556 3561-3562 3576-3580 3589 3605 3610-3613 3619-3625 3628 3632- 3634 3638-3640 3664-3665 3667 3670-3671 3673-3677 3684 3686-3691 3716 3724-3725 3742-3744 3747 3760-3761 3780-3781 3815- 3816 3822-3824 3826 3830 3837-3838 3870 3880 3882-3883 3895 3897-3905 3911-3919 3939-3951 3955-3957 3959-3960 3966-3971 3997-3998 4014-4015 4036-4039 4055-4056 4060-4064 4071-4075 4077-4079 4082-4084 4093 4098 4101-4102 4114-4116 4119-4123 4136 4138-4143 4220-4223 4230-4235 4243- 4244 4252-4253 4255-4257 4260 4267-4270 4285-4288 4322 4335-4337 4342 4363 4383- 4384 4391-4393 4400 4430-4432 4439 4451-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult kidney	Invitrogen	AKT002	1-2 70 278-283 313-315 379-380 457 491- 492 574-577 582 604 652-653 699-701 707 709-711 719-722 764-771 794-795 814-816 822-823 840-844 906-909 924 944 950 963 975-988 993 995 1017-1021 1042-1043 1063- 1067 1070-1071 1076 1079 1110-1113 1117- 1119 1128 1137-1143 1172 1182-1184 1193 1208-1212 1220-1221 1235-1242 1278-1280 1287 1297 1315-1318 1323-1328 1355 1357- 1358 1360-1371 1374 1397 1405-1406 1414 1418-1420 1425 1457-1462 1488 1507 1515 1536-1538 1547-1548 1551-1552 1559-1560 1579 1626 1656 1664 1674-1682 1685-1689 1691-1693 1706 1708 1710-1716 1719-1721 1728-1734 1737-1739 1753 1773-1774 1845- 1851 1870-1875 1897 1903-1911 1913-1914 1925 1948-1949 1951-1953 1978-1979 1981- 1983 1990-1991 2004-2005 2017-2020 2027- 2030 2038 2048 2054 2062-2064 2072-2074 2076-2077 2116 2118 2125-2133 2156-2160 2174-2176 2179-2181 2186-2188 2208-2210 2214-2215 2224-2228 2275 2277 2296-2297 2321 2377-2379 2391 2397-2399 2421 2428 2452-2454 2473-2474 2492-2494 2499 2528- 2531 2536 2560 2579-2584 2592 2594-2595 2608-2616 2706 2734 2781 2785 2818 2843- 2845 2854 2861-2862 2886-2887 2974-2975 2979 2984 2996-2998 3008 3100 3139-3147 3149 3151-3152 3156-3157 3184 3195 3218 3250-3252 3260-3267 3269 3313 3325-3327 3336-3338 3341-3344 3424-3427 3550-3552 3554-3556 3590 3624-3625 3628 3658-3660 3663 3693 3791 3822-3824 3943-3948 4004 4040-4042 4055-4056 4076 4093 4109-4111 4232-4235 4241-4242 4275-4277 4534 4549 4622-4623 4633-4634 4740-4741 4764-4766

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult lung	GIBCO	ALG001	78 136 138-139 175-177 313-315 324-325 341-344 413-414 440-441 456 491-492 511 557 652-653 677-678 728-733 784-786 794- 795 822-823 849-851 855-856 885-886 919- 920 954-960 975-988 992-993 997-999 1003- 1006 1017-1021 1026-1027 1042-1043 1053- 1054 1075 1088 1129-1130 1143 1182-1184 1189-1191 1198-1201 1208-1212 1271 1297 1300-1301 1317-1318 1352-1355 1374 1407 1422-1423 1455-1462 1481-1484 1488-1489 1497 1507-1512 1516-1517 1532-1535 1541- 1548 1551-1556 1582-1584 1588-1589 1591 1603-1604 1611 1617-1619 1663 1723 1727- 1734 1742-1746 1753 1780-1783 1814-1817 1831-1834 1852 1870-1875 1919-1922 1925 1951 2005-2007 2038 2058-2061 2072-2074 2086-2087 2116 2118 2121-2136 2144 2153- 2155 2163-2168 2179-2181 2186-2187 2214- 2215 2223-2228 2230 2234-2242 2277 2283 2296-2299 2331 2380-2382 2389-2390 2467- 2469 2473-2474 2499 2536 2553 2564-2571 2574-2575 2604 2672-2674 2677-2680 2749- 2750 2759 2761 2774-2776 2843 2855-2856 2913 2957 2960 2969-2973 3081 3084-3085 3098-3099 3156-3157 3167-3168 3213-3214 3220-3222 3226-3228 3238 3256 3280-3282 3289-3290 3319-3322 3333-3335 3409-3410 3442 3466-3468 3558-3560 3588 3621-3625 3628 3689 3776-3777 3815-3816 3893 3908 4040-4042 4068-4069 4114-4116 4136 4232- 4235 4291-4295 4335-4337 4404-4407 4439 4545 4672-4674 4756-4757 4796-4797 4804- 4805 4886 4907-4909 5001-5003 5046-5047 5095-5097 5142-5143 5387-5388 5464-5466
lymph node	Clontech	ALN001	39-40 143-148 154-156 269 278-283 313-315 445-446 728-733 736-742 764-771 814-816 822-823 931-936 950 961-962 994 1000-1002 1017-1021 1129-1130 1139-1142 1151-1153 1182-1184 1198-1204 1244-1246 1256 1319 1359 1398-1399 1425 1438 1455-1462 1478 1504 1507 1511-1512 1532 1539 1547-1549 1553-1556 1575-1576 1617-1619 1648 1659- 1660 1663 1719-1721 1735-1736 1753 1755- 1756 1839-1844 1857-1859 1919-1922 1925 1951 1993-1998 2004 2038 2042-2043 2048

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2060-2061 2086-2087 2107 2111-2114 2118 2125-2130 2137 2144-2145 2191-2195 2208- 2210 2214-2215 2223 2254 2277 2288-2291 2296-2297 2394 2470-2472 2483 2526-2527 2554-2556 2649 2774-2776 2852-2854 2861- 2862 2865 2888 2896-2897 2965-2968 3029 3133-3135 3189-3191 3242 3250-3252 3280- 3282 3289-3290 3312 3333-3335 3411-3417 3577-3580 3638-3640 3716 3817-3821 3878- 3879 3962 4023 4090-4092 4134 4140-4141 4219 4285-4286 4581-4582 4796-4797 4864- 4865 4907-4909 5001-5003 5261-5267 5272- 5274 5323-5325 5332-5333 5335-5343 5423- 5425 5444
young liver	GIBCO	ALV001	48-50 78 100-110 210-211 255-257 261-266 278-283 286-287 313-320 332-333 381-383 395 419 435-436 491-492 548-553 574-577 652-653 677-678 709-711 755-757 784-786 789-793 799-803 806-808 822-823 840-844 852-854 910-914 916-918 924 944 969 995 997-998 1056-1057 1063-1068 1085 1089- 1091 1116 1120-1121 1128-1130 1139-1142 1151-1155 1172 1177-1179 1182-1184 1189- 1191 1198-1201 1205-1207 1217-1218 1220- 1221 1230-1232 1249-1256 1269-1273 1290- 1291 1300-1301 1310-1314 1323-1328 1357- 1358 1360-1362 1374 1410 1418-1420 1479- 1484 1497 1507 1516-1517 1527-1531 1541- 1546 1551-1552 1557 1579-1581 1585 1590 1592 1613-1619 1626 1656 1664 1685 1691- 1692 1694-1698 1701-1702 1708-1709 1723 1725-1726 1735-1739 1753 1759-1762 1765- 1771 1773-1774 1780-1790 1796-1798 1827- 1829 1835-1838 1848-1852 1865-1875 1882- 1885 1903-1911 1913-1914 1919-1922 1925 1951 1964-1965 1978-1979 2005 2031-2034 2060-2061 2075 2086-2091 2096-2097 2118 2144 2153-2160 2174-2176 2188 2200-2201 2223-2228 2234-2242 2244-2245 2281-2282 2288-2291 2321 2358 2380-2382 2414-2415 2423-2424 2427 2447 2451 2469 2477-2479 2484-2485 2503-2504 2510 2533 2543-2544 2560 2564-2571 2579-2584 2587 2648 2761 2836-2839 2843 2865 2873-2874 2879-2881 2945-2946 2951-2952 2957 2974-2975 3013- 3014 3076-3078 3139-3147 3151-3152 3156- 3157 3181-3183 3195 3226-3228 3242 3250- 3252 3280-3282 3299 3310-3311 3328-3330 3345-3346 3403-3404 3456 3462 3561-3562 3599-3601 3619-3625 3628 3654-3657 3815-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult liver	Invitrogen	ALV002	35-37 62 70 107-110 131-132 175-177 192 233 255-257 261-266 278-283 313-315 337 354 365 374-375 445-446 450-451 478 491-492 652-653 801-803 840-844 848 852-854 903-905 944 954-956 995 997-998 1003-1006 1026-1027 1032-1034 1042-1047 1049 1056-1060 1063-1071 1078 1089-1091 1117-1119 1139-1143 1151-1154 1158-1159 1177-1181 1188-1191 1193 1205-1207 1217-1218 1230-1232 1278-1282 1307 1310-1314 1323-1327 1337-1345 1351 1360-1371 1380 1451-1454 1485 1533-1535 1547-1548 1569-1574 1592 1626 1640-1647 1656 1663 1691-1692 1708-1709 1723 1725-1726 1735-1739 1759-1762 1770-1771 1773-1774 1827-1829 1835-1844 1913-1914 1919-1922 1925 1948-1949 1954-1962 1981-1983 2010-2013 2025-2026 2054 2060-2061 2118 2171 2174-2176 2186-2190 2193-2195 2208-2210 2223 2254 2267-2270 2276-2277 2296-2297 2308 2322 2338-2340 2380-2381 2499 2533 2536 2543-2544 2560 2579-2584 2629-2631 2648 2659-2662 2665 2741-2743 2800-2801 2828 2843 2865 2879-2882 2905 2914-2917 2925-2929 2957 2960-2962 2974-2975 3013-3014 3054 3089 3156-3157 3181-3183 3199 3220-3222 3229 3310-3311 3328-3330 3371-3373 3462 3466-3469 3472-3473 3536-3543 3577-3580 3667 3749-3752 3793 3997-3998 4014-4015 4036-4039 4082-4084 4096-4097 4282 4330-4331 4376-4377 4381 4451-4452 4616-4621 4633-4634 4636-4637 4649 4687-4689 4738-4739 4754-4755 4768-4771 4796-4797 5050-5052 5057-5065 5082-5083 5130-5131 5145 5148-5149 5164-5167 5229-5231 5335-5343 5367-5368 5387-5391 5414-5415 5451-5453
adult liver	Clontech	ALV003	341-344 370-371 849-851 946-949 1177-1179 1202-1204 1626 1759-1762 1770-1771 1913-1914 2484-2485 3328-3330 4403 4998-4999 5130-5131
adult ovary	Invitrogen	AOV001	12-13 32-34 39-40 42 44 47-50 52 63-64 70 74-78 87 100-110 116-119 133 135-139 153

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			173 175-177 185 201-205 212-215 220 222 227-230 233 245 267-268 277-283 286-287 291 301-303 313-315 321 341-344 357-361 364 372 376-377 379-380 394 396-398 436 445-446 459 462 474 478 491-495 509 511 520-524 538 543 545 551-553 561-562 574- 577 583-594 604-607 611-620 629-630 641 652-653 677-678 682-684 697 699-703 707- 711 719-722 728-733 743-744 747-750 755- 757 764-771 784-786 789-795 801-803 806- 808 814-816 822-825 836-837 840-844 855- 856 863-869 871-875 879-886 889-897 899- 908 910-914 916-920 924 927 930-936 944 950-962 964-966 969 971-988 990-995 997- 1006 1008-1009 1017-1027 1032-1040 1042- 1047 1049 1052-1054 1068 1070-1071 1075- 1076 1078-1079 1081-1082 1089-1091 1095 1108 1117-1121 1128-1142 1151-1156 1158- 1164 1171-1173 1175 1180-1185 1189-1193 1198-1207 1217-1218 1220-1221 1228-1232 1235-1242 1244-1246 1249-1256 1269-1271 1278-1280 1287 1290-1293 1297-1301 1307 1315-1328 1332-1335 1348-1359 1363-1371 1374 1380 1383-1384 1386-1389 1395-1396 1398-1399 1403-1410 1413-1417 1421-1423 1426 1432 1435-1436 1438-1444 1446-1449 1451-1464 1467-1473 1475-1480 1485 1488 1491-1494 1498-1499 1504-1505 1507-1512 1515-1517 1520 1527-1538 1541-1548 1550- 1557 1569-1576 1580-1589 1591 1603-1608 1611-1612 1617-1619 1621-1623 1625 1629- 1632 1638-1645 1648-1654 1656-1658 1663- 1664 1666-1670 1674-1682 1685-1686 1688- 1692 1694-1698 1701-1702 1707-1709 1717 1719-1721 1723 1727-1739 1743-1746 1753 1755-1756 1758 1763-1769 1780-1783 1792- 1817 1827-1830 1835-1838 1848-1853 1860 1865-1877 1879-1885 1900-1911 1915-1922 1925-1936 1948-1953 1964-1965 1978-1979 1981-1983 1990-1991 1993-1998 2000-2002 2004-2005 2017-2024 2027-2037 2042-2043 2045-2048 2052-2061 2066-2067 2076-2077 2080-2082 2086-2091 2093-2094 2096-2100 2111-2115 2118 2125-2133 2138-2147 2151- 2160 2174-2177 2179-2181 2186-2187 2189- 2195 2197-2201 2204-2215 2223 2229 2231- 2232 2234-2242 2251-2252 2254-2262 2264- 2265 2267-2271 2273 2275 2277 2281-2284 2286-2291 2296-2300 2321 2331 2380-2381 2386-2392 2395 2397-2399 2403 2414-2415

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			4674 4681-4683 4691-4692 4740-4741 4748-4749 4751-4753 4764-4766 4777-4780 4784-4786 4796-4797 4804-4805 4812 4820 4854 4861-4865 4874-4875 4886 4902 4907-4910 4912 4918-4920 4923-4925 4953 4956-4957 4976-4979 5001-5003 5025 5040 5050-5052 5057-5065 5085-5088 5095-5097 5109 5115 5123-5127 5148-5149 5154-5157 5173 5222-5224 5241-5242 5251 5259 5261-5267 5276-5277 5281 5284-5289 5308-5309 5329-5330 5335-5343 5367-5368 5387-5391 5399-5401 5408-5410 5421-5425 5427-5429 5431-5433 5439 5455 5464-5466 5485 5490-5491
adult placenta	Clontech	APL001	313-315 491-492 605-606 719-722 736-740 834-835 950 971-979 1017-1022 1151-1153 1182-1184 1215-1216 1410 1418-1420 1532 1539-1540 1564-1566 1639 1719-1721 1747-1751 1870-1875 1925 1966-1974 1984 2101-2102 2230 2424 2510 2524-2525 2574-2575 2645-2647 2668 2818 2873-2874 3323-3324 3462 3483 4040-4042 4101-4102 4581-4582 4793-4795 5188-5189 5376
placenta	Invitrogen	APL002	12-13 192 364 491-492 520-521 709-711 755-757 789-793 840-844 885-886 975-979 1026-1027 1042-1043 1050 1070-1071 1076 1117-1119 1160-1164 1202-1207 1215-1216 1272-1273 1320-1321 1351 1360-1362 1380 1400-1401 1442-1443 1473 1553-1556 1564-1566 1603-1608 1621-1623 1694-1698 1724 1737-1739 1743-1745 1747-1751 1780-1783 1860 1948-1949 2062-2064 2072-2074 2101-2102 2111-2114 2146-2147 2186-2187 2204-2207 2310 2434-2435 2470-2472 2488 2511-2513 2594-2595 2645-2647 2677-2680 2696-2697 2737-2738 2831-2832 2836-2839 2899-2900 2925-2929 2954 3065-3067 3195 3199 3220-3222 3288 3313 3336-3338 3391 3403-3404 3466-3468 3536-3543 3624-3625 3638-3640 3932-3933 4082-4084 4273-4274 4291-4295 4410-4412 4701-4709 4740-4741 5431-5433 5435-5437
adult spleen	GIBCO	ASP001	78 137 154-156 175-177 213-215 274 278-283 313-315 324-325 332-333 341-344 346-349 420 456 479-480 491-492 511 530 557 612-620 652-653 659-660 677-678 699-701 728-733 741-744 764-771 784-786 814-816 822-823 849-851 924 944 950 964-966 975-988 994-995 997-998 1000-1002 1008-1009 1049 1052 1070-1071 1078 1088-1091 1128-1136 1151-1153 1171-1172 1193 1195-1196

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1202-1204 1217-1218 1220-1221 1256 1269- 1271 1287 1294-1297 1315-1318 1332-1333 1349-1350 1352-1354 1359 1363-1371 1374 1383-1384 1386-1387 1397 1408-1409 1414 1418-1420 1422-1423 1425 1440-1441 1446- 1449 1486 1497 1507-1512 1514 1516-1517 1527-1532 1540-1548 1551-1552 1575-1576 1586-1589 1597 1603-1604 1612 1617-1619 1621-1623 1629-1632 1634-1637 1640-1645 1654 1656 1663 1686 1691-1692 1708 1710- 1714 1719-1721 1723-1724 1727 1737-1739 1746 1753 1765-1769 1773-1774 1780-1783 1796-1798 1807-1817 1827-1834 1853 1857- 1859 1870-1885 1903-1911 1913-1914 1919- 1922 1948-1949 1951 1964-1965 1978-1979 2025-2026 2035 2038 2040-2043 2045-2047 2054 2060-2061 2072-2074 2076-2079 2086- 2087 2111-2114 2116 2118 2131-2133 2137 2144 2148-2150 2153-2155 2178 2182-2183 2214-2215 2223 2230 2234-2242 2281-2283 2298-2299 2303-2304 2310 2331 2380-2382 2405-2413 2421 2440-2441 2452-2454 2456 2461 2469-2472 2488 2510-2513 2551 2560 2573 2603-2604 2608-2616 2650 2696-2697 2719-2720 2726 2747 2754-2758 2803 2818 2831-2832 2843-2845 2854 2861-2862 2873- 2874 2914-2917 2945-2946 2974-2976 3153 3158 3167-3168 3170-3171 3195 3210-3211 3215-3216 3226-3228 3250-3252 3258-3259 3280-3282 3289-3290 3336-3338 3385 3403- 3404 3428-3429 3466-3468 3536-3543 3561- 3562 3591-3593 3621-3625 3629-3630 3632- 3634 3716 3784-3786 3792 3815-3816 3878- 3879 3886 3935 3966-3971 4014-4015 4023 4036-4039 4060-4061 4077-4079 4090-4092 4098 4100 4126 4142-4143 4228 4232-4235 4239-4240 4335-4337 4374-4375 4400 4404- 4407 4451-4452 4554-4555 4598-4601 4622- 4623 4662 4668-4671 4740-4741 4796-4797 4832-4834 4864-4865 4907-4909 4912 4956- 4957 5001-5003 5034-5036 5074 5095-5097 5123-5124 5148-5149 5154-5157 5241-5242 5261-5267 5272-5274 5298-5302 5310-5311 5329-5330 5335-5343 5427-5429 5440-5441 5485
testis	GIBCO	ATS001	47 81-82 123 136 154-156 175-177 179 227- 230 278-283 313-315 341-344 366-367 379- 380 456 491-492 574-577 604 652-653 677- 678 682-684 699-701 743-744 764-771 784- 786 811-816 822-823 826-828 879-881 885-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	3895
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	2639-2642

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult bladder	Invitrogen	BLD001	154-156 175-177 301-303 341-344 652-653 659-660 950 980-988 997-998 1042-1043 1069 1075 1139-1142 1160-1164 1193 1244- 1246 1307 1508-1510 1575-1576 1717 1728- 1734 1746 1805-1806 1870-1875 1882-1885 1903-1911 1981-1983 2004 2006-2007 2038 2060-2061 2072-2074 2118 2191-2192 2273 2283 2294-2295 2344 2639-2642 2721 2747 2818-2819 2914-2917 3112 3212 3280-3282 3424-3427 3470-3471 3536-3543 3664-3665 3691 3760 3791 3795-3800 4014-4015 4082- 4084 4335-4337 4613 4796-4797 4864-4865 4960 5001-5003 5241-5242 5387-5388 5431- 5433
bone marrow	Clontech	BMD001	30-31 42 48-50 74-78 114-115 120-123 137 143-165 175-177 213-215 227-230 232 235 278-290 297-303 305-309 313-315 324-325 335 341-344 354 379-380 394-398 435-438 440-441 447-455 462-471 491-492 513 516 520-521 538 551-553 557 561-562 641 652- 653 661-671 674 677-678 680-684 699-701 709-760 763-772 794-795 822-823 849-851 857-859 863-869 882-886 889-897 909-914 916-918 921 924-926 931-936 944-945 950- 956 969 980-988 992-995 997-1021 1026- 1027 1032-1034 1038-1040 1049 1053-1055 1070-1071 1075 1079 1108 1110-1113 1128- 1136 1139-1143 1151-1154 1173 1182-1184 1186-1187 1193 1198-1204 1217-1218 1220- 1221 1228 1230-1232 1249-1256 1264 1269- 1271 1274 1281-1282 1290-1291 1294-1297 1317-1319 1322-1345 1348-1362 1374-1379 1386-1387 1397-1399 1405-1407 1414-1417 1422-1423 1425 1437-1438 1440-1441 1444 1451-1464 1470 1479 1485-1489 1497-1500 1504-1505 1507-1512 1514-1515 1518-1520 1522-1526 1532-1563 1567-1576 1582-1585 1588-1589 1603-1608 1612 1621-1623 1625 1629-1632 1634-1637 1646-1648 1655-1656 1659-1660 1663-1664 1666-1670 1685-1690 1694-1698 1701-1702 1707-1708 1710-1716 1719-1721 1723-1724 1728-1739 1746 1752- 1753 1755-1756 1765-1771 1773-1779 1805- 1813 1830-1838 1853 1857-1860 1870-1875 1879-1881 1894-1896 1913-1922 1925-1936 1948-1951 1963 1966-1974 1978-1979 1993- 1998 2000-2003 2005 2017-2020 2027-2030 2036-2056 2060-2064 2066-2067 2080-2082 2086-2087 2095 2098-2102 2107-2108 2111- 2118 2121-2150 2153-2168 2172 2174-2177

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2191-2195 2202-2203 2214-2221 2223 2229 2231-2242 2246-2248 2254 2262 2264 2273 2283 2288-2291 2294-2299 2302 2311-2312 2327-2330 2358 2377-2379 2387-2403 2418 2422-2424 2427 2440-2441 2443 2448-2465 2467-2469 2473-2474 2480 2488 2495 2510- 2513 2519-2520 2528-2531 2560 2572 2592 2598 2604 2628 2644-2648 2650 2656 2677- 2680 2686 2698-2699 2715 2719-2720 2722- 2744 2749-2750 2754-2758 2760-2761 2768- 2771 2774-2776 2781 2783 2785 2793-2820 2824-2826 2829 2843 2846-2847 2863-2867 2873-2874 2888 2891 2894-2895 2904-2905 2931-2939 2945-2946 2965-2973 2976 3008 3011-3012 3017-3022 3029 3041-3049 3054 3100 3102-3105 3150 3166-3175 3181-3186 3188-3194 3204 3208-3209 3212 3220-3222 3226-3230 3235-3243 3245-3252 3256-3273 3276-3277 3280-3283 3285 3289-3290 3299 3304-3307 3319-3322 3341-3346 3372-3373 3402 3406-3407 3422 3424-3427 3438-3441 3446-3449 3456 3466-3468 3470-3471 3486- 3487 3491-3495 3505-3506 3508-3513 3536- 3543 3550-3552 3557-3562 3566-3573 3576 3598-3607 3609-3614 3616-3628 3663-3665 3673-3677 3682 3707 3724-3725 3729-3730 3742-3744 3754 3761 3792 3794-3809 3817- 3821 3826 3828 3836-3861 3867-3869 3878- 3879 3881-3884 3897-3905 3911-3919 3955- 3957 3969-3971 4023 4028-4029 4052 4055- 4056 4082-4084 4094-4095 4101-4107 4109- 4120 4136 4142-4153 4156-4159 4167-4178 4208-4211 4215-4223 4227-4247 4267-4270 4275-4277 4285-4286 4291-4296 4383-4384 4430-4432 4494-4496 4501-4503 4517-4529 4531-4536 4554-4555 4572-4591 4596-4601 4624-4626 4649 4651 4662 4664-4665 4691- 4692 4729 4738-4741 4761-4780 4793-4810 4832-4834 4862-4865 4884 4907-4910 4923- 4928 4930-4931 4933-4935 4937-4943 4945 4961-4985 5001-5003 5038-5039 5050-5052 5080 5114-5115 5137-5141 5148-5149 5153- 5157 5180 5190-5192 5241-5242 5250 5252 5254-5277 5303-5305 5307-5325 5327-5343 5345-5354 5367-5374 5376-5379 5381-5385 5387-5388 5397-5398 5444 5460-5461 5464- 5466 5485
bone marrow	Clontech	BMD002	175-177 249-250 254 258-260 301-303 313- 315 324-325 413-414 440-441 491-492 540 574-577 580-581 592-594 599-601 612-620

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			652-653 724-733 741-750 804-805 814-816 846 849-851 889-897 903-905 910-914 957- 960 970 992 994 997-998 1010-1014 1023- 1027 1038-1040 1089-1091 1095 1110-1113 1128 1202-1207 1217-1218 1235-1236 1256 1271 1297 1319 1330-1333 1348-1350 1352- 1354 1357-1358 1383-1384 1397 1457-1462 1479 1491-1494 1497 1504 1507-1512 1532 1547-1548 1551-1552 1575-1576 1621-1623 1646-1647 1686 1719-1721 1727 1743-1745 1753-1754 1763-1764 1773-1779 1796-1798 1805-1806 1814-1817 1827-1830 1839-1844 1848-1851 1913-1918 1925 1993-1998 2040- 2043 2048 2052-2054 2060-2061 2078-2079 2088-2091 2116-2118 2131-2142 2148-2150 2172 2174-2176 2191-2195 2223 2246-2248 2318-2320 2537-2538 2553 2604 2638 2702- 2705 2709-2711 2713-2714 2739 2781 2796- 2798 2803 2931-2939 2961-2962 3026-3027 3055 3130 3159-3162 3181-3183 3246 3250- 3252 3304-3307 3402 3536-3543 3793 3847- 3849 3925-3926 4024-4025 4060-4061 4209- 4210 4228 4252-4253 4267-4270 4574 4581- 4582 4729 4787 4796-4797 4858 4907-4909 4974 4991-4993 5021-5023 5050-5052 5056 5148-5149 5260-5267 5272-5275 5278-5279 5335-5343 5377-5378 5416 5423-5425 5485
bone marrow	Clontech	BMD004	728-733 849-851 1349-1350 1486 1860 2050- 2051 2134-2136 2148-2150 2234-2242 2803 4209-4210 4598-4601 4652-4653 4907-4909 5261-5267 5272-5274
bone marrow	Clontech	BMD007	396-398 440-441 453-455 491-492 712-718 764-771 814-816 846 849-851 1096-1104 1146-1147 1315-1316 1486 1497 1522-1523 2134-2136 2148-2150 2223 2803 3250-3252 4598-4601 5001-5003 5050-5052 5310-5311
adult colon	Invitrogen	CLN001	1-2 32-34 64 175-177 251 278-283 452 478 814-816 832 870 889-897 944 957-960 1044- 1047 1069 1117-1119 1128 1139-1142 1195- 1196 1217-1218 1317-1318 1386-1387 1511- 1512 1547-1548 1640-1645 1709 1770-1771 1860 1870-1875 1882-1885 1948-1949 1952- 1953 1981-1983 2088-2091 2146-2147 2156- 2160 2174-2176 2208-2210 2254 2347-2348 2511-2513 2604 2629-2631 2737-2738 2831- 2832 2852-2853 2865 3035-3036 3156-3157 3220-3222 3246 3339-3340 3554-3556 3632- 3634 3663 3673-3677 3693 3780-3781 3870 3949-3951 4272 4275-4277 4330-4331 4534 4636-4637 4651 4668-4674 4776 4796-4797

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL016	210-211 910-914 995 1128 1479 1617-1619 1626 1784-1790 1913-1914 2901-2903 2979 3831-3833 4796-4797 5001-5003 5075-5077 5154-5157 5414-5415
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL021	175-177 237-240 652-653 801-803 849-851 950 993 1042-1043 1063-1067 1156 1310-1314 1332-1333 1485 1511-1512 1533-1535 1746 2148-2150 2182-2183 2186-2187 2223-2228 2233 2253 2484-2485 2843 2979 3189-3191 3250-3252 4796-4797 4907-4909 5001-5003 5050-5052 5196 5226
adult cervix	BioChain	CVX001	1-2 32-34 52 56 70 107-110 123 125 133-134 137 140-142 153-156 175-177 195-196 212 227-230 233 278-283 288-290 301-303 313-315 324-325 335 341-344 365 379-380 394 396-398 491-492 514 520-521 539 583-590 597-598 611 682-684 697 699-701 708 719-722 810 814-816 822-823 840-844 857-859 863-870 873-875 879-881 885-886 889-897 899 903-905 909 915 919-920 925-926 931-936 950-953 957-962 975-988 992-995 997-998 1000-1002 1022 1032-1034 1044-1047 1049 1052 1069 1075 1110-1113 1129-1130 1144-1145 1154-1155 1165-1170 1172-1173 1182-1184 1198-1204 1215-1216 1220-1221 1256 1263 1271 1287 1297 1300-1301 1319-1321 1323-1328 1352-1355 1360-1371 1374 1397 1400-1401 1410 1413 1421 1440-1444 1455-1464 1470 1475-1477 1479-1480 1487 1491-1494 1504 1507-1510 1515-1517 1524 1547-1548 1551-1552 1557 1569-1574 1599-1608 1611 1620 1625 1639 1648 1653-1654 1657-1658 1663 1683-1685 1690 1715-1716 1723 1735-1736 1753-1756 1763-1764 1780-1783 1792-1795 1805-1806 1827-1829 1835-1844 1852 1870-1877 1879-1881 1896 1925-1927 1951 1964-1965 1993-1998 2000-2002 2005 2021-2024 2031-2035 2038 2042-2043 2048 2050-2056 2058-2059 2062-2064 2066-2067 2072-2074 2078-2079 2086-2087 2096-2100 2111-2114 2116 2118 2137 2143-2144 2146-2147 2156-2160 2177-2181 2191-2192 2216-2221 2223-2228 2234-2242 2249 2251-2252 2254-2257 2273 2275 2277 2280-2282 2296-2299 2302 2327-2331 2333-2334 2341 2344 2349-2356 2358 2368 2377-2381 2389-2390 2423-2424 2456 2467 2483 2490-2494 2499 2510-2513 2546 2549-2550 2560 2563 2573-2575 2591 2594-2595 2597 2603-2604 2628-2631 2645-2647 2651-2655 2706 2713-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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diaphragm	BioChain	DIA002	574-577 1230-1232 1524 1605-1608 2116 2143 2843 3795-3800 4060-4061 4598-4601
endothelial cells	Stratagene	EDT001	1-2 32-34 38 45-46 56 70 74-77 137 140-142 165 173 175-177 187-190 195-196 213-215 220 231 278-283 294-295 313-315 330 332- 333 341-344 346-349 364 366-367 379-380 395 445-446 474 491-495 511 520-521 531- 532 545 548-553 574-577 612-620 652-653 682-684 697 704-706 709-711 719-722 801- 803 811-816 822-823 836-837 863-872 879- 881 885-886 889-897 899 903-914 919-920 927 930-936 944 950 954-962 964-966 969 971-988 993-995 997-998 1000-1002 1007- 1014 1017-1021 1026-1027 1032-1034 1036- 1040 1042-1052 1068-1071 1075-1076 1079 1089-1091 1095 1110-1113 1117-1119 1128- 1136 1139-1143 1151-1153 1155-1156 1160- 1164 1172 1192-1193 1198-1204 1217-1218 1220-1221 1235-1242 1244-1246 1249-1255 1281-1282 1287 1294-1297 1300-1301 1315- 1319 1328 1337-1345 1349-1355 1357-1359 1374 1380 1386-1387 1390-1393 1397-1401

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	2639-2642
esophagus	BioChain	ESO002	885-886 1639 2223
fetal brain	Clontech	FBR001	153 278-283 863-869 1156 1400-1401 1626 1691-1692 1727 2118 2229 2604 2645-2647 2844-2845 3174 3763 3780-3781 4090-4092 4140-4141 4545 4835
fetal brain	Clontech	FBR004	855-856 1017-1021 1470 1580-1581 1839- 1844 1978-1979 2052-2053 2084 2171 2249 3197 3451-3455 3713 4960
fetal brain	Clontech	FBR006	30-31 39-40 74-77 116-119 130 137 143-148 175-177 187-190 195-196 216-218 223-226 366-367 388-390 400-404 465 491-492 520- 521 557 602-603 607 647-649 652-653 670- 671 676 680-681 685 698 724-727 743-744 760 763 789-793 814-817 824-825 829-831 836-837 849-851 855-856 885-886 889-897 944 994 997-998 1000-1002 1017-1021 1026- 1027 1042-1043 1068-1069 1076 1089-1091 1095 1139-1142 1151-1153 1156 1176 1182- 1185 1192 1220-1221 1228 1230-1232 1332- 1333 1349-1350 1357-1358 1389 1394 1400- 1401 1403-1404 1408-1409 1413 1455-1456 1507-1510 1520 1605-1608 1617-1619 1629-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	Clontech	FBRs03	1870-1875 1878 3424-3427 3554-3556 4907-4909 5137-5140
fetal brain	Invitrogen	FBT002	32-34 59-60 92-96 124 128 137 180-182 192 195-196 278-283 341-344 436 491-492 520-521 583-590 607 647-649 652-653 677-678 778-783 789-793 822-825 849-854 882-884 950 957-960 964-966 971-974 980-988 1026-1028 1038-1040 1042-1043 1050 1070-1071 1076 1127 1156 1205-1207 1230-1232 1271 1281-1282 1322 1337-1345 1349-1350 1360-1371 1386-1387 1400-1401 1414-1417 1427-1431 1435-1436 1470 1507-1510 1532 1603-1604 1617-1620 1633 1649-1653 1674-1682 1691-1692 1694-1698 1708 1710-1714 1727 1737-1739 1765-1769 1773-1774 1780-1783 1805-1806 1839-1844 1852 1870-1875 1882-1885 1896 1925 1964-1965 1978-1979 1990-1991 1993-1998 2031-2034 2058-2059 2084 2109-2110 2118 2173 2186-2187 2193-2195 2202-2203 2208-2210 2233 2254 2278 2288-2291 2305-2306 2414-2415 2496 2511-2513 2537-2538 2558-2559 2573 2579-2584 2590 2597 2604 2629-2631 2639-2642 2659-2662 2672-2674 2696-2697 2719-2720 2741-2743

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal heart	Invitrogen	FHR001	909 1089-1091 1128 1256 1514 1621-1623 3354 4228
fetal kidney	Clontech	FKD001	30-31 137 154-156 212 278-283 313-315 326-327 370-371 379-380 491-492 551-553 595 602-604 665-667 680-681 736-740 743- 744 822-823 900-902 950-956 995 1023-1025 1035 1085 1089-1091 1182-1184 1230-1232 1300-1301 1332-1333 1353-1354 1357-1359 1386-1387 1446-1449 1457-1462 1479 1515 1532 1551-1552 1580-1581 1588-1589 1612 1617-1619 1629-1632 1663 1667-1670 1719- 1721 1724 1746 1752-1754 1796-1798 1831- 1834 1845-1847 1896-1897 1925-1927 1951 1981-1983 1993-1998 2035 2045-2047 2111- 2114 2118 2144 2224-2228 2253 2360 2422 2440-2441 2502 2510 2526-2527 2549-2550 2645-2647 2650 2693 2763 2774-2776 2781 2831-2832 2844-2845 2879-2881 2898 2913 2960 2974-2975 2979 3031-3032 3054 3198 3230 3276-3277 3304-3307 3372-3373 3442 3446-3449 3491-3495 3536-3543 3714 3780- 3781 3853 4030-4031 4055-4056 4093 4581- 4582 4679 4864-4865 4907-4910 5001-5003 5038-5039 5050-5052 5142-5143 5148-5149 5329-5330 5372-5374
fetal kidney	Clontech	FKD002	313-315 551-553 699-701 743-744 784-786 1017-1021 1173 1182-1184 1403-1404 1753 2055-2056 2116 2118 2223 2253 4598-4601 4907-4909 5001-5003
fetal kidney	Invitrogen	FKD007	45-46 491-492 849-851 950-953 1507 1575- 1576 1746 2060-2061 2086-2087 2134-2136 2204-2207 2223-2228 2380-2381 2579-2584 3242 4581-4582
fetal lung	Clontech	FLG001	64 350-352 453-455 551-553 736-740 822- 823 863-869 997-998 1000-1002 1035 1042- 1043 1193 1275-1277 1317-1318 1374 1648 1674-1682 1707 1727 1746 1753 1830 1835- 1844 1852 1870-1875 1951 2004 2066-2071

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal lung	Invitrogen	FLG003	195-196 278-283 341-344 388-390 395 450-451 491-492 849-851 879-881 885-886 950 971-979 995 1128 1193 1237-1242 1269-1270 1386-1387 1450 1507 1514 1605-1608 1709 1746 1780-1783 1830 1835-1838 1848-1852 1860 1865-1875 1990-1991 2010-2013 2060-2061 2072-2074 2094 2174-2176 2233 2253 2283 2526-2527 2579-2584 2594-2595 2836-2839 2844-2845 2888 2896-2897 2913 2951-2952 2979 2985 3008 3123 3149 3200-3202 3212 3258-3259 3280-3282 3466-3468 3508-3513 3536-3543 3605 3629-3630 3691 3749-3752 3793 3840-3841 4016-4018 4114-4116 4258 4330-4331 4598-4601 4897 5102-5104 5119 5276-5277
fetal lung	Clontech	FLG004	154-156 971-974 1070-1071 1182-1184 1527-1531 1701-1702 1753 1896 3462 3629-3630 5001-5003 5241-5242
fetal liver-spleen	Columbia University	FLS001	1-13 24-27 29-50 52-99 111-113 115 126 133-134 136 140-142 154-156 166-192 195-222 227-230 232-236 241-283 286-287 291 307-310 313-327 330-334 336-361 365-367 369-375 379-383 386-394 396-420 422-431 435-446 453-456 461 474-475 478-481 483-505 507-532 534-545 548-553 557 561-562 565-567 569-577 580-581 583-607 611-620 629-631 633-650 652-653 655-662 682-684 699-701 704-706 709-711 724-727 736-740 743-744 747-750 755-759 773-829 832-835 839-854 857-877 882-886 889-905 909-921 924 927-966 968-969 971-988 990-995 997-1014 1017-1050 1052-1055 1058-1059 1063-1074 1076 1078-1082 1085-1088 1092 1094 1096-1104 1107-1108 1110-1113 1115-1121 1124 1127-1145 1148 1150-1175 1177-1223 1225-1256 1263-1289 1292-1301 1307-1327 1332-1335 1337-1345 1349-1350 1352-1355 1357-1371 1374-1379 1386-1387 1389-1393 1395-1397 1400-1401 1403-1406 1408-1410 1414-1423 1425 1432 1434 1437-1438 1440-1444 1446-1462 1467-1473 1479-1480 1485-1486 1495-1500 1504 1507-1510 1513-1514 1518-1519 1522-1524 1527-1538 1540-1548 1551-1557 1559-1576 1579-1608 1611-1623

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver- spleen	Columbia University	FLS002	3-11 24-27 35 38 42 44 48-50 57 67 70 73-77 85 88 98 107-111 136-142 151-153 165 173 195-196 198 201-205 210-215 219 222 232- 234 236 245 252-254 258-266 277 291 316- 320 332-333 337 354 357-361 365 374-375 381-383 394 406 415-416 418 436-438 445- 446 461 478-480 486 489-490 520-521 527 538 540 543 548-553 574-577 599-601 607 612-620 647-649 677-678 682-685 699-706 709-711 736-740 747-750 755-759 777 788- 793 814-816 818 822-828 833 852-854 863- 869 873-877 885-886 889-897 899-902 906- 914 916-920 924 927-936 946-949 951-956 961-962 969 975-988 990-991 993-995 999- 1014 1023-1037 1041-1047 1052 1055 1063- 1067 1070-1071 1076 1080 1085 1088 1108 1110-1119 1124 1128-1142 1144-1145 1148 1151-1156 1158 1160-1170 1172-1175 1177- 1184 1186-1187 1192-1193 1195-1197 1202- 1204 1208-1212 1215-1218 1220-1221 1225- 1227 1235-1236 1244-1246 1249-1256 1263 1266-1273 1278-1280 1285-1291 1297-1301 1307 1315-1316 1320-1327 1332-1333 1349- 1350 1352-1355 1357-1371 1374-1379 1385- 1387 1389 1395-1397 1405-1406 1410 1414- 1417 1421-1423 1425 1427-1432 1437 1442- 1444 1451-1456 1463-1464 1470-1473 1475- 1477 1479-1480 1485 1498-1499 1515 1536- 1538 1540-1546 1550-1557 1559-1560 1580- 1585 1597 1603-1608 1612-1616 1620 1625- 1627 1629-1632 1638-1653 1656 1661-1662 1664 1667-1682 1685 1691-1692 1694-1699 1701-1704 1706-1707 1709-1714 1717 1719-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver-spleen	Columbia University	FLS003	210-211 341-344 849-851 1089-1091 1177-1179 1310-1314 1320-1321 1349-1350 1440-1441 1514 1557 1624 1648 2042-2043 2134-2136 2223 2253-2254 2511-2513 2533 2843 2979 4163-4166 4273-4274 4687-4689 4738-4739 4998-4999 5075-5077 5414-5415 5452-5453
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver	Clontech	FLV002	1411 1605-1608 1625 4581-4582 5323-5325
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fetal muscle	Invitrogen	FMS001	3-11 154-156 216-218 278-283 313-315 341- 344 388-390 395 478 491-495 511 591 652- 653 704-706 814-816 822-823 889-897 903- 908 925-926 928-929 931-936 946-950 957- 960 980-988 993 1017-1021 1048-1050 1063- 1068 1171 1297-1299 1307 1320-1321 1359 1444 1507-1510 1514 1533-1535 1540 1553- 1556 1585 1605-1608 1639 1694-1698 1710- 1714 1717 1746 1753 1773-1774 1780-1783 1805-1813 1860 1879-1885 1915-1918 2004 2042-2043 2107 2118 2134-2136 2148-2150 2161-2162 2197-2199 2254-2257 2281-2282 2503-2504 2665 2686 2824-2826 2843 2852- 2853 2896-2897 2979 2985 3054 3058-3059 3159-3162 3213-3214 3226-3228 3280-3282 3299 3323-3324 3365-3366 3372-3373 3658-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal muscle	Invitrogen	FMS002	341-344 652-653 1298-1299 1389 1400-1401 1507 1727 1746 1753 2042-2043 2191-2192 2224-2228 2761 2979 3123 3257 4285-4286 4410-4412
fetal skin	Invitrogen	FSK001	1-2 39-40 70 92-95 137 157-159 175-177 213-215 246-247 278-283 291 298-300 313- 315 341-344 365 370-371 388-390 419 445- 446 452 478-480 511 516 522-524 538-539 548-553 580-581 597-598 602-603 633-634 647-649 652-653 677-678 685 709-711 784- 786 789-793 814-816 824-829 849-851 863- 870 879-884 903-905 909 919-920 925-926 946-949 957-960 980-988 992-994 997-1002 1010-1014 1017-1021 1035 1042-1047 1050- 1051 1076 1078 1110-1113 1117-1119 1129- 1130 1151-1155 1160-1164 1182-1184 1198- 1204 1237-1243 1256 1271 1290-1291 1307 1310-1314 1320-1321 1323-1327 1351 1355 1357-1359 1380 1385 1390-1393 1400-1401 1414 1418-1420 1432 1435-1436 1450 1457- 1462 1479 1488-1489 1507-1510 1524 1533- 1535 1547-1548 1550-1552 1567-1568 1575- 1576 1579 1585 1588-1589 1611 1617-1619 1621-1623 1653-1655 1663 1686 1688-1689 1691-1692 1694-1698 1703-1704 1710-1714 1743-1746 1753 1765-1771 1773-1774 1780- 1783 1807-1813 1830-1834 1848-1852 1865- 1878 1882-1885 1903-1911 1915-1918 1925- 1927 1954-1962 1964-1965 1981-1983 1990- 1991 2006-2007 2017-2030 2038 2054 2068- 2071 2076-2079 2088-2091 2098-2100 2107 2118 2145 2153-2155 2173 2177 2179-2181 2188 2191-2192 2204-2210 2214-2215 2246- 2248 2251-2253 2267-2271 2277 2280 2286- 2291 2305-2306 2310 2338-2340 2376 2386 2432 2434-2435 2437 2469 2483 2490-2491 2510-2513 2526-2527 2560 2563 2572-2573 2588-2589 2594-2595 2603 2628 2659-2662 2696-2697 2734 2741-2743 2754-2758 2782 2787-2789 2813 2819 2824-2826 2828 2831- 2832 2843-2845 2855-2860 2865 2873-2874 2905 2914-2917 2925-2929 2945-2946 2951- 2952 2955 2961-2962 2965-2975 2979 2981- 2983 2985 2989 2996-2998 3000 3008 3023 3082 3109-3110 3151-3153 3156-3157 3167- 3168 3195 3213-3216 3220-3222 3234 3247-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal skin	Invitrogen	FSK002	313-315 341-344 366-367 551-553 971-974 1038-1040 1151-1153 1271 1353-1354 1507-1510 1588-1589 1755-1756 1870-1875 1903-1911 1926-1927 1952-1953 2017-2020 2027-2030 2078-2079 2197-2199 2377-2379 2669-2671 2677-2680 2931-2939 3167-3168 3189-3191 4082-4084 4613 4907-4909 5423-5425
fetal spleen	BioChain	FSP001	175-177 743-744 1171 1202-1204 1457-1462 1753 2060-2061 2116 2143 2223 2253 2728-2729 4167-4168 5001-5003 5335-5343 5444
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	GIBCO	HFB001	3-11 32-34 39-40 42 78 81-82 100-110 116-119 124-142 154-156 165 175-177 195-196 201-205 212-218 220 278-283 286-287 291-296 313-315 335 341-344 346-349 366-367 379-380 388-390 396-398 419 456-461 491-492 511 551-553 557 561-562 574-577 583-590 651-653 676-679 682-694 697-711 743-744 784-786 804-805 814-816 822-825 848-851 855-859 863-869 871-872 882-884 899-902 915-918 927 930-936 944-945 951-953

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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macrophage	Invitrogen	HMP001	244 278-283 440-441 445-446 794-795 855-856 995 999 1017-1021 1353-1354 1507 1582-1584 2223 4228 4864-4865 5490-5491
infant brain	Columbia University	IB2002	32-35 39-40 45-47 64 70 74-77 81-82 92-95 100-110 116-119 124 126 136 154-156 175-177 180-182 195-196 213-218 227-230 246-247 254 278-283 291 296 340 346-352 362 364-365 388-390 413-414 419 445-446 459 491-492 509 511 551-553 574-577 579-590 592-594 607 652-653 675-676 680-681 743-744 755-757 789-793 796 806-808 824-825 832 849-851 855-859 863-872 900-918 924 927 944 951-956 964-966 971-988 990-995 997-998 1008-1009 1022 1026-1027 1036-1040 1042-1043 1049-1054 1069-1071 1088-1091 1110-1113 1117-1121 1127 1129-1130 1139-1143 1154-1155 1159 1172-1173 1175 1180-1181 1192-1193 1198-1207 1217-1218 1220-1221 1230-1232 1235-1236 1256 1263 1274 1281-1282 1290-1291 1297 1300-1301 1307 1315-1316 1319-1321 1328 1334-1335 1349-1350 1357-1359 1363-1371 1394-1399 1402-1404 1410-1411 1413-1420 1422-1424 1427-1431 1437 1439-1441 1444 1451-1462 1465-1470 1479 1485 1498-1499 1507-1510 1540 1547-1548 1550-1552 1580-1584 1586-1587 1592 1603-1608 1617-1620 1638-1639 1646-1648 1653 1656 1664-1673 1693-1699 1719-1721 1727-1734 1737-1739 1743-1745 1752-1756 1763-1769 1773-1774 1780-1783 1805-1806 1814-1817 1830-1834 1848-1852 1865-1885 1896-1897 1899 1903-1911 1926-1927 1951-1962 1964-1974 1978-1979 1990-1991 2000-2003 2010-2013 2017-2020 2025-2030 2052-2056 2058-2061 2066-2067 2092 2098-2100 2131-2133 2138-2144 2151-2152 2161-2162 2171 2177 2186-2190 2200-2201

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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lung, fibroblast	Stratagene	LFB001	137 313-315 435 491-492 579 822-823 885- 886 910-914 944 950 961-962 994-995 997- 998 1000-1002 1026-1027 1049-1050 1052 1068 1075 1079 1110-1113 1129-1130 1143 1172 1182-1185 1192 1202-1204 1266-1267 1274 1287 1294-1296 1298-1299 1307 1315- 1318 1351 1374 1395-1396 1400-1401 1407 1411 1418-1420 1444 1455-1456 1473 1485 1507 1516-1517 1532-1535 1547-1548 1553-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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leukocyte	Clontech	LUC003	1-2 48-50 154-156 195-196 286-287 313-315 324-325 395 520-521 557 602-603 772 784- 786 814-816 822-823 863-869 885-886 906- 908 944 954-956 963 980-988 995 1050 1080 1122 1129-1130 1182-1184 1192 1198-1201 1317-1319 1348-1350 1353-1355 1357-1358 1374 1432 1450 1507 1516-1517 1532-1535 1547-1548 1664 1686 1715-1716 1737-1739 1753 1814-1817 1857-1859 1888-1893 1903- 1911 1919-1922 1950 1984 2010-2013 2035 2038 2054 2058-2061 2116 2118 2125-2133 2178 2191-2192 2223 2278 2572 2574-2575

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	1-2 52 96 138-139 278-283 313-315 479-480 491-495 511 799-800 822-823 829 847 863- 869 871-875 889-897 944 951-953 957-962 980-988 993 1017-1021 1038-1040 1042- 1043 1129-1130 1172-1173 1182-1184 1202- 1204 1220-1221 1237-1242 1269-1270 1290- 1291 1337-1345 1359 1400-1401 1403-1404 1432 1435-1436 1438 1442-1443 1457-1464 1475-1477 1489 1505 1507 1524 1532 1536- 1538 1547-1548 1551-1556 1575-1576 1585 1603-1604 1611 1617-1619 1648 1663 1688- 1689 1691-1692 1701-1702 1715-1716 1719- 1721 1724 1735-1736 1746 1755-1756 1780- 1783 1845-1847 1876-1877 1882-1885 1925 1954-1962 1981-1983 2005 2045-2047 2058- 2061 2088-2091 2115 2118 2138-2142 2144 2178 2189-2190 2197-2199 2223 2254 2266 2277 2281-2282 2284 2298-2299 2310 2347- 2348 2389-2390 2418 2424 2427 2440-2441 2443 2510-2513 2548 2591 2597 2637 2659- 2662 2781 2783 2814 2824-2826 2843-2845 2857-2860 2898 2905 2945-2946 2955 2969- 2973 3008 3029 3094-3095 3130 3166 3170- 3173 3195-3196 3226-3228 3240 3258-3259 3339-3340 3438-3441 3443 3459-3460 3574- 3575 3577-3580 3589 3599-3601 3635 3658- 3660 3691 3753 3815-3816 3828 3878-3879 3941-3942 3966-3968 4077-4079 4104-4105 4121-4122 4132-4133 4142-4144 4241-4242 4275-4277 4287-4288 4326 4391-4393 4546- 4548 4672-4674 4679 4737 4796-4797 4835 4902 5055 5057-5065 5085-5088 5280 5308- 5309 5389-5391 5421-5422
mammar y gland	Invitrogen	MMG001	1-2 12-13 39-40 47 62 81-82 96 116-119 126 173 175-177 180-182 195-196 213-215 227- 230 236 246-247 258-260 274 278-283 313- 315 321 341-344 346-349 354 365-367 399 419-420 445-446 450-451 478 491-492 520- 521 538 543 580-581 583-590 602-603 607 629-630 647-649 652-653 670-671 677-678 682-684 697 709-711 728-733 743-744 764- 771 789-793 796 801-803 806-808 814-816 840-844 870 879-881 885-886 900-905 909-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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induced neuron cells	Stratagene	NTD001	313-315 548-553 682-684 814-816 903-905 909 944 950 969 993 1017-1021 1026-1027 1036-1037 1070-1071 1088 1285 1294-1296 1315-1316 1322 1357-1358 1363-1371 1403- 1404 1520 1536-1538 1620 1629-1632 1638 1663 1701-1702 1707-1708 1724 1753 1770- 1771 1915-1918 1925-1927 1950 1993-1998 2017-2020 2025-2026 2058-2061 2083 2121- 2124 2144 2151-2152 2197-2199 2331 2386 2469 2573 2596 2628 2752-2753 2843 2898 2925-2929 2961-2962 2969-2973 3172-3173 3189-3191 3224-3225 3253-3255 3310-3311 3428-3429 3470-3471 3673-3677 3760 3969- 3971 4014-4015 4082-4084 4090-4092 4100 4114-4116 4140-4141 4272 4285-4286 4470 4616-4621 4691-4692 4761-4763 4864-4865 4907-4909 5137-5140 5298-5302
retinoic acid induced neuronal cells	Stratagene	NTR001	195-196 278-283 388-390 743-744 855-856 995 1038-1040 1139-1142 1418-1420 1533- 1535 1780-1783 1903-1911 2060-2061 2223 2592 3289-3290 3969-3971 4598-4601
neuronal cells	Stratagene	NTU001	74-77 195-196 246-247 278-283 294-295 341-344 388-390 491-492 566 652-653 680- 681 743-744 755-757 784-786 801-803 855- 856 863-869 900-902 919-920 950 964-966 995 997-998 1000-1002 1076 1159 1235- 1236 1294-1297 1432 1451-1454 1507 1533- 1535 1605-1608 1648 1667-1670 1688-1689 1691-1692 1694-1698 1703-1704 1746 1753 1765-1769 1831-1834 1848-1851 1900-1902 1925 1966-1974 2060-2061 2088-2091 2095

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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pituitary gland	Clontech	PIT004	175-177 227-230 491-492 796 822-823 849-851 992 995 1017-1021 1042-1043 1160-1164 1182-1184 1202-1204 1215-1216 1220-1221 1300-1301 1317-1318 1320-1321 1398-1399 1410 1479 1507 1540 1553-1556 1582-1585 1591 1625 1648 1657-1658 1663 1708 1753 1870-1875 1925 2060-2061 2068-2071 2118 2447 2604 2696-2697 2715 2774-2776 2843 2871-2872 3021-3022 3100 3203 3331-3332 3339-3340 3424-3427 3577-3580 3684 3787-3788 3959-3960 4549 5431-5433
placenta	Clontech	PLA003	1052 1215-1216 1694-1698 1919-1922 2116 3969-3971 4672-4674 5001-5003 5241-5242
prostate	Clontech	PRT001	42 165 246-247 335 511 548-550 675 847 873-875 879-881 889-897 910-914 946-949 980-988 993 995 1008-1009 1038-1040 1049 1128 1154 1157 1173 1182-1184 1202-1204 1297 1317-1318 1352 1357-1359 1398-1399 1414 1457-1462 1485 1498-1499 1524 1553-1556 1629-1632 1648 1683-1684 1688-1689 1718-1721 1746 1753 1770-1771 1792-1795 1831-1834 1860 1870-1875 1879-1881 1925-1927 1990-1991 2005 2035 2038 2045-2047 2055-2056 2060-2064 2083 2088-2091 2118 2144 2179-2181 2202-2203 2229 2254 2277 2283 2296-2297 2303-2304 2315 2337-2340 2387 2418 2423 2427 2445 2456 2468 2475 2492-2495 2510 2536 2543-2544 2546 2549-2550 2574-2575 2591-2592 2604 2645-2647 2649 2659-2662 2712 2721 2749-2750 2760 2857-2860 2871-2872 2894-2895 2909-2911 2925-2929 2951-2952 3005 3013-3014 3017-3020 3029 3081 3100 3121 3148 3174 3199 3226-3228 3242 3250-3252 3276-3277 3280-3282 3558-3560 3606-3607 3694-3696 3765 3891 3962 4067 4101-4102 4232-4235 4383-4384 4461-4464 4533 4546-4548 4581-4582 4796-4797 4882 4886 4899 4907-4910 4967-4970 5073 5078 5295-5296 5431-5433
rectum	Invitrogen	REC001	39-40 61 64 278-283 298-300 491-492 561-562 652-653 789-793 870 879-881 957-960 997-998 1007 1042-1043 1070-1071 1131-1136 1159 1217-1218 1235-1242 1272-1273 1275-1277 1317-1319 1363-1371 1380 1386-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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salivary gland	Clontech	SAL001	48-50 116-119 154-156 175-177 313-315 396-398 491-492 543 591 784-786 826-828 910-914 924 950 994-995 999 1023-1025 1036-1037 1049 1128 1202-1204 1230-1232 1237-1242 1297 1322 1332-1333 1352 1418-1420 1446-1449 1473 1480-1484 1498-1499 1507 1511-1512 1533-1535 1541-1546 1667-1670 1686 1746 1763-1769 1792-1795 1839-1844 1857-1859 1865-1875 1882-1885 1919-1922 1948-1949 1951 1978-1979 2017-2020 2055-2056 2118 2125-2130 2138-2142 2146-2147 2179-2181 2251-2252 2255-2257 2273 2280 2286-2287 2395 2403 2405-2413 2423 2499 2536 2591 2629-2631 2700 2712 2781 2784 2843-2845 2855-2856 2898 2965-2968 3008 3021-3022 3075 3236 3280-3282 3319-3322 3462 3491-3495 3632-3634 3778 3867-3869 3966-3968 4291-4295 4333 4581-4582 4598-4601 4681-4683 4729 4953 5001-5003 5148-5149 5270 5272-5274 5406-5407 5464-5466
salivary gland	Clontech	SALs03	341-344 1089-1091 1435-1436 1511-1512 1664 1708 4907-4909 5272-5274
skin fibroblast	ATCC	SFB001	491-492 1089-1091 1182-1184 1685 2005 2223 5423-5425
skin fibroblast	ATCC	SFB002	175-177 1089-1091 1182-1184 1688-1689 1763-1764 3289-3290 5423-5425
skin fibroblast	ATCC	SFB003	366-367 840-844 1089-1091 1557 1688-1689 2005 3313 5423-5425
small intestine	Clontech	SIN001	154-156 179 191 201-205 212 277 341-344 357-361 435 457 652-653 698 873-875 944 969 997-999 1032-1034 1048 1063-1067

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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skeletal muscle	Clontech	SKM001	1-2 154-156 175-177 216-218 245 313-315 346-349 354 574-577 849-851 928-929 957-960 971-974 1003-1006 1032-1034 1076 1300-1301 1334-1335 1395-1396 1403-1404 1432 1550 1691-1692 1735-1739 1746 1830 2049 2118 2548 2560 2592 2629-2631 2746 2785 2819 2843 3121 3181-3183 3310-3311 3432 3663 3737-3738 3943-3948 4534 5095-5097
skeletal muscle	Clontech	SKM002	1688-1689 2234-2242 2288-2291 3795-3800 5423-5425
skeletal muscle	Clontech	SKMs03	1688-1689 3795-3800
skeletal muscle	Clontech	SKMs04	1585 3536-3543 3795-3800 5154-5157
spinal cord	Clontech	SPC001	30-31 74-77 123 134 154-156 175-177 213-215 301-303 313-315 421 491-492 520-521 751 796 822-823 849-851 855-856 863-869 871-872 889-897 909 924 927 950-953 964-966 980-988 997-998 1017-1021 1026-1027 1049 1053-1054 1089-1091 1127 1151-1154 1159 1173 1175 1182-1184 1189-1191 1215-1216 1220-1221 1230-1232 1319-1321 1349-1350 1355 1359 1363-1371 1388-1393 1398-1399 1422-1423 1432 1446-1449 1470 1532 1539 1541-1546 1551-1552 1569-1574 1582-1584 1649-1653 1663 1685 1688-1689 1707 1715-1716 1727 1735-1736 1792-1798 1831-1834 1839-1844 1915-1922 1951 1992 2005 2017-2020 2035 2042-2043 2057 2060-2061 2072-2074 2086-2087 2096-2097 2118 2143-2144 2173 2186-2187 2193-2195 2208-2210

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult spleen	Clontech	SPLc01	491-492 548-550 561-562 641 652-653 801- 803 863-869 944 969 971-974 995 1128 1171 1205-1207 1271 1290-1291 1330-1331 1353- 1354 1508-1510 1547-1548 1551-1552 1605- 1608 1621-1623 1625 1694-1698 1743-1745 1753 1796-1798 1827-1829 1848-1851 2054 2066-2067 2098-2100 2111-2114 2179-2181 2193-2195 2537-2538 2604 2925-2929 3017- 3020 3234 3240 3250-3252 3289-3290 3402 3536-3543 3667 3975-3983 4114-4116 4136 4549 4652-4653 4691-4692 4796-4797 4907- 4909 5001-5003 5050-5052 5144 5241-5242 5270 5335-5343 5346-5354 5389-5391
stomach	Clontech	STO001	47 134 154-156 286-287 394 440-441 468 707 754 950-953 961-962 995 1041 1050 1070-1071 1075 1160-1164 1182-1185 1195- 1196 1256 1414 1507 1511-1512 1524 1638 1648 1664 1674-1682 1687 1724 1746 1780- 1783 1819 1952-1953 2093 2118 2121-2124 2188 2216-2221 2234-2242 2251-2252 2258- 2260 2273 2424 2464 2511-2513 2522 2548 2626 2645-2647 2650 2664 2675-2676 2686 2726 2820 2842 2898 2957 3008 3114 3172- 3173 3197 3258-3259 3285 3310-3311 3374- 3382 3428-3429 3456 3508-3513 3584-3585 3693 3882-3883 3906 3969-3971 4241-4242 4400 4498-4500 4672-4674 4910 4967-4970 5431-5433 5497
thalamus	Clontech	THA002	14-22 52 70 96 131-132 154-156 235 296 313-315 354 400-404 436 551-553 709-711 822-823 829 964-966 969 997-998 1026-1027 1038-1040 1044-1047 1051 1129-1130 1154 1175 1182-1184 1193 1244-1246 1249-1255

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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thymus	Clontech	THM001	28 39-40 42 52 125 137 157-159 165 175-177 198 235 274 277 284 366-367 394 450-451 491-492 499 516 583-590 605-606 659-660 707-711 764-771 822-823 840-844 847 852- 854 863-869 899 944 950-953 980-988 997- 999 1017-1021 1026-1027 1075-1076 1080 1131-1136 1139-1142 1173-1174 1182-1184 1202-1204 1230-1232 1290-1291 1308-1309 1359 1380 1389 1397 1410 1414 1418-1423 1434 1444 1450 1470 1479 1485 1507 1511- 1512 1516-1517 1524 1551-1557 1569-1574 1597 1611 1617-1619 1659-1660 1663 1686 1709-1714 1719-1721 1727 1746 1753 1763- 1764 1792-1795 1827-1829 1857-1859 1876- 1877 1879-1881 1915-1922 1926-1927 1954- 1962 2000-2002 2031-2034 2038 2049 2054 2060-2061 2098-2100 2118 2125-2133 2138- 2142 2145 2148-2150 2153-2160 2191-2192 2214-2215 2246-2248 2254-2257 2267-2270 2273 2280 2284 2298-2299 2301 2307 2338- 2340 2427 2456 2468 2490-2491 2536 2542 2561-2562 2604 2730 2739 2752-2758 2820 2843 2866-2867 2873-2874 2913-2917 2919- 2920 2954 2974-2975 3009 3025 3035-3036 3088 3094-3095 3117 3149 3170-3171 3210- 3211 3226-3229 3235 3238 3250-3255 3283 3289-3290 3314 3342-3344 3428-3429 3508- 3513 3591-3593 3605 3608 3624-3625 3632- 3634 3636 3689 3691 3723 3772 3778 3780- 3781 3784-3786 3815-3816 3864-3865 3882- 3883 3891 3897-3905 3925-3926 3958 3962 4093 4100 4112-4116 4126-4130 4228 4287- 4288 4581-4582 4598-4601 4652-4653 4662

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			4796-4797 4839 4910 5000-5003 5137-5140 5148-5149 5190-5192 5272-5274 5317-5320 5384 5483
thymus	Clontech	THMc02	39-40 52 74-77 92-96 136 154-159 168 175- 177 244 258-260 301-303 316-320 365-367 400-404 462 471 491-492 498 516 522-524 531-532 551-553 557 602-603 607 647-649 670-671 697 699-701 709-711 728-733 784- 786 822-823 829 833 840-844 863-869 885- 886 925-926 931-936 944 950 971-974 993 995 997-999 1003-1006 1017-1021 1042- 1047 1070-1071 1075 1110-1113 1128 1131- 1136 1171 1182-1184 1192 1202-1207 1271 1275-1277 1315-1319 1322 1332-1333 1357- 1359 1363-1371 1389 1398-1401 1405-1407 1432 1440-1441 1446-1449 1455-1462 1467- 1469 1479 1507-1510 1524 1526 1533-1535 1540 1551-1552 1569-1574 1588-1589 1617- 1619 1634-1637 1646-1647 1656 1694-1698 1701-1702 1707 1715-1716 1727 1743-1746 1754 1763-1764 1792-1795 1831-1834 1839- 1844 1848-1851 1857-1860 1870-1877 1879- 1881 1903-1911 1913-1918 1952-1962 1966- 1974 1981-1983 2010-2013 2017-2024 2048 2052-2053 2060-2061 2072-2074 2080-2082 2086-2087 2098-2100 2131-2133 2138-2142 2148-2150 2153-2160 2178 2191-2192 2196 2208-2210 2214-2221 2230 2234-2242 2249 2286-2287 2331 2338-2340 2360 2388 2391 2464 2511-2513 2519-2520 2537-2538 2604 2645-2647 2651-2655 2657-2658 2672-2674 2677-2680 2737-2738 2741-2743 2781 2829 2846-2847 2896-2897 2901-2903 2918 2976 3009 3068 3124-3128 3138 3196 3215-3216 3220-3222 3230 3240 3250-3252 3274 3289- 3290 3299 3310-3311 3331-3332 3394-3395 3403-3404 3406-3407 3459-3460 3466-3468 3535-3543 3554-3556 3591-3593 3654-3657 3729-3730 3737-3738 3768-3769 3795-3800 3817-3821 3846 3867-3872 3878-3879 3882- 3883 3925-3926 3969-3971 3975-3983 4100 4106 4285-4288 4291-4296 4326 4343-4347 4360 4376-4377 4439 4529 4534 4542-4544 4581-4582 4598-4601 4613-4615 4622-4623 4629-4632 4651 4657 4660 4672-4674 4729 4747-4749 4796-4797 4864-4865 4903 4907- 4909 5001-5003 5046-5047 5130-5131 5148- 5149 5210 5241-5242 5261-5267 5276-5277 5298-5302 5313-5315 5322 5329-5330 5332- 5333 5335-5343 5346-5354 5421-5425 5440-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5442
thyroid gland	Clontech	THR001	1-2 47 62 70 74-78 100-106 134 136 138-139 154-156 175-177 185 191 197 222 231 237- 240 252-253 278-283 313-315 332-333 341- 344 357-361 365 379-380 394 400-404 415- 416 419 437-438 463 491-492 511 513 574- 577 583-590 631 652-653 670-671 685 699- 701 704-707 728-733 796 822-823 840-844 847 863-870 889-898 903-908 910-914 916- 918 927-929 931-936 944 951-953 969 971- 974 980-988 992-995 997-999 1003-1006 1008-1009 1017-1021 1032-1034 1036-1037 1049 1052-1054 1056-1057 1063-1067 1070- 1071 1075 1079 1110-1113 1117-1121 1128- 1136 1154 1172-1173 1175 1180-1187 1198- 1204 1217-1218 1220-1223 1228 1235-1236 1243-1246 1249-1255 1266-1267 1269-1271 1275-1277 1286 1297 1300-1301 1307 1310- 1319 1323-1327 1332-1333 1349-1350 1353- 1355 1359-1362 1374 1386-1387 1389-1393 1395-1399 1403-1404 1412 1414-1420 1427- 1431 1438 1440-1444 1446-1449 1455-1456 1463-1464 1470 1473 1479-1480 1488 1507- 1510 1520 1524 1536-1538 1547-1548 1551- 1552 1558 1569-1574 1582-1584 1586-1589 1611-1612 1617-1620 1639-1645 1648 1657- 1658 1663-1665 1667-1670 1683-1684 1686 1691-1692 1701-1702 1707 1715-1716 1723 1735-1739 1746 1753 1755-1756 1765-1771 1773-1774 1780-1783 1792-1798 1805-1813 1827-1834 1839-1844 1848-1852 1870-1877 1897 1903-1911 1915-1918 1925-1927 1951 1954-1962 1964-1974 1999-2003 2005 2010- 2013 2017-2020 2025-2026 2036-2038 2042- 2043 2045-2048 2050-2059 2062-2064 2066- 2071 2075 2083 2086-2091 2093 2101-2102 2111-2114 2116 2118 2125-2133 2143-2144 2156-2160 2163-2168 2173-2176 2179-2181 2186-2187 2200-2210 2223 2230 2253-2260 2262 2267-2270 2273 2288-2292 2296-2297 2303-2304 2327-2331 2358 2377-2379 2386 2418 2421 2423 2427 2434-2435 2444 2449 2452-2454 2467 2496 2502 2510-2513 2534- 2536 2549-2550 2554-2556 2564-2571 2573- 2575 2598 2604 2626 2629-2631 2645-2648 2650-2655 2657-2662 2672-2676 2686 2700 2702-2706 2709-2711 2726 2741-2743 2746- 2748 2760-2761 2763 2772 2777-2778 2805- 2806 2813-2814 2818 2828 2833 2843 2852- 2853 2861-2862 2866-2867 2898-2900 2905

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2913 2925-2929 2945-2946 2965-2973 2992 3008 3010-3012 3021-3022 3024 3084-3085 3088 3094-3095 3123 3131 3133-3135 3138 3153-3158 3170-3171 3189-3191 3195 3210- 3212 3218 3220-3222 3226-3228 3240 3242- 3243 3256 3258-3259 3279-3282 3288 3297- 3299 3313 3319-3322 3325 3331-3335 3342- 3346 3372-3382 3399 3408 3418 3424-3429 3438-3441 3444-3445 3456 3466-3468 3474 3477-3478 3516-3517 3522 3524-3532 3535 3544-3545 3554-3556 3558-3562 3577-3580 3583 3586 3589 3591-3593 3602-3605 3610- 3613 3628 3638-3640 3658-3660 3673-3677 3680 3685 3691 3693 3708 3724-3725 3747 3762 3791-3792 3804-3807 3815-3816 3822- 3824 3867-3869 3871-3872 3886 3891 3895 3908 3930 3949-3951 3962 3966-3971 4004- 4007 4014-4015 4024-4025 4033-4034 4043- 4045 4093 4100 4104-4105 4109-4111 4123 4126 4140-4141 4169 4220-4223 4230-4235 4241-4244 4275-4277 4379-4380 4383-4385 4435-4437 4461-4464 4520 4522 4537-4544 4568 4581-4582 4598-4601 4633-4635 4640 4681-4683 4691-4692 4764-4766 4785 4796- 4797 4864-4865 4873 4890-4891 4907-4910 4980 5085-5088 5092 5107-5108 5147-5149 5154-5157 5241-5242 5280 5308-5309 5329- 5330 5335-5343 5369 5389-5391 5399-5401 5406-5407 5423-5425 5427-5429 5442 5448- 5450 5464-5466 5497
trachea	Clontech	TRC001	1-2 39-40 52 231 288-290 306 379-380 511 822-823 889-897 909 951-953 963 990-991 1026-1027 1052 1110-1113 1129-1130 1182- 1184 1272-1273 1292-1293 1297 1300-1301 1307 1349-1350 1352 1363-1371 1397 1440- 1441 1457-1462 1511-1512 1532 1547-1548 1586-1587 1612 1648 1664 1667-1670 1687 1690 1708 1735-1736 1746 1770-1771 1876- 1877 1900-1902 1948-1949 1951-1953 2000- 2002 2004 2021-2024 2036-2037 2054-2056 2060-2064 2118 2422 2452-2454 2470-2474 2511-2513 2604 2659-2662 2681-2685 2748 2879-2881 2898 2925-2929 2974-2975 3026- 3027 3170-3171 3223 3242 3260-3267 3394- 3395 3446-3449 3456 3663 3673-3677 3686- 3688 3761 3969-3971 4014-4015 4140-4141 4275-4277 4477 4554-4555 4570-4571 4664- 4665 4761-4763 4864-4865 4878-4879 4892 5241-5242 5272-5274 5438
uterus	Clontech	UTR001	116-119 137-139 278-283 313-315 379-380

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			491-492 548-550 583-590 592-594 789-793 814-816 822-823 930 995 999 1050 1068 1143 1202-1207 1230-1232 1297 1323-1327 1351 1363-1371 1383-1384 1388 1425 1438 1451-1454 1507 1551-1552 1582-1584 1627 1663 1688-1689 1691-1692 1719-1721 1746 1753 1755-1756 1765-1769 1792-1795 1839- 1844 1878 1919-1922 1951 1988 2017-2024 2045-2047 2055-2056 2118 2193-2195 2208- 2210 2254 2273 2296-2297 2444 2469 2552 2604 2665 2696-2697 2768-2771 2781 2802 2861-2862 2955 3156-3157 3419 3451-3455 3577-3580 3708 3729-3730 3749-3752 3880 3934 3966-3968 4043-4045 4062-4064 4239- 4240 4374-4375 4629-4632 4666 4796-4797 5024 5148-5149 5181-5183 5389-5391 5485

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Table 2

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1	5498	C	1	239	322	MGGALLKEPILSPGGGKGKIFFWGPQN*
2	5499	A	2	1441	2129	SVIA*SCRASVASKQS*PTLLPSACARPHA\STVDAPASGGAPRASSPSSDCLWSTSSSSTPLSASASSS/SPPSFNP AADARGSQPGARGRSCSPSSSERH VRRRVSAARQAGAASAGGGRQAG LAGRSGLSA/SRSSARASSSATPALA QSTPSSSESECAPLKSRSGLTSSL SKP AS*ATLGKKKSGSSWRFPPEHGR HPLSASCWNKSVAAAAAPTGATAP PKAGP
3	5500	C	3	36	236	MGPTIPDXSXXFFWRKPITWMPTWEGTSNVGPQPLSSSKSLHSXRGHPAPIPTGQAGPRDSGPGASP*
4	5501	A	4	109	300	GGGKQIPFKGGKFKWGPVPVLKKG EREKPGGNPKKTPWKKASSRPAPRI HPCFT*HAPDPRPLY
5	5502	A	5	2	73	
6	5503	A	6	27	375	EHSQVVRQALCFGTASQRPSSQPPAPS GPGPPGEPG*ERLCASHKAFISHKQS H*SPQ*PCQAGVTL SRLQTTSNPRPH SQKGLRGPRQTLSLTSQPTACSEN SQGSQPSPKRTL
7	5504	B	7	50	204	XKEGSLCDEYWNPAANLINVCSLFL RQGPRLALMQGEPVDKGLGVLL ENK*
8	5505	A	8	379	623	ATTVSVPFTAKLLERPGLHLLVFLP NLQFPLQPLVS*LALLRGSTLTQV PSAPDKPLLVSPPAKHPPVPPSCGP GLQG
9	5506	B	9	185	366	XHPGDGFRPNQEGDERPARKKTWV RDGGPHQGLFRSFHPQFFSRPSRAT AHVPAVYFSVEWX*
10	5507	A	10	29	308	WLPPNPGRRRREARQEEDLPGWW APSGPLPQLPSAVLQTPQGHGPRA SL**SVCFSFADKEGSLCDEYWNPA A/KPH*RLQPLPSTRPEISPL
11	5508	A	11	663	1269	TAGTWAVASLGRKNCGWKLRLKE ALMGPTIPDKSSPLAGLSSPFWFG RKPITLECPTWERDPRNVGPPAPSP ARKSLPQPTGTTLPYSPRDKAGPK KTLGPRG/APL*VRRTRPLN*WTPA DLGVRTRGAGPLPDAGTLRPRGA VEPSVSACGKWAPSPTSQCCEGR CDAVPKHEGLAHTVLSINVPVLN QKKKKK
12	5509	A	12	190	715	
13	5510	A	13	270	713	KLTLDCQFTG*QR*KFNG*NLRNR/ HSPSRWDGAKPLYKALKL*SSSSSV GAFIFIFTRSLRAYLFSFAH/LRRPL LAGHLLCSPEQAVELSALLAQTKFG DYNQNTAKYNYEELCAKELSSATL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NSIVAKHKELEGTSQASAEYQVL
14	5511	A	14	1575	1968	REMGRFRHVGQTGLELLTSGDLPTSA SQSAGITGVSHHTWPKTLFVLRQSL TLSPGLECSGTISAHCSPLPCSSNS CAPASRVAESTEAAHH/LCPDNLHISS REGASPCWPGCS*TPELKRPAHPCR DQLGH
15	5512	A	15	185	720	KVSHVYFLHRHGNHPISQTFPHLS PLSIPQONCHCHGPFMSWCRIKYL GIQLTRDVKDLFKEN*KPLLSKIKED TNKWKNI PCSWIGRINIVKMAILP/K ELEKTTLKFIWNQKRACIAKTILSQ KNKAGDITLPDFKLYYKATVTKTA WE/QNRDIDQWNRIEPISEITPHIYNY LIF
16	5513	A	16	1114	2193	GSFTKRVRRAFKVLRDNPVAKLS QVKKHWHYFTWNHKLRLKIAKILSK KNKPGGITLPDFKL*YRATVSKTVW YWHKNRHINQWNRIRNPEANAHTY I*LIFDKGAKNIHWVKTSLFNKWCW EN*ISICKEWEKISANYPSDKGLITR IYKEL/K/QL*EKKSNNLIKQAKDL NRHFSKEDK*MANRHMKKCSMLIT REMQUIKTTMKYHFTPVKMVYIQA GNDKCWQGCGEKGTFFVHC*WECK LV*PL*RTVWRFLEKL/E/LELP*DPA IPLLGIYPK*RKS/CVKEITVAKIWK QPKCPSTDKWIKKMWYIYTMDYYS ALKKNEILSFPTTWMEKIVILSVIG QSQDKDKCMFSLICGS
17	5514	A	17	149	328	WQDPLQDPCCHQPFHLCRLR*TLH* LRQQ*WPLLRLRQKIMLILLNTHP EHPCVLLDL
18	5515	A	18	615	734	ENSCWTATLQMGKNWQSL*PVLTS YYR*DNSYWREILQV
19	5516	A	19	1	181	MRARRLPWALTVAELGWDQTGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSA*KLATF FTFVGLSSMNCLMLSKG*GTAKSF ATFFTFVGLLSSVYPLMSS
20	5517	A	20	1	665	
21	5518	A	21	401	1739	DNSHWRETLQM*RMWQSF*PFFNP C*T*ENSYW/MRNPTNVKNVAKLL AIPQPLLIIR*LILKRNPTNVKNVTKL LSDSQPLLNK*YMLERNSTNVKNV AKLLIDLQILLYISFILERNLTSVKN VAKHLTGPQALLNIKDFILERNPSN VKNVAKHLYGLQP*LDIRGYTLER NPTNVKNVAKLLAILQPLLNIREFIL ERNPTNVKNVAKLLAVLQPLLNIRE FILERNPTNVKNVAKLLAIPQPLLIIR
22	5519	A	22	618	1655	DIPERNASNVKNVSSHFAVYTKTQ HKCVYITEKSCCKEKECTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIICAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKECGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIHH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKECGKGFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTKHKIHHTEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKECGKAFFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIHHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKECG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFFRSSTLTKHKTIHTGEKPY KCKECGKAFKHSSALAKHKIHHAGE KLYKCEECGKAFNQSSNLTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFFSQPSHLT THKRMHTGEKPYKCEECGK/RF*PI LNPYYT*DNSYWRETLQM*RMWQ SF*EIFNSY*T*DNSYWRETLQM*R MWQSI*PILNPN*TYEDAHWRETIQ M*RMWESF*SILKAYYT*DNSYWR ETLQI
23	5520	A	23	1	3476	MTLNEHAAFKHLFNKAHLAPPLIHL TLSGHSTCFREHRVGAKSNNPPASK GVWALQSARVKFAETTAGQKGMN TTWVFYYPNVASTWWGAMIPVHV VLPGGCHDASTLGDKEKRAGEAVL NVPGFQDSLESHGRIVNCLIPDVQE NNPSTGNESWLKSHQRLGEPTSRR WLITLPVTSRSNSIGHLKGTPGKSKE EIKATVCAPTLKNGFWIAERVMTVS GHEGAASSRALREELRLLFSSCAQG RLTPHIAGYPSKAKLREERSGSNICC SAIFAVLQPLLLIPRGTGSGVDLLQT PTDLQLRVLTVRRKTNKQEGHPHQ NPTCTSPSSKTKDRSTRRNVKKDTQ ELNSALRQVDLIDIYRTLHPKSREYT FFSAPHRTYSKIDHTVGSKALLSKR KRTEIITNCLSHHSAIKLELRIKKLTQ NRSTTWKLNLLNNDYVWHNEMK AEIKIFFETNENKDTTYQNLWDTFK AVCRGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTSHKASRRQEITKI RAELKEIETQKNLQKINEFRS/W/PW QRHNKKKVKFWTNTPEHQCKNPQ *NTGKPNPAAHQKGYPP*SSGLHPW DARLVQHTKINKRNPSYKQNRQK PHDYLNRCRKGL*QNSTALHAKNS Q*IRY*WDVSQNNKSYL*QTHSQYH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SECAETGSIPFENWHKTGMPSLTTP QHSGVSSGQGNHAGERNKGYSIRK RGSQIVPVC*HDCAFRKPYGLSPK SP*ADKQLQQSLRIQNQCTKTTSILI HQ*QTNREPHE*TSIHNCFKENKIL RNPTYKGCEGPLQGELOTTAQ*NK RGYKQMEEHSMMLMGRRI SYHENG HIAQGNLQIQCHPHQATNDFLHRTG KNYFKVHMEPKKSPHHQGNPKPKA QSWRHHTT*LQTLQGYSNQNSMV LVPKQRYRSMEQNRALRN NATYLQ LSDL*QT*EKQAMGKGFP**TVLG KLASHM*KAETGSLPYTLYKN*FK MD*RLKR*T*NHKNPRRKPRHYHS GHRHGQGLHV*NTKSNGNKSQNG QMGSN*TKELLHSCRNYHQSEQAT YKMGENFRNLLI*QRANIQLQRTQ TNLQEK NKQPYQKVGKGHEQTLK RRHLCSQKTHEKMLIITGHQRNAN QNHNEIPSHTN*NGNH*KVRKQQG HG
24	5521	B	24	1	8442	MIPARFAGVLLALALILPGTLC AEG TRGRSSTARCSLFGSDFVNTFDGSM YSFAGYCSYLLAGGCQKRSFSIIGDF QNGKRVSLSVYLGEFFDIHLFVNGT VTQGDQRVSMPLYASKGLYLETEAG YYKLSGEAYGFVARIDGSGNFQVL LSDRYFNKTCGLCGNFNIFAEDDFM TOEGTLTSDPYDFANSWALSSGEQ WCERASPPSSSCNISSGEMQKGLWE QCQLLKSTSVFARCHPLVDPEPFVA LCEKTLCECAGGLECACPALLEYAR TCAQEGMVLYGWDH SACSPVCPA GMEYRQCVSPCARTCQSLHINEMC QERCVDGCSCPEGQLLDEGLCVST ECPVHSGKRYPPGTSLSRDNTCI CRNSQWICSNEECPGECLVTGQSHF KSFDNRYFTFSGICQYLLARDCQDH SFSIVIETVQCADDRDAVCTRSVT RLPGLHNSLVKLKHGAGVAMDGQ DVQLPLLKGDLRIQRTVTASVRLSY GEDLQMDWDGRGRLLVKLSPVYA GKTCGLCGNYNGNQDDFLTPSGL AEPRVEDFGNAWKLHGDCQDLQK QHSDPCALNPRMTRFSEACAVLTS PTFEACHRAVSPLPYLRNCRYDVCS CSDGRECLCGALASYAAACAGRGV RVAWREPGRCELNCPKGQVYLQCG TPCNLTCSRSLSPDEECNEACLEG FCPPGLYMDERGDVCPKAQCPCYY DGEIFQPEDIFSDHHTMCYCEDGFM HCTMSGVPGSLLPDAVLSSPLSHRS KRSLSRPPMVKLVCADNLR AEG LECTKTCQNYDLECM SMGCVSGCL CPPGMVRHENRCVALERCPCFHQ KEYAPGETVKIGCNTCVCRDRKWN CTDHVCDATCSTIGMAHYLTFDGL KYLFPGEQYVLVQDYCGSNPGTF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RILVGNKGCSHPSVKCKKRVTLVE GGEIELFDGEVNVKRPMDETHFE VVESGRYIILLGKALSVVWDRHLS ISVVLKQTYQEKVCGLCGNFDGION NDLTSSNLQVEEDPVDFGKSWEVSS QCADTRKVPLDSSPATCHNNIMKQ TMVDSSCRILTSDVFQDCNKLVDPE PYLDVCIYDTCSCESIGDCACFCDTI AAVAHVCAQHGVVTVWRTATLCP QSCEERNLRENGYECEWRYNSCAP ACQVTCQHPEPLACPVQCVEGCHA HCPPGKILDELLQTCVDPEDCPVCE VAGRRFASGKKVTLNPSDPEHCQIC HCDVVNLTCACQEPGGLVVPPTD APVSPTTLYVEDISEPPLHDFYCSRL LDLVFLLDGSSRLSEAEFEVLKAFV VDMMERLRISQKWVRVAVVEYHD GSHAYIGLKDRKRPELRRIASQVK YAGSQVASTSEVLKYTLFQIFSKIDR PEASRIALLMASQEPQRMRSRNFVR YVQGLKKKKVIVIPVGIGPHANLKQ IRLIEKQAPENKAFVLSSVDELEQQR DEIVSYLCDLAPEAPPPTLPPDMAQ VTVGPGLLGVSTLGPKRNSMVL DV AFVLEGS DKIG EADFNRSKEFMEEV IQRMDV GQDSIHVTVLQYSYMVTV EYPFSEAQSKGDILQVR EIRYQGG NRTNTGLALRYLSDHSFLVSQGDRE QAPNLVYMTGNPASDEIKRLPGDI QVVPIGVGPANVQELERIGWP NAP ILIQDFETLPREAPDLVLQRCCSGEG LQIPTLSPAPDCSQPLDVILLD GSSS FPASYFDEMKSFAKAFISKANIGPRL TQVSVLQYGSITTIDVPWNV VPEKA HLLSLVDVMQREGGPSQIGDALGF AVRYLTSEM HGARPGASKAVVILV TDVSVDSVDAADAARSNRVT VFP IGIGDRYDAAQLRILAGPAGDSNVV KLQRIEDLPTMVTLGNSFLHKLCSG FVRICMDEDGNEKRPGDVWTL PDQ CHTVTCQPDGQTL LKSHRVNCDRG LRPSCPNSQSPVKVEETCGCRW TCP CVCTGSSTRHIVTFD GQNFKLTGSC SYVLFQNK EQDLEVLHNGACSPGA RQGCMKSIEVKHSALSVELHSDME VTVNGRLVSPYVGGNMEVNVYG AIMHEVRFNHLGHIFTFTPQNNEFQ LQLSPKTFASKTYGLCGICDENGAN DFMLRDGT VTTDWKTLVQEWTVQ RPGQTCQPILEEQCLVPDSSH CQVL LLPLFAECHKVLAPATFYAICQQDS SHQEQVCEVIASAHLCRTNGVCV DWRTPDFCAMSCPPSLVYNHCEHG CPRHCDGNVSSCGDHPSEGCFPPD KVMLEGSCVP EEA CTQCIGEDGVQ HQFLEAWVPD HQPCQICTCLSGRK VNCTTQPCPTAKAPTCGLCEVARLR QNADQCCPEYENGRLVSPYVGGN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion)
						MEVNVYGAIMHEVRFNHLGHIFTF TPQNNFQLQLSPKTFASKTYGLCG ICDENGANDFMLRDGTVTTDWKT VQEWTVQRPQTCCPILEEQCLVPD SSHCQVLLLPLFAECHKVLAPATFY AICQQDSSHQEQVCEVIASIAHLR TNGVCVDWRTPDFCAMSCPPSLVY NHCEHGCPRHCDGNVSSCGDHPSE GCFCPPDKVMLEGSCVPPEACTQCI GEDGVQHQFLEAWVPDHPQCQICT CLSGRKVNCTTQPCPTAKAPTCGLC EVARLRQNADQCCPEYENPCPLGY KEENNTGECCGRCLPTACTIQLRGG QIMTLKRDETLQDGCDFHCKVNE RGEYFWEKRVTCPPFDEHKCLAE GGKIMKIPGTCCDTCEEPESNDITAR LQYVKVGSCKSEVEVDIHYCQGKC ASKAMYSIDINDVQDQSCCSPTRT EPMQVALHCTNGSVVYHQVLNAM ECKCSPRKSSK*
25	5522	A	25	364	477	VIEHLVSQDGLDFLTS*SARLGLPKC WDYRREPPRPVH
26	5523	A	26	6838	7166	GSRRPGCHCNSHTGRRSSRHRGHL SPAASRGHPSPSAGPPRS*GARRPSL YAGYEA YLSGGGAGRPGHPWQLLP HASVSQGCCAGQAAGR*RSCTQR RGQSSPGQSQ
27	5524	A	27	817	1299	RKSHIFFFFLRWSLALSPRLECSGA ILAHCKLLLP/GFKPFSCLSQPSSWD YRHPPRPANFLYF/SVETGFHHVSQ G\GLNLLTS*SAHLSLPKCW\DYRRE PPRPAENLSSLTQYLECTQFEIHLGS QTALEGRLVPVITYPLGGVEISGHPV FLTSSCGR
28	5525	A	28	506	761	DGVLLLLPRLECNSAILAHRNLRPL/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLELLTSR* SARPRPPKIA
29	5526	A	29	71	425	CRRKGVNMNAPLGGIWLWLP LLT WLTPEVNSSWRYMIATGGSCRVMC YNELGLVSRRLCQRYSPCILTIIY GEAKVLFVCGLSLLVHWPNCAPSF RDNT*LLRFLHVIIVLLRPL
30	5527	A	30	263	463	
31	5528	A	31	287	2919	MASFPPRVNEKEIVRLARTGELLAP AAPFDKKCG\RENWTVALAPDGSY FAWSQGHRTVKLVP\WSQCLQNF LHGKTNVTNFKQFKDLPRQNSDG GSEKIKPREHIIDCGDIVWSLAFGSS VPEKQSRCVNIEWHRFRFGDQQLL ATGLNNGRIKIWDVYTGKLLNLV DHTGVVRDLTFAPDGLILVSASRD KTLRVWDLRDDGNMMKVLRGHQ NWVYSCAFSPDSSMLCSVGASKAV VAAILV*LRLCWHHSHTGAQWC*L GRKSGISGYRAGGDLYHRMK*PCIR LQGVLYVHRCWSMSTFCFSFFLFF FKVISPTVKYTDS*VN*FSSFMELGV

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						*QVKPI*CKVFGFQMVS LCYFLEFF QIPEISYVFDSI*NL YLFSFRNNVLCL CRKKKNQKGLLYSKRRDCLRLN LQ AHI*YNRLK*TLESCLEL FCTVNY*S LESKIVYELILK*LNC FIFK*LMIVVS LGKIRWLNFDLLKCNCIIFIK*HFHF VMWFN ILVVCQRNFIWL*IFYLLAV SVSLPRLKLV TQAYCKQVIISKGDA NGVTIC*PYVFCLYIF*KSGSFWKKK EKGVCST*PYLFPYILVN*FLE*MDF SIALWLNCIAFILCLGLFLN*HLTETF EIEFACLP*LT*RLILI*L*H*AYSLNY S*FIMLNILIKFSSFSIRCAILSSVCLN EAITFAFLLQVFLWNMDKYTM MRK LEGHHHDVVACDFSPDGALLATAS YDT*VYIWDPHNGDILMEFGHLFPP PTPIFAGGANDRWVRVSFSHDGLH VASLADDKMVRFWRIDEDYPVQV APVSNGLCCAFSTDGSLAAGTHD GSVYFWATPRQVPSLQHLCRMSIRR VMPTQEVQELPIPSKLLLEFLSYRI
32	5529	B	32	51	285	XGDEKGAAQVA AVLAQHRVALSV QLQEACFP PGP IRLQVTLEDAASAA SAASSAHVALQVFSELGFPPAVQR WVIGRCL*
33	5530	A	33	38	347	FGVAPGV SFLHHPRPHPARATASTR RAWNPQALPQPSGSSAVGSPSPRC HRGRTEWQCPVMDTITIWNSLGPP VLVGEVGSTFPTAGCLGR LPPGSR WSLE
34	5531	A	34	331	1257	FRGCHRGKDRMAARVTHHQ PWAQ KHALASWSPPEASTLKGPPEADL PRSPGNLTEREELAGSLARAIAGGD EKGA AQVA AVLAQHRVALSFQLQE ACFP PGP IRLQVTLEDAALPHPPAS SAHVALQVHPHCTVAAPGSRFFSE LGFP PAVQRF IGRCLCVPERSLAS YGV RRDGDHAFLYLLSA/RSR S/LQ PQDLALKNPQEDGRGTWTLVSPHIG GYPQGPTAQLPPACPSPLPA\SWSCP FRHLHSM POKRPGCEMCSTQRPCT WDPLAAAST*QPPEVTRGEWPFPH KSDISR PPLNSGDLY
35	5532	A	35	616	1017	LYWEKIIFSNLKT PETFLVMTSNIF HIFWEGNKLPHYTTQFSGFYFILWY FRDRASL\CRPVWGAVVWS*LTAA SNSW\VRCS SCLGLPSSWSLSPMPPH SANFKFY*FHLIFVGDGGLAVLFRL VLNSWPQAI
36	5533	A	36	3	283	FYTQNIFYSVESKLHTSTL*D\HYFFF FFETESYSIAQGGVQWGNLGS LQPP SPGFKQLSCLSLPSSWNYRCAPCP ANFVFLVEMGFHWIKPG
37	5534	A	37	260	569	RENLDLGEAFISRCLPLHSLAYFLH NLSFKSREMHN MVFKS*QALKFIRR IENNHL LFYFYFYFERKSLAHSPLG NGVGLCLKKKKNNNGSYKVLVWSF DSTE

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38	5535	A	38	468	849	TSEEFQQFTIHLTGVLHCHPDLETG GYKTF*WKSLEN*IAFFFFSETESPS APRLECSGSISAHCNLLPGSSDSPAP ASRIAGTTGTHHHARPFIILLVKEGF HHVGQPGKLKLLTSGDPPAPASQSA
39	5536	A	39	97	448	GSHEQPWEVVTGSRQPAR*SSR*AI MRKPRAAVGSGHRKQAASQEGRQ KHAKNNSQAKPSACD/GDVAEVTA FRGSLLSWYDQEKRDLPWRRRAED EMDLDRRAYAKWPTLQDLASASL EEVNQLWAGLGYYSRGRRLQEGA RK
40	5537	A	40	990	1812	RLPLGRRSPSEAAGAETAPSSLSAA MTPLVSRLSRLWVRWTCIAIMRKPR AAVGSGRKQAASQEGRQKHAKN NSQAKPSACDGR*DGPGQAGICW SVHLLRA/EATLPRGPVWGLWAR *GQVNSVL/DANPFPPVWVSKVML QQTVATVINYYTGWMPVTPGEEG KGHGSDPR*EPLLWGGCREGFLYH LHP*PCLFLPAWGYRSGPTLQDLGR AFLEEGDQL\WAGLGYYSRGRMP EDTPARNGTAQRSLPQHRLPLNEW LEWRDLACREP
41	5538	A	41	360	652	IYLAGAQWLTSLVILVWPKPRVDH LRSGVRDQPGQHGETSSLLKIQKLA RRHGACL*SLLGRWRQENHSNPG DRGCSELR\CTPAWATEGDSVLKKK
42	5539	A	42	1400	1823	NEKKSFLRQSL/DSVAQAGVQWC DLGSLQTPPPRFTPFSCSLSPSSWDH RCPPPRPP/RFCFFLYF**RQDFTMLA RLVSNS*LQ/CDPPTLASKSAGITGM SYCTRPNQAGVQWWDLGSLQAPPP RFTPFSCSLSPSSWDYRH
43	5540	A	43	227	481	KKKKELEKGNMD*IQSSRR\ETIKM RAKIF*TTNTKLMKKNKTRSLVSEN FNKIGKALARLRKKEKTPITKVRNE TEDITTNFIE
44	5541	A	44	1374	1835	ILPCNKPPWNSMACTTKHLSRSQAY RSAGAFIHWTGEAGVGSALLSLAL QKPWANQGIFPCGGRSQRGVSRN TRVWVQARNWY*VTPTHRVLWMR TAPRALAASSAAS\PSAVGSPVAA\ PSQPGLMTQMATTATEVVVGYAV GHTLSYSENI
45	5542	A	45	1	1470	
46	5543	A	46	62	526	EEKLKKGKSFQEYSGSLLLSIASVGF LSPTDIAIAVPRQWEEMRPLDIV*LA EPEEVEVLEPEEDFEQFLPVINEMR EDIVSLTREHGIRAYLRNRSKL\WRL DNML\QIKTQVEASEESALNHPPNP GETAEG\RAAKRCEKAEEKARELQ KAK
47	5544	A	47	721	1030	MGPWEPRPQMRT*CLLPLKPNSPPP TPSEE/PGHLPK*PLEVI*WPSPSPGF P/PAFRGQ*ARGHPPPPQWNTPFSP PQQ\PLSAGKT*PLTPFPALPYLGTG

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						RK
48	5545	A	48	66	386	PMEIFVDDEANLTLHGVQQYYLKL KDNEKNRKLFDLLDVLEFNQGVIFV KSVQRCIALAQLLVEQNFPAAIHR GMPQEE/QFKDFQRRILVATNLFGR GMDIERVNI
49	5546	A	49	434	858	CLSHTMDPYSPNLRPPTPPHNRWVI FVKSVQRCIALAQLTSGSRNFPAAI HRGDGPREGGGFFRVFRQF*RFNNG RIFVGYQPILGRGMGHSRRVNI AFN YGHAWRVFDTYLAFGVGQRQGRF WATKGFLFTFCVPMED
50	5547	A	50	1	660	LALARNKSLNLKHIKHFILDECCKM LEQLDMRRDVQEIRMTPEKQVM MFSATLSKEIRPVCCKFMQDPMEIF VDDETCLTLHGLQQYYVKLKDNE KNRKLFDLLDVLEFNQVVIFLKSQV RCIALAQLLVEQNFPAAIHRGMP Q\EERLSSVFSSFKDFQRRILVATNL FGRGMDIERVNI AFNYDMP\EDFAD TYLHRVARAGRFGTKGLAITFVS
51	5548	A	51	143	387	QPCLTRY*DTRCTNQ*ETTS*RLCKE PFRPGSFRPNWHLANVVENIERLQL VS\TLRLIEEDSSLN*YSIIFHSESYR YN
52	5549	A	52	2	1360	VCVCVCVCVCVRQSLAPLPRLEGS VSILTHCNRLRLGLSDSPASARGA GTTGMCHHTWLMFLFLVETGFRHV GQAGLELQTS\DPALPPKCDYR\I VNHARP*HSFYRIRLGDQNVMA GQRPASMPCPVFLVQMSPAAVST VREWAPDSQRGHRDGHAKLWGVA DSPAPACPCTFGVTHETGWGSHLPS PKRQS/CYKGSQRPTQPQVIKQAPSS MATIPIHQGDVEGGASWFTPPSAET DPRSGPRTLREGKCR*LSPYSSIKP GLKMG*IRDFHSTKEKF*WGQIDL LIFESLLTRRERANDFVVEGPTQL*L V*SIMNANLNSRKAELPNNGTSTA MGSASSFSVCLFYERETPRKAAAH* ENVWELTRRFFIFEMEFCSVAQA GAQWCHLGLSLQPAHHEFK*FSSA/S LPSGCDYRHPPPCANFFYF*WVDGV PSRCPGWPR
53	5550	A	53	218	380	RKMKNYPAPFAPRPIYSSPPPPQE/P Q*GGRDMAAIW*GALSIPPPVDDL PLG
54	5551	A	54	76	376	YKIIFVLETCMYKVICRFANNTMHL SYTVIHKDPGKGRGIISPNLFYFIYFE MEF/SLLMRPLECNGTAILAHRNLH LPGSSNSPASAS*VAEITGMCTMP
55	5552	A	55	97	437	WTRTHRASTCHVAYQEDGLLHLRN TNDPENFPKSYHYHRIIGGASG*QA TAREATHYDGDVIDLDFVTPPLG TTWGLEGTCENGDSLADLMHQSP LVGQPTEDFRNTGGH
56	5553	A	56	22	424	ALGMAHITLFFFFLLFCDSLALSPR

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						LQCSGTISAHCNLPVPGFKQFSCLSL LGSWDYRCMPPC/RWLTFFVLVET GFHHVGGAGLELLTSGDPPALA/FP KC*DYRR\DPRAWALFVFLT*FFSKL KYHKAKEKWS
57	5554	A	57	514	835	QFIFNVNKINSKTIKDRWGPVGVF TPVIPQHFGRPQQANHLRSGVRD\H PGQQGETPSLLKIQK*AGHGRGHL* TQLLRRLRQENHLNLGGGGCSEPRS RHCTPAW
58	5555	A	58	234	457	SKTENIKYWL VHGELETALHRWRN SKMAY*LGK\QFLINLRTQLPYDSAI PFIGCIPFKYECWTYNKDLFTHVYI
59	5556	A	59	1	336	
60	5557	A	60	192	432	FDNFLNSPTWAGHGGGSL*SQHFGR LRRVDHLRSGI*DQPG*HSKTPFL/ KNTKISWAWWRTSEIPAAREAEAG ELLELG
61	5558	A	61	81	439	CEHHKAHPPPVSPYQSMAPSFTQRL RPKEQVSPTMPFSLVSTPIHLTSGTP AGLPASIPGPLQSPWPSTTGT\PKI QGPSPARPAQNSPVASS*ATSSWP ARPPWTPLHSSLPALAA
62	5559	A	62	297	561	SQHFGRPRQVDHLQSGVQDHPVQ RGETPSLLKIQKLARGGGARL*SQL LRLRLRQENHLNPGGGGCNEPI*HR CSPA WAI*DSVSKK
63	5560	A	63	3	808	FFFWEPEKAFIEEFEGVSSSSSPSQL GQQRKQDAGVLHWSNLSALKNLNV PPPPPGWCLWGTAALSSSQAGRG SGIGRGGGESGGTG/ASSAEGEAPG GIVSCA*GPGCRSSGAKGLRLRAS SLQAPAAALIQAAPGVR*TGLGPYL SAVHAGPAAAAAALPGCLSPASP AAPVGATPRA\GPLNSENHRCPPGP PGPQFGLGPLGPGSGPWA\AHSQ NMRAAESAAAAWLSVPSQSPRLSP SSSSSSSPTAWNFSRPRDAGLR
64	5561	A	64	1005	1150	AWAWVCVSSGLGAPCGDGCCRGR GVASKCC\CAGGGCVSVG*GNVCA RA
65	5562	A	65	3	230	LVEMGFHQPGQHGETPSLQKI*NKK \LAGHGGTCL*S*LLRRLSQEDGLSL GGRGFSEPLCHCTPA*TTEQGLKK
66	5563	A	66	317	503	KKPKPPKPPWEPTTFG/TPAFIPPRGI WFLIAPCGWV*EEGPGSGGPWPWC PLGKTHGEGGKP
67	5564	A	67	523	741	ERGFFFGPHPGGRGKKLG*WGPPFP GLKEFSPLRPP*EGGLRGPPPLPG/SF LGFLRKGGFKHGGQGGQNPGGG
68	5565	A	68	498	778	VTINMMTGIVPYISILMLNVNGLSA/ PLERRRLAEWIKIHKPNICCLQEIHL THKDSYRLNVKEWKIFHTNGNSK *AGVAIVMSEKTDKATTV
69	5566	A	69	187	488	KRFGKNGFYPCGPGGLKPRALKEPP PLTPQRGGITSSPPPQPKKTLFFGY WPKKSL*INPQGGNLNPSQGGKP\WG

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						GFPFLDNYGGCWNRPPGGPWGGYLK
70	5567	A	71	1006	1979	GLGASILDSTTSTWSWNASRLIGL KNSLFFFEME/FSLLLPRLECSGTISA QV\NLRLPCSSDSSASASRVAGITGM CHHAQLIFVFLVEKGFHHVQGAGL ELTASGD/PTCLGLPKCWDYR/R*AT APGLFFFFLRQSFTLVAQAGVQWR DLGSLQPPPPPRFKQFSCSLSPSTWAS WVYRHAPPCPANFVFFFFFFFFLVE KGF\SMLLRLVLNS*PHDPDPASAS QSAGITGVSHHTRPMSFKNIYFFFF FFETESRSVAQAGVQWRDLSSRQP PPPGFKRFSCSLSSSSWDYRRVP/PM PG*FCIFRRDGVSPRWSGWSQTPDL K
71	5568	C	72	126	472	MADCCAKQEPERNECFQHKDDNP NLRLVRPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAK SSMNFGMKGRRLRPNRDSSVPVSK NLEKELSKHVARLSQRFP*
72	5569	A	73	3	873	HELLSTPLAFGTMKGVT\ISLLFLFS SAYSRGVFRDAHKSEVAHRFKDL GEENFKALVLIFAQYLQQCPFEDH VKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEIA \DCCENKEPERNES/CFCNHKKDNP N/LPPIG*GPEVGC CGTGFFMDNG RRTFLEKILIMEIGQEGHPYFLWP RELLFLLKRVLKLFTGMLAKLAGL KLACLLAKARWDFRNEGKASSAKQ RLQCASLQKFGERAFKAWAVTRLS QRFPKAEFAEV\SKLVTDLT
73	5570	A	74	849	1277	YNTTKLVPLYLCKMIFLLFCYVYVL RQCLA/SVAQAGMQWHNHSSLSK* PP\GLK*SSHLSLSSWDYRCVPQRF SLLFIFCRRKGFFPILA*AGLEQLGSR NHLALASHLSVGIIIGVSYHTQPVL TAAIAMVLYFVNKLSVLL
74	5571	B	75	120	323	ITRRYAEFSSALVSINQITIPNERTMQ LLGQLQVEVENFVLRVAAEFSSRKE QLVFLINNYDMMLGVLM*
75	5572	A	76	154	432	QLPEAGGPGLQEPLQLGELDITSDEF ILDEV DVHIQANLEDEL VKEALKTG VDL*LHSGERTTRD*QLPEAGGPGL QEPLQLGELDITSDEFILDEV DVHIQ ANLEDEL VKEALKTGVDLRHYSKQ VELELQQIEQKSIRDYIQESENIALS HSQITAC
76	5573	A	77	2	630	FFFVSGPAAHDLFHAVMGRTLSMT LKHLD SYLADCYDAIAVFLCIHIVL RFRNIAAKRDVPALD/RVTEFWSLM PNRPRTLLVLHDSALTDSY*PGIIN LYSHSFAPEAVVLLFDS PFSNHCPPT PTTSY*PLN*MMPHSLPSPNIPCW LTSDD*AHRYWEQVLALLWPRFELI LEMNVQSVRSTDPQRLGGLDTRPH YVREGKGNKG

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77	5574	A	78	175	2385	QLPEVRLRGMAAAATMAAAAREL VLRAGTSDMEEEEGPAGG\GPGLQE PL\QLGELDITS\DEFILDE\VDVHIQ ANLEDELVKEALK\TGVDLRHYSK QVELELQQIEQKSIRDYIQESENIA LHNQITACDAVLERMEQMLGAFQS *PSGSIKL/CRFRTLQEQSGAMNIRL RNRQAVRGKLGELVDGLVVPALV TAILEAPVTEPRFLEQLQELDAKAA AVREQEARGTAACADVRLDRLR VKA\VTKIREFILQKIYSFRKPMNTY QIPQTALLKYRFFYQFLGNERATA KEIRDEYVETLSKIYLSYRSYLGR MKVQYEEVAEKDDLGMGVEDTAKK GFFSKPSLRSRNTIFTLGTRGSVISPT ELEAPILVPHTAQRGEQRYPFALF RSQHYALLDNSCREYLFICEFFVVS GPAAHDLFHAVMGRITLMTLKHLD SYLADCYDAIAVFLCIHIVLRFRNIA AKRDVPALDRYWEQVLALLWSRF ELILEMNVQSVRSTDPQRLGGLDTR PHYITRRYAEFSSALVSINQTPNER TMQLLGQLQV\EVENFVLRVGSW SFSFKGREAACVFWIQQLTWMLG VLME*ERAADDKEVESFQQLNA RTQEFIEELSPFGLRWHL*KEAE ALIERGQAERLRGEEARVTQLIRGF GSSWKSSVESLSQDVMSFTNFN GTSHIQGALTQLIQL\YHRFHRVLSQ PQLRALPARA*AHSTFHHL
78	5575	A	79	1333	1561	PLFIQLPGLPRMLTQFN*TNHS*SK CQD/HSVCSWVKAFWRAVVAHAC NPSTLGG*GMRITRSGVRD*TDQHG ETH
79	5576	A	80	132	356	KDKIHIIISILKKFDKI*YSLIHK\TL*K LGME*TYLNIHKVIYDRPTASIIISGE KLKSFPLKSGR*QECPLL
80	5577	A	81	108	335	NKDKIHIIISILKKFDKI*YSLIHK\TL* KLGME*TYLNIHKVIYDRPTASIIISG EKLKSFPLTSAR*QECPLL
81	5578	A	82	3	6742	
82	5579	A	83	499	1018	PTRVFSITAKLINGGVAGLVGVTCV FPIDLAKHSPQQPALGKPCYKGMIR LPDRRLGRRASSAMYRGAAVNLT LGTPEKAIKLAANDFFRLLMEDG MQRNLKMEMLAGCGAGMCQVVV TCPME*PTRVFSITAKLINGGVAGL VGVTCVFPIDLAK\TRRSNQHWHESH VTKE*SDCLIEDGSGGG/PSSAMYR GAAVNLTGTPKAIKLAANDFFRR LLMEDGMQRNLKMEMLAGCGAG MCQVVVTCPEMLKIQQLQACWTP GRPSSGLGLSTLHLQVLHNWFGFHP QAPLCHPHCLG
83	5580	A	84	3	305	GTRQGCPLSPL*FNTVLEILVRHS/RS SSSSSSCLTADP/MVLHIENPKGSIK *VLELINEFSQVAGYKINM/QKTVAF LYTNN*LSKKEIKKTIQFIASKRT

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84	5581	A	85	39	281	KPRCIVSFFSMVVEA*ASIVK*EKEK IGNQGTKL**FEEMI/LYIGNSRASA DTLLEIKDFSKISGYRFNIHQSVMF LYFSC
85	5582	A	86	456	712	NIITYLFIFVTESCTVVQAGVQWCD LGSLQPPLPGSSDPHASTS*VAGIT GVSHGAWLIFFSFFPFLRRSLPLSLQ FGQQSETLF
86	5583	A	87	218	468	NNFFSSRVLLSPRLECN/SRI*AHCN LR/LPGFKRFFCLSLPSSWDYRLLPP RPANFLYF/SV*TGHHVVQASLELL TSDDPPAL
87	5584	A	88	372	666	NVCFIRTGTDCIIEHNGMKLAITKE KLEHLQ/YVWK/LNRFLNNQGVKEE ITREIRKYFEMNENKNTKYQN*ECV MTTVCRGKFIAANVHIKKQDSNYV R
88	5585	A	89	36	350	KLQLHNLKARIAAIHQAA*LTPIPT LWEAKAGRFLEPREVKASLGQ/P** GTHVHKTYKIARAWVAKHLWVPS YFKRLEVRRVALSPRGV/NGCS*RLI LPLPSQP
89	5586	A	90	58	375	VFYNKTTFKVFIIAICSLIYFVCLHSI VI*FFIL/CYCRVSEIFGYRCFIIKLL KSLL*L*FVPLFILFACILLF/WLNC YFLRLSTIVFF*KKLLIVLTFFFLYRS IIFS\CFYLLLSFF\CFFGCTL/CSCLC LQLCLFFSFSYFLIHVLR
90	5587	A	91	107	355	DMILYIENPKDSSKNPLGLINKYSK VAGYKINTQKSAFL*TNNYLKN*P /MRTIPFTIAASSSYLETYLTMEVKD LYTENYKM
91	5588	A	92	31	358	NVKSGQNLTMGEGSVSQGSIFSSLG GHRTVSVVMTMVRRCRPAHRLSR WLPSTASSGTQ*GP*NC*PNPPITLLR PPRPRQRCPSLCQFPP*TSRQRPSQ PPQGPEFP
92	5589	A	93	1	1253	MRIPSFLNLQDFEDKMEIKRYRPE GPLATSAQSHVSTAPLISTQIPHVP PLFLDCRHLTPASLFDQTLIPKKAPS NCVTDYSYRKTSEIHGSLFLILNLQF RTSTSNCCFSGSGKEALTGSIGRERS PLLAQTPFPTLKKSQRSATLECDEE ASLWENPLRDHGLFPASEHRLPLPL NQQKGPPLRTPAAHSPPNFAGWMP PVASSEGLTSIYSQLSPIGPPGRRRQ RGCPY*VQLHGDWPLCTAVYT*AR RSVAL*SRFCG*QTRR*TRWQRNPP VCSG/HKLREFPLKLELFPQIQDP HGFVISVGQVRGH*STQKLYGPIRS ASPGADGGARGRRGFDCGSPPPAP NLHPGARALPGSCWSHLPGVRSQE VSFLDSGSGSRVNPPTAEDEAWESG LCSSHPACQEHTKDL
93	5590	A	94	216	1374	RPQGMVSSPPPKLLLDPLAQLFS GQQDPQPLEKPHLQCLGRELGSGR RGGGWSPGVENRSQTLFFPGHRAP

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						APGDAEGSGP*SFSGDARPTGHLLP PRKG\HL*SSGELRPGRCNSLQAFG/ HRGLGVPRGALGVSLAGSSFPPR RRPSG*AANNSVASEGAR*ALGRG/ GPEAMP/DEFVRGVSGG*GPRGRSR LLIEW*TEAMFADPTRTAGGVGTD GKLLPVPQDH*ARPWKPREIRAVS RAGHVG/LPAC*EIPAQSLSGPRGA SAAIFGSCVPHGGSTRAGMVVRVA RGSPRGEQGLVLTR\GTTRTCGMNS SSPLAFSPLKSPG/MGGQLAGP/PGA PSARWSHGGSGRWCGRGVVGQE LVSWIHRSVTGSPhKFVGCWRQTS
94	5591	A	95	282	612	
95	5592	A	96	19	1153	DLTPGKWDQQEPGRARAPGWRLG AGGGEPQSNPLFPAPRTCPRGCR NWPIKLLCNGKKPEAPGGARGASL SEPSPLPGWPWSTGSEADLEDRT\ ERPKGFDSDVEMLK*NPVNPCE GERGCSRAGSTLESPGESSAQVQE KKDYAQQWF/SNRGQLRPHMPLPT PLGH*AAAGGSGRENVPLGMCLVS GGDRCC*TPCNPRWEGPSPTPK*PF RQRWRNSRVRSIAHGILADGIHGF DQLDLGSEKAPASEGTLEVLPRAN GGVALPVA*RWEDGRRHRLQGV GDQLSAP\GLPGKSFLSSPPRFPHP DSL*C*GCRGLGPL*CRGCPRLTSG ASPLPPPGNLVGGSGPDPSPSCQ LLPPGKHL
96	5593	A	97	429	945	KSVLSTLNWAQPRHWPETLPWVPS *PETSLPPPGGS/APPTPDM*LN SAS PNSAPPAC*NPSPACRLSSLPAITPV S QDPTPSTEQAPKFAFTPWLPAAAS P FKAQTASKG*PSHMWLPLPLLTFF P KPV\PSALLP*APSQPPKGVQAPS Q QHPLTPSHRTCSAGLLTP
97	5594	A	98	178	603	SQHFGPRWTNHLRS*IQDHPG\QHG KTPSLLKILKKLAGHGG AHL*SQL LGRLRHENHLNPGGGGCSEPR\CH T AAWMTE*DSVSKKKRPGTVAHAC Y YPSTLGGQGGRITRSRDRDHPCQY G ETPSLLKMQKLAGHGGTRL
98	5595	A	99	405	689	GSFLFFCFFF*DRVPPCSPGWSAVV QQPQLTSALTWSGSHLSLSSWEHR DV\PPCPG*FFIFCRDGV/LTVLHRLV SNFWAQSILPPWPPKVLGL
99	5596	A	100	3	307	FFFLEPSLACRQAECNAHLAH/CKL NSWFTPFSLSLRNSWNYRCPPSRL GNFFVFLVETGFHCVSHDGLDLLTS *SVRLSLPKCWDYKGESLHRAQNY LDL
100	5597	A	101	279	469	PKMAQTQKGYLHLILALMCFYFRN TQAKKNLKRDC*RPSPMPKDLACC KSIQNKIKQIGRKK
101	5598	A	102	265	446	
102	5599	A	103	283	398	NWQEKCTFQIIGGRKRMSFRILINF

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						FHN*DRTVCYVP
103	5600	A	104	283	397	NWQEKCSFQIIGGRKRMSFRILINF FHN*DRTVCYVP
104	5601	A	105	2	1012	AEALVESFWKAKQHTKEELKSLQA KDEEKNENEKAKAACSAAMEEDS EASSSTGDSSQGDNNLQKLGDDV SVDTDSIRRVYTRLLSNEKIEIAFLN ALVYLSPNVECDL MYHKVYSQDPN YLNLFIIVMENRNLHSPEYLEMALP LFCAMSKLPLAAQGKLIRLWSKY NADQIRRMETVQQLITYKVISNEF NSQNLVNDDDAIVAASKCLKMIYY ANAYAVTKNLGLYYDNRIRMYSER RITVLYSLVQGGQQLNPYLRLIVRCD HIIDDALVRLEMITMENPADLKQFY/ RGI*RRTRWVAAFWDRASEPKANSI GFGGSQLWMPTPVASYT
105	5602	A	106	966	3172	
106	5603	B	107	1	2271	MAGKASESWRKVKDTSCMAVTRE NEKDAKAETPDKTIRSRETYHKN MWETAPMIQIISQGVTPTTHENYGS TIQDEIWCLTNFCLDDMLSFLVESC TNHCAYCLNVWYRKRAAAKHLIER YYHQLTEGCGNEACTNEFCASCPTF LRMDNNAAAIKALELYKINAKLCD PHPSKKGASSAYLENSKGAPNNSCS EIKMNKKGARIDFKDVTYLTEEKV YEILELCREREDYSPLIRVIGRVFSSA EALVQSFRKVKQHTKEELKSLQAK DEKDEDEKEKAACSAAMEEDSE ASSSRIGDSSQGDNNLQKLGDDVS VDIDAIRRVYTRLLSNEKIETAFLNA LVYLSPNVECDLTYHNVYSRDPNY LNLFIIVMENRNLHSPEYLEMALPLF CKAMSKLPLAAQGKLIRLWSKYNA DQIRRMETVQQLITYKVISNEFNS RNLVNDDDAIVAASKCLKMVYYA NVVGGVDTNHNEEDDEEPIESSE LTLQELLGEERNKKGPRVDPLETE LGVKTLDCRKPLIPFEFINEPLNEA LEMDKDYTFIVETENKFSFMTCAF ILNAVTKNLGLYYDNRIRMYSERRI TVLYSLVQGGQQLNPYLRLKVR RDH IIDDALVRLEMIAMENPADLKKQLY VEFEQGVDEGGVSKEFFQLVVE EIFNPDIGMFTYDESKLFWFNPSSF ETEGQFTLIGIVLGLAIYNNCILDVH FPMGCLQEANGKRNFSVTWETLT QFLYQSLKDLIGV*
107	5604	A	108	264	378	
108	5605	A	109	297	353	
109	5606	A	110	1034	1195	MQKKMIFQQTAPLNPVQTV*RHP TPKRKECPSLRRQSTLLRMMWYLP CDQWS
110	5607	A	111	1075	1826	LGLQNRNFGYKKHFWVLT DSEPAG VGGGEEWFFSLGSR TDRSGAISPLI TLRTLAAKGAHQALTKTMMMSD KKRI*VTFLFEFKMGRKAVETTCNI

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						NNAFGPGTANERTVRWWFT\KLCK GDEGLEDEEP*WPDPLEVDSDLLR TIKAD\PLTT\TREVAEEFNIDHSMV FPHLKQIGKVKKLNK*VPHEPSKN KLA\FLEASSLILCENNNEPFLSRIVTW DENWILYDNH*QPAQLD*EAPKPN LHQQ
111	5608	A	112	540	724	EAMFYTWEGEWAQEIFVGLKKIRL GNIAHAYNPSTLGG*GGQIA*AQEF DTSLDNIARVS
112	5609	A	113	1	370	QRSRGRGSLRIGQTCLRRDMLSQEL PRLEFPLLLLLMLLMPPPCPAHRA TLFDPTWESLDARQL\PAWFDQAKI GILIHGVLGTGPSYCIERV*RNWQM EKIPKNVEFMTDDYPPRYTHEDF
113	5610	A	114	151	379	PFYVENP**YTLKNFLELISNYNKV AKYKINIQRSIYFLYASHKQVDFKV QTQ/LPFTLA/SL/RMK*FSISLTK*VQ D
114	5611	A	115	17	214	KQRLSYCIYKTTKTYATYKEIHR/LE VNGCKRIYHANTNQKKAGVAILISD KKHLRQEYYQG*KEML
115	5612	A	116	249	675	QYISVTRCHISMLTLNLNGSNAPLK RYSLTE*IFLNDTTV/CIPRHTDRLKV KG*RKTCYTNRKQKQ*/GAILMPD KTDVMSSSSSSSRK*IIVKGSILQED MTIQNIYTPNTIAP/R*VKLILLGLK G*IHSNTIMVGKFSIR
116	5613	A	117	67	373	FCDCHHFILMFKSPHIWPVGIFSSWL LCFFWACLHHSLSIALLSCTKRYSG LILYFLCSSFEITVSSKSSVSF*RRMV FRNQVLGSRCACCC*GVAAPRPPF
117	5614	A	118	366	795	AWVEQSKVLIKEGGIQLLLTIVDTP GFGDAVDNSNCWQPVIKYFDSKSQ DYLNAESQVNRQMPGNRVHCCCL YFIAPSGHGPHLN*RLPPSGRIG*YM FVTTWHCLLLRLKPLDIEFTKHLHE KVNIPLIAKADTLMPEEC
118	5615	A	119	105	702	AGSSVSLGFCPAAA AHKPRGGALR LPVFRRAQQGPDYALAGVARQPA GTCRRRCNRSHCRAEDPQWPTPAA APAAHSPHMSLGESGLGKLILNSLF LTDLYSPEYPGPSQRIKKPVQVYILV FLIDDKLE*Y*YTQSTCCNFHYAS\Q SWQPAINYIDSKFEDYLNESRVNR CQMPGNRVQGCLYFIAPSGHGPH N
119	5616	B	120	7	177	MSVSARSAAAEERSVNSSTMVAQQ KNLEGYVGAFANLPNQVYRKS VKRG FEFTLMVVE*
120	5617	A	121	2114	2945	KSVAFLCTNNVQVQAENHIRNVVIS VTI\APIHKIKYQRMYPKEVKELR ENYKTLMEIIDDTKKWKNI/C*W VGRK/LIYRYNTIPIKLSFFTELEK KILKFIWNQK/HSRIAKAIL/AQKYK AGGITLPDFKLYYKTTVTKTAW/Y WYKNRHRDQWNRTEPEIKPYTCN

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						QLIFDKINKNKQ*GKDILFNK*CWK NWLPICRRMTLGPYLSPTKITSRW ITDLNVRLQTLNILEENLGKLNMDIS /VGKEFMTRP/PKAYATKTKIDK*DL IKLKSFC
121	5618	A	122	3	113	GLDLLAS*SARLGLPKCWDYRSDW GPGPVCGLCRG
122	5619	A	123	145	540	FFVFFVEMGFHCVAKAQAYNIFFFF LRWSLALSPRECCGAISVHCKLRL PGSRHSPCLSLPSSWDYRRLPPRPA NFFFVFLVETGFHPC*PGMGLDLLT S/SIRPASA/FPKCWDYRA*AIAPGK MRLFNSL
123	5620	A	124	739	835	LAKISNSDVLKLSMLHKSSENSISHK TGAERNKYLLIKLKVI*LLTL*VNIC FFQLQFYVK*SFQIYVAWKVLIRQS Y*FLPVIFSIYFFYL*LIFV/CDTFCF *SHFLLFIFYVYFNLVTMRITYNILEL *HFNLNLFQKFNHHPKFYCYIYIAL L/CFMLLM*QIISLFIVYHVTDLLITF YAFAP*IM*KIKSRVTNQNYNRTVF MFVY/YLPLPESFVYSYLLIYLHSY CLEFIYFNLKDLTLPECQ\FRDKWIF FQF*KKIRKCLNFS/CHF*RISFPAIYF SIDRFLHYFKYIIHCLLAFKVSAREIS C
124	5621	A	125	48	492	HPTGPGRSHPRPCPRSLTSLAPSP WPPGSLQRSLLDPQRSPWRPRTQAC TRSAHALRHTIPRSTLGVTVGLEAA PPPQHLRAKGT/PPVPGAQPPPGPRP WPTQLRERPSPEPPPGGLPGSKTP ALPARPRVG*MGPKAQPHPTF
125	5622	A	126	536	669	YLNVGWVGVMAHTSNPSTSGG* GGWST*GQELKTILTSLVKHS
126	5623	A	127	793	829	GRCHLAHGGVQGSRIKPQQLGAWG RRQRDIGNRGSRGLWGEKEEKAGE RKDEPALARSTSQAPSRHPCIFNPL GVRYPRWALHPQLCAPP*AHVSVS TQIPRQRPQVAVTSLVPPISG*FRAP QGKLPNGQMLYGRHPHPLQAPPTA RASPSHVLTLTGTEQPPRA*THSPEK W*GVPAWLRTSPRPRVGRREQVT LIWPKQN*SAESPPSHRAYPEIPFR LLCLQPRTGPVLLGP*SSKCPEPPC\ TKSKPGWGKACSPLTGPCLPSP/PDL PSVPSPSPVLPDPNRTATASRNPTV TERYLNASLCWSQPDLPQGPIITDM PSAPAVPLTSDNCPSMSPAPSGKAV RQMPPGTWWGSG
127	5624	A	128	322	386	IRCFALRFSSLLSFIHLY*DT*HPDT* HPDIQTPGHL/HTQTPDTRTPGHPDT ETPDTQTLRRLTPRHLDT*HSDTQT PDTQTPGHSTPRNL
128	5625	A	129	323	516	AGGRFPSPWDPFSSRGSQASKPVRMP PTR*MRR/RGRQPCPGHRRRTQLFA VSAPSRDLQNCRRERF
129	5626	A	130	238	583	MADKQISLPAKLINGGIAGLIGVTC

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						VFPIDLAKTRLQNQQNGQRVYTSM SDCLIKTVRSQGYFGMYRGA AVNL TLVTPEKAIKLAANDFFRHQLF*GR AEA*PCLKRLLGGFWG
130	5627	A	131	3	492	SSGLGCAGTRDSQLSIRRLSSTRRS GGGGDGDGTPARDLQLGWLHLLH GSGDRRGIECAIKRKDQGVNQKK KKKRTSKLGRMSSCSNVCGSRQAQ AAAEAGGYQRYGVRSYLHQFYEDCT ASIWHEHEDDFHILRSPTRRS/SYIFE GVDSFSGTLL*YLAWTG
131	5628	A	132	1	245	GPGTGPEPWTPYS*EGDPRGRPRPR PLGPPP/TAHAADGSYRHSASGPGS WTSPFPSPGGGEKSGRTGQRVWKF GFWSWLCH
132	5629	A	133	554	1049	GRTGGGLGLLHGHTRLADTDLLDR GMLKDTLAQAPPPPLGEAYCHQGP GPWAGGGALSPGTRLQAGIQG/P/PE PQLPQLRPEPRP*PP/AQVVAGCGPA DLPPGGCGPGSCGCSPHR*TAFIKTSA NPATLAGVGWG*GHPEGVPHASE TGSDLQL*PTAIGHTGGPW
133	5630	A	134	798	1083	DPVGKGNVELPGRIAHCFHCLPVLH VCLSLSVLCVCFVLFWCFTSLF*RII VFERYLTFLVCVLC*GLCFICTCF YCSLVF*LFASCFLYSS
134	5631	A	135	71	484	EIFCYCVKYTYIQTHAPFKFRFIYL FRDRVSL*PRLECCGVVLAHCNLR/ LPGPK*SSHLSLLSSWDYRRTPPMPS WFLCFS*RRGPHHVIVQGLELLGSS SLPALASQCWDYRREQWPWG*KVF LSSAYCLFHLY
135	5632	A	136	186	434	SQHFGRRQLDAPRSGI*DQPGQHG ETPSLLKIQKLAGHGGRRL*SQL/LE RL/RQENHLKPGGGGCSEPRSRHCIP AWVTERD
136	5633	A	137	1638	1904	GGWITRSGDRDPSLAKHGETPSLLK IYKLAGRGGRSL*SQLRRLRQEN GINPGGRACSKPRSHCTPAWATG DSASKK*KIKKKVV
137	5634	A	138	421	1155	KICGSYYPLFLATFSEESFQSMLIK TTLSLNVGLVLSWKR/VQGAS/GKL QGLSEFCESQGAQNLT/LRALRLHLD LQIGEKLLVKVDAKTKAQLDEWK AKKKAS\NGNARPRNCHLMTDEEA LDEETKRRDQMIKGAIEVLTREYSS ELNAPSQESDHP/RKKKKKEKKEAIF RRFPVAPLAIPYPLITKEDISAIEMED DYIDLISREISIFRDTHKRSYGD*CK MKLSAWKVTRNRINWKKRK
138	5635	A	139	338	395	
139	5636	A	140	340	1248	RPLVLANCIQEVIRIVDMQVPLISG MQ/AWFNIVKQINVIYHLNIMKDEN HIIHGEKAFHKIQHPVIMEILNKIE REGWYLNNTKTIHEMTTAEITSQKG WNAFPVGSMMQE/CLSPLLFN/LIL AVLARAMK*/QKEIKLIEIRKKEVKL

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						YLFVDDMIFCAENHKESTKILLELS NIFSGFAQYSISTKN*LNHFTFNNKQ L*KKILK/QLPLAGELK/RKKYLKIN VKRSEVFTLKSTNIDAND*KHI*RH NPY*WFGKINIVK*LYNNPM*FRFN MISIKIPISFC*RNKKQAGKMAHVC WPG
140	5637	A	141	47	411	
141	5638	A	142	1	343	GRLQAITDKRKIQEEISQRLKIEED KLKHQHLKKALREKWLLDGISSG KEQEEMKK/RKSTKEEAILKKLSIE RTTEDIIRSVKVEREERAESIEDIYA NIPDLPKSYIPS
142	5639	A	143	460	976	LLRIGKEAELGGRGRLPGHSQIKRK LQEEISQK/RV*KLGEDKLKHQHF DK/VPLREKWLPRWNPASGKEPGR D*RSQNQPRPSTQIPGS*NKVSLRLE KEIQDLEKAELQISTKEEAILKKLS IERTTEDIIRSVKVEREERAESIEDI YANIPDLPKSYIPSRLRKEIN
143	5640	A	144	79	533	SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*HLSSFHQA VVGMIQPSHSQFLMKRKAASPRKL EWEH/LQPLHPMTLLYR*DGKPF* VLLSTYTYCSSRDRPKSSGKNARRF PAHGSS
144	5641	C	145	354	416	MKESPGGELPQTGKKPVFLF*
145	5642	A	146	3	145	SSSSDFAGQTL*STQTVQN*FKKVL KPGRLYPVPIATMGIKEPLIS
146	5643	A	147	214	464	FCGLLLLHPVSADF*PAELINTQEPQ ERCQLDTGESSRVQHTLPSCPVCQG GTAELSRNVMIGASELKCLHPSPKL EYILPGN
147	5644	A	148	246	730	SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*QLSSTGAAL PLASLSRERAWVDDGKHRLTTPMT VPQRAVQQL*ETSG**DWRQKVQIF QQA VVGMIQPSHSQFLQREDVIML RPFGLHLSWEENGs
148	5645	A	149	12	288	FGGGYIPTWGKGEGILALELNHDIS REFCSAPALASRPPTPPPLLPPT/PP LPAPRSPADATPRRVGGPLR*ALKP RAPGPGWSRRRCRSWW
149	5646	A	152	106	344	KQILLPPRLEG/NGQNSG*WKFLP GPSLFSCPSFQTSGNYGPPQQAIF WKFKIKTGFGVVTREGLNFLTSGSA PLGS
150	5647	A	153	38	349	RTAKSGSTKFSLSNSKYGTVLAVLF MKKILVLRSPKKNQDQTVKYIKRPL TSLKIREIHIKTALLYLLE*KLKLF DDTCH**AWRNYCWVVCVLIQPL WRQMW
151	5648	A	154	220	970	ESRTRGAEAAAGLAPSCTSPQAHGPA PLPTHVCCGVAIGMEPGHTAISPVV ELAVHLTGLVSSHDA LGMMPSQQG

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						*QWGRQRGLASGN*GRMSFPNSWP VTPICAARLPPGLLLICGFDGAGHSD RSEGF*GLRFPFCFKRQ/RSHSVSQA RV*WCDHGSLQPPSSGLK/HPPVSA SQVAGTTGMWHRAWLVCLFETES CSVAQARVQWRDLGSLQPLRPGFK QSSCLSLSSWDYRHHVAPCLASLFV CLRRS
152	5649	A	155	193	369	HLN**FSNLIFFETESPSVTRGIISAH RNPRLPGSSDSPTSASRVAGTTDT
153	5650	A	156	626	1017	FDSCFLFCFVCLRQSSVAQAGVK WHGLSSLQVPPPGFTFWSLSLRSS WDYRHPSPHLANVFCFLGFFVFLVE RGF\TVLARIVSIS*PHDPPTPASQN AGITGVSHCAWPTLVCLNAKFSIVV FVHKD
154	5651	A	157	1	336	TVSQAPSPESNPHGRRGDYHRKLIG QTFEWV/VRRHGGRAIGPRLSRVTK AAGARPEPKDFGFPEAARRVMGIT PVLDLGRQPVRGALVELRGAGHWR AGGGTGSCGIPARL
155	5652	A	158	2	320	VVAVSQAPSPE/SEP*FPVTRGHHGR HGDYHRKLIGQTFEWV/VRRHGGRA AIGPRLSRVTKAAGARPPAGAGEG/ LDRVGFDLINARIPPAKGANGSSPPR GACDRPEVI
156	5653	C	159	177	380	MPTGADPLRGGDACIYQIKTNPVSP SPAPAGGRAPAALVTDNLGPIARP PWRRRPIRTSAPINFRW*
157	5654	C	160	1	417	MDATCHGCLQFQIMRNKKFQLLSP SSQHFRMTASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXGRPV *
158	5655	C	161	1	403	MDATCHGCLQFQIMRNKKFQLLSP SSQHFRMTASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX*
159	5656	A	162	513	1086	QPQVASSYSAGQGRRWNTPSLGKIT RSGDRDPG*HSETPSLLKIQ/KLAG CGGRHL*SQLLRRLRQENGVLGG GGCSEPLRHCTPAWATE*DSISKK REKKKKKERKKKKRKKKKWKKE RGRGEAGEEQEEGERRRDKKKK EKKEREETREGRRRRRRKKRR RRKKKEERTTKRRRRTRKKK
160	5657	A	163	2	935	WRRSTPAPSATSASPSRCL*SQLLG RMRQENRLNLGGGCSEPRSCHCT LASPAGTQSCSRCTSQQGVQSDIPC TAAAPETAPRRGSAGGTWCRRRAP P
161	5658	A	164	34	1026	LLALGQSSCL*SQLLGRMRQENRLN LGGGCSEPRSCHCTLASPAGTQSC

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						SRCTSQQGVQSDIPCTAAAPETAPR RGSAGGTWCRRRAP
162	5659	A	165	45	69	RKNQRIYQIARKRLNEMARISPLRS MIILNVSGLNFLPKRCRLAEWTISSP DPIICCL/QKTHFTG/KDIYRLKIKGW KKIFHANGSQ*QTAMMNTNRERTK GYTK
163	5660	A	166	48	72	RKGQRISEIAIKRLNKMARISPLISII LNVSGLNFLPKRYRRAEWTISSPDP IICCL/QKTHFTG/KDIYRLKIKGWK KIFHTNGSQ*RTAISQSAMCNNNRE RVKGFPG
164	5661	A	167	118	639	ATVPSQQLIFDKDSKAIQWRDTLNFN KWCY*IN*ISTCKKLDIDSYLAPR\T KINPKRILDLNVKPKTIKCLQENTGE NCWDFGSGKHFLDMTPKMQSTK*Q ISKLIKI*NFSSKTQHFALLIIRIF*KTL LTGSKYKATTWKK/VFVNHIPDKRL ISQIQELFRTQ\TKNPTSDW
165	5662	A	169	435	808	KNLCNNKKFHRDEGWAQCLTPVIP ALSEARSRLYHLR\SGVRN*PGQHG *KHGLYWIMQNLAG\RGGTCL*SQL LGQLRQENSLNLQGGGCSEPRSRHC TPAWVTERDSVSTTTTKIFTRMNLN R
166	5663	A	170	167	197	VKFHKIKLDGEDTTYGGFDGPGLM YVYLISSDGH*FTQLHQEL
167	5664	A	171	45	259	ARMNSKLALA*ALQKRLRHQSNV FSMFDQSQIQEFKEAFNMIDQNRDG FIDKEDLHDMLASLGELGQQQG
168	5665	A	172	90	468	IMKLLTRAGSFSRFYSLKVGP*AKAK ATAAPAGAPPQPDLEFTKLPGKW LIAPLENYPPG**IGWFIKAGT*SEDF NALGTTHLLSTTCSVTNGASSFTIT RGIESADGPLTVTASREYMDHTVE
169	5666	B	173	89	186	XLKYFQTVTDYGKDLMEKVKSP ELQAEAKVLL*
170	5667	B	174	85	298	XLEGALVRRQAKEPCVESLVSQYF QTVTDYGKDLMEKVKSP ELQAEAKSYFEKSKEQLDTPDQEGWERELV*
171	5668	C	175	279	533	MAKDLMGEGPRTPELHAERQVFTF EKFKGSSLTPLDPRKAWERELGLTS LELIFRGNFGNHSLATPVESFPRTIW SFQTPGWAF*
172	5669	C	176	260	389	MDFFAQKKKKKVCMYVHMSTQR WLPNETNQINVLGFLNFLSC*
173	5670	A	177	84	1008	KVCCRYRKANGGKSPVQEVDPDG APEGAPLQQGP\PGWLPPLTTQSVS APPGGESPTENQPMFKQTDPMKMS FWTKMGSPTLSPNSV\AVSHFSPH FISN*EWEQNQPLSLVLSGRGDELH SDGGQKTQGLDKQLPRGWHGLV SFGRAACSKLGKNLRPQEIWSSKL HLPIPESQC*SPLVGVEQWGKLG S VGLLLQPKGGIPTALSPALPAGHP TLPYGNNAAGTDLRLHTEPEGPHGEP GLPARWGQDGMEPRWAAAGLGKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YLLQASRGVGVSETGQVGFLEFGKKT KSNRLIAVNDVSVHLL
174	5671	A	178	79	336	NCCNTIKSISEKP/LANSIR*AKKQEG FFQISGIRQGCLLSSFLFILEVLARG NR*D/IKCIQIGKKVKLSLFSETMR FNIWKRLR
175	5672	A	179	3	370	SVCVRAHESVVKSEDFSLPAYMDR RDHPLPEVAHVKHLSASQKALKEK EKASWSSLSMDEKVELYRIKFKESE AEMNRGSNEWKTVVGGAMFFIGFT ALVIMWQKHVGLASKWDYEKNE WKK
176	5673	A	180	24	1173	RAVAAGSGGRMLATRVFSLVGKRA ISTSVCVRAHESVVKSEDFSLPAYM DRRDHPLPEVAHVKHLSASQKALK EKEKASWSSLSMDEKVELWVLKG PTGAPSSSRKRVCDRAHFWAYC LESSLAQEGCSAGVSGHCARAPVY VLTSHLALPADRIFC*APFSVLSSGS LSAYLLGKT*LTVNY*KKLITMHSV WDERGRKITGLNRP*YCNSKK*FC SFNLHLKRTVCIFFLPCPVTCLRGHV CARMCVNMMWGLVYPSALCFL HKCGFGEKWLNVAAEAGAADLCAC KWLSSLPPVYRIKFKESEFAEMNRGS NEWKTVVGGAMFFIGFTALVIMWQ RHVYVGPLPQSFDEKWEVAKQTKR MLDMKVNPIQGLASKWDRV
177	5674	A	181	1	738	RRSQRYPFPLHGDRLAAGCGRSLPR SRGAPRRGLALFRSRDTGCRGRSRQ GSGGRMLAYQGYFTLVGKRAISTS VCVRAHESVVKSEALFASQPYMH RR*HHPCPEVAHVKHLSQCPEGT* KEKEKAFLEASLSMDEKVEVVFAL KFKESEFA*RLNKGAPNRVKGDRFV WAGAIVSFNRVFTALRLSCWQKIH YVYVGPLPRKSF*QKSGLAKQTQEG CLDNEGEPPSQGLASKWVPEKNE WKK
178	5675	A	182	82	395	ICSFAPSSIFWGSFTGTCSSTSVRA AAPPGETPQRPSMDAHMTGRKGRLS *TSFTWMTALLGVWTSVSVVW FDLADYDD*L*ALAIYDADGDVRF LRGLSH
179	5676	A	183	134	594	VITLTVSPALVANNSARGTLTPAP/P LPTGSRRTGEPWEPDGLGSSSLASC *NPPGAPGPKS*SQTGRPALPALASR LSGPLLQLPCFLSVPRSPERAPGPRH KLLLLQSLMAVSFISQFKCHLPGEV LPDRAAPGGSWPGDSRALTKSPCT
180	5677	A	184	3	404	
181	5678	A	185	2	851	AAAPAPAPAPTPTPEEGPDAGWGD RIPLEILVQIFGLLVAADGPMPLGR AARVCRRWQEAASQPALWHTVTL SSPLVGRPAKGGVKAEEKLLASLE WLMNRFSQLQRLTLHWKSQVHP VLKLVGECCPRLTFLKLSGCHGVTA DALVMLAKACCQLHSLDLQHS MV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ESTAVVSFLEEAGSRMRKLWLTYSSTTTAILGDLLGSCCPQLQVLEVSTGIRNRNSIPLQLPVEALQKGCPLQVLRLLNLMWLPKPPGRGVAPGPGFPSLEELCLASSTCNFVS
182	5679	A	186	2	568	EFGKDSCGNISAAAPPLSAQVFTAPEADPHPLEVSGTTPRVEGESSRL* LHITCDTLGLVSTLGSSTLGAQRCSVMSACLPGLSFLFPAGRYQRRGHP SRPGMGRKEVTAKAVRVGLAPATLSVSLVDLSLSPNPSCPSVSPQLVGECCPRLTFLKLSG\CHGVTCLTLWSC LAKACCQFHKPW
183	5680	A	187	2	333	ARDSTSTTEMNPQVLFQRV**QFLLI TTSWRKVISQTFGRLVDTGSKL/TV QMPRISSPSVRVAACGGQVIDGVLL KVQLTVDP*T*WTDLVIFS/SAFE*VI GIDILGSECS
184	5681	A	188	2	363	AREVFTQHS\HLTYH*TIHTGEKPYK CIECGTAFGVRSCLSIHLVVHTG*LP YRCHECGMVFMNRNTHLVRHQLIHT GEKPYMCNECGRAFIHNSNLATHQ AIHTGEKPYICTECGTVFTQN
185	5682	A	189	361	1026	RKYLPPRPTFNAEALPLKVRIWGRGLISKLYH*LYQEL*L*LYQGLITILLE KKLI*KLDKNLNRHFSKEDIQMANR HMKMYSTSLNREMQUIKTTMRYPSP PQLKYLLSQKTGNKNC*RGCGEKG TLVH/WWKCILVQPLWRTVWRYL/ RKLKIELPYNPAIPLVGIPKERKSV Y*R*ICSMFTVALLAIAKIWKQSKCP SADEWINKIWAYTTEYYSAIK
186	5683	A	190	158	366	FIISMNFVFLYFVFDLSINEILLGLKE WSIYLSS/DHSLSSLCSFYLLLLMFFL CMLLLLLLCSHIS*P
187	5684	A	191	10	284	
188	5685	A	192	3	438	LFISLLSISEKIIENCWV*LSAARS*A LRKLAFF*ATRSFF*ARDILGRFHLF F/CNFFLGLLFIDWILSYSSMSFLIHL LHPAGQQQASTICCSHCQANLHTIF WQFVCIRCADYHIPLYTGISNLNDI SVCHTNYHPVIGVW
189	5686	A	193	497	752	DGVLLLLPRLECNSAILAHRNLRPL/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLELLTSR* SARPRPPKIA
190	5687	B	194	922	2057	YPNRFPLVMDSEKQRNFNAESTIGS HIHGPRIVAGLHAPTLMEEDDALQ ETVRASIRKEQRNSRHDGGDGIRKA HAAIPRESRSMKRSRKEVKKRW NRPKMSLAQKKDRVAQKKASFLRA QERAAES*
191	5688	A	195	1492	1790	SQTLGGRRGGQITKSGDREHPG*HSE TPSLLKIQK\LAGHGNGCLWSQLIRR LRQENDMNPGGRCSEPRSCHCTP AWVTEQDSISKKKKQKQKEGLGGS A

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192	5689	A	196	178	572	QAGSCTRTSQPRDSRGSDIQPVGLA FGRTPAELQELHLSRPRGRGAVWA CGSLEPGPLPLLSITSGSQPSLQLSSL PQSPLFCPLPPF/PPRPPPRVGLVPPP *LTHVPG LQPTGRPPSPSRSPAPPP Q
193	5690	A	197	209	684	PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPSRHR DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLFHGAQVLAQLLGTSEE DSMVGTL YDKMY
194	5691	A	198	2	720	IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPLYTRHRMLGPESVPP PKRSRSLMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVVNVGGEYDPSRHR HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLFHGHKLVAQLLGTSEEDS MVGTL YDKMYENFVEEVDVND GISQWAEGEPRYALTTLSARDARL NPTWNHPDQDTEAGFKRA
195	5692	A	199	209	684	PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPSRHR DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLFHGAQVLAQLLGTSEE DSMVGTL YDKMY
196	5693	A	200	2	720	IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPLYTRHRMLGPESVPP PKRSRSLMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVVNVGGEYDPSRHR HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLFHGHKLVAQLLGTSEEDS MVGTL YDKMYENFVEEVDVND GISQWAEGEPRYALTTLSARDARL NPTWNHPDQDTEAGFKRA
197	5694	A	201	94	660	LHLKNSDGYCLIVYQKRFIPVTFIHF CFLILSLKFNNIPLNIFANGEKYFVY KFTYSYVVKFLT\CFVELPVNCLFI SFSHFLLMSFVIFL**ILGMLYVLVL LIFNFTYICIVIAFY*LFVVIQTFLHFY LLKFNLFL*SFSGFCVLLRRVIPRI YICFIRILYNSTLFTSTYLEE*FSFDM
198	5695	A	202	3	347	FFEMEF/SLLLPRLECNGVILVHCNL RLPGSNDSPASAS*VAEII GVCTASS *IFVFGTLTQ*KSRLVDQAGLELLA PASSDPILTSQSAGITGVTTDIQPPF FLSSFANTEWT
199	5696	A	203	32	403	APIPDAMGHFTEEDKATITSLWGKV NVEDAGGETLGKLLVVPWTQRF DRFGNLSSASAIMGRR*VKAPG*NV \LTS LGDALMHLDDLKAPLANLRER T/CDQGCWVNPENF*LLGNVLVTVL AI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
200	5697	A	204	94	361	FCQLDSLYTESQSLADSTVL*LAEHM KFIKTSY*GALDTFTKHLQMSVDA YE**MISILNPSSLSERQSLLLFIVLD LSLVPYLLIFE
201	5698	C	205	265	408	MTLSCSNLVFFFLFKITVFIMTMVTP QCKGGPDSVCFSTLFVNKCPV*
202	5699	A	206	10	419	MRGGHSWARKGGMRGLIRNERES GGGEQTD*ASKLKRGNRNITPFAY MDTY\ASSSSSSSSSSSSSSSSASKLE AELGQTGLLPIPLGGGGGAFSTKT VRSGESEGLWKQRKRWLEGRGCR VSGWECGAEAMK
203	5700	C	207	165	248	MDTYXXXXXXXXXXXXXXXXXXXXX FQARS*
204	5701	C	208	337	428	MILRVDDFVPLALLPQSFPHRSHYD PNPAA*
205	5702	A	209	531	1860	PSKPPNQCFLSLSQATSAGTHLSQD TESLTQVAKGIS*GSQGHGGGTL*M RGGHSWARKGG/H*EGSSGMRGRA VEGNKQTRLLN*NGEIQTEPLLHT WTLTVQMRKVTPREGELSCPRASK LEAELGQTGLLPIPLGGGGGALSTK TVRSG\GVRGVFGSRENDGLWKVD VEGSVAGSRAGA*AMKGEPKQIPK LTL*S*P*ENPNGNAVFS*ARGKL*/ SFTKTLGAPAGAPAPAPP\GPRWPP PA/DCGHTRPPLPSESLEELKAGDS PSLALDSLSP*PPPTPPAGPRRSQGP GAPAGALGSRCPRQVQKQTTLSG* RGRAGAGNTRRRGSGPHAAPIGSV DLRSGAPATAGPCG\RAASVGAGPR RGRGGRG\LPAPPWGT*GAPKGPRR RGPAGWSQTGSARPCGPWASRGGP KPRPCVHGGRRPGDAPGVVTPRC GR
206	5703	A	210	32	452	
207	5704	A	211	38	618	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVPWTQRF FDSFGNLSS\PSAIMGNPKVKAHGK KVLTSLG\DAIKHLG*SQRAPFAQA* SELALVTKLHVDPGGTFKLLGEML LVTRFWAIPFSAKEFHPWRLQA\SW QKQKMAEDGDLELASALVPSRLPL SSLAHECRAFQGYGFILASNYK
208	5705	A	212	137	368	DGVYLWTHRPYCGLSLNFSGSVIIV LP*VKAYGWMVLTSLGDAIQPLAD PECSF\GQLRELRCMDLHVDPEDFR LLGK
209	5706	A	213	60	317	FPCLVCCTLQENSGKPILCPRRTTAQ LGPRRNPAWSLQAGRLFSTQTAED KEEHLHSIISSS*SVQDYTSKHKFQA STYKH*SIA
210	5707	A	214	3	406	HEDKLCTVATLRETYGEMADCCAK HEPERNECFLOHTDYNANLSRLMR PEEDVMCTAFHDNEETFLKKYLYDI ARRHPYFYDPELLIFANRHKAFTD CSQAGD*AAWLVPKLDLYEL*A

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
211	5708	A	215	1	2953	TSCIIISKCANL MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCAATYKLCHEPELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGDAHKSEVAHRFKDLG\EEDFT ALVLIAFAQYLQQ*PFEDHVKLANE ATEFAKTCVADESAIENCDKSLHTL FG\DKLCTVATLARETYG\EMADC\C AKQGT*GEMECFFATQRMNDPNLP PIGWRTRGWMWMLHCFFHDNEGD IF*KKYLLWKLPGRTSFTFYGPPELL FLWLKR/RIKAGFLQEC\CQGWLD*S WPACLAAGSDELSGMKGKAS\SAK QRLKASLQKIWEKELSKPWAVAR LSQRFPAEFAEVSKLVTDLT\KVHT ECCHG\DLLECADDRA\DLAKYICE\ NQDSISSKLKECC\KPLLE*FHCLA EVENDEMP\ADLPSLAADF\VENKD V\CKNYAEAKDVFLGMFLYEYARR HPDYSVVLLRLAKTYETTLEKCCA AADPHECYAKVFDEFKPLVEEPQN LIKQNCLEFEQLGEYKFQNALLVRY TKKVPQVSTPTLVEVSRNLGKVG KCKKHPEAKRMPCAEDYLSVVLNQ LCVLHEKTPVSDRVTKCTESLVNR RPCFSALEVDETYVPKEFNAETTF HADICTLSEKERQIKQTALVELVK HKPKATKEQLKAVMDDFAAFVEK CKKADKETCFAEEGKKLVAASQA ALGLTPLGPASSLPQSFLKCLEQV RKIQGDGAALQEKLCAATYKLCHE ELVLLGHSLGIPWAPLSSCPSQALQ LAGCLSQLHSGFLYQGLLQALEGI SPELGPTLDTLQLDVADFATTIWQQ MEELGMAPALQPTQGAMPAFASAF QRRAGGVLVASHLQSFLEVSYRVL RLHAQP
212	5709	A	216	1060	1259	TKFGQHKGKTPSLLKI*KLAGHGGAH LKSQLPGRHENHNLNPGGGGCSEPR LCHCTPAWVTKRDCLKK
213	5710	A	217	2	354	SAAAGQGEENQLEASLDALLSQVA DLKNSL/EEFHLQVGERVWPADLLN TLNKVLKHEKTPFRNQVIPLVLSP DRDEDLMRQTEGRVPVFSHEVVPD HLRTKPDPEVEEQEKQLTTV
214	5711	A	218	90	329	
215	5712	A	219	2	632	QPSFLCVILVYLGDPVPPIGAEKRRS TLEASLDALLSQVA*SEELSGEFHL QVG\DEYGRLTWPSVLDSICLAFLD SMNTLNKVLKHEKTPAVP*PGHHSS GCCLQDRR*KISCRQT*KDGCFLSA H*GKSLDHLEKPSLDP*KLEEQEKQ LTTDCSPAFGADAAQKQIQSFE*NV

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						FQTFLGENQQRGSEDSWRFSGRTRLLTPTDT
216	5713	C	220	309	479	MIHYSSSYSEFKSSRELHIKFKFPVSTSCGAFGSKIKWKVLSEVVEETQESEQPEVL*
217	5714	A	221	76	525	PQPLGPQPQQRPSRLASCCGAAAPCSWVEGAIGHAPPHGLPIMSNGYRTLSQLNDLKKENFSLKRIYFLEERMQQKYEASR\EDIYKR\NTELKVEVESLKRELQDKKQHLDKTWADVENLNSQNEAELRPQFEERQQETEHVYELLEK
218	5715	A	222	534	1310	PRNEFTQQFCFIDSFFLVTLKIEALQCSHRSSRRSGEKVPFVQTYSLRAFEKPPQVQTQALRDFEKHLNDLKKENFSLNVRIYFLEERMQQKYEASREDIYKR\NTELKVEVESLKRELQDKKQPSGLKPWA\DVENLQPVQNEAELRRQFEEP\QQE\TEHVYEL\LENKMQLLARNSRLATE*TMRGWQLLVERQRKGV*TWKLSGET*RESPKNWGRCPREQVKPDPLHLRPLAQKGKDLKKIMLGSPNHIKNASDQ
219	5716	A	223	32	360	TGSKIRNIKGIIHIGREEMKLILFTNYILVCRE/NPKIMFKLLALISRY*ATVAGCNIYIPPTPKLNFDIVG*ILLAKKLF TNANNNIRYLGINLIINDGHHSKEIYIISL
220	5717	A	224	2	761	APTPTGQRVVRATPAQSA\PVRLRRRSYDVNNPIPSNLKSEAKKA\KILREFTVEITSRNGPDK\NPGSTVI\AKAK\GLANSCLLNQSPGSLVTFQ\RGPGV\VARL\PDGK\WSSPFS\ALGIAGFG\GFEIGI*GIQTLV\ILEF\DDPCC*EAF AKGGNLT\GGNLTVA\VGPLGRNLEGNV\ALRSSAAVFTYCKSRGLFAGVSLEGSC\IERKETNRKSVQKVILIESVMRK*YFKS*YNLQSTFIYSFYNMWF
221	5718	A	225	299	541	SQHFGRLTQADHLKS*VQDRPGQHGEIPSLQKIQKLAGHGGASL*SQLLGLLRQENHLNPGGGGCSE\PTPGWATE*DSV
222	5719	A	226	198	660	LLLALLFNTVLRFTVCLFLFQAPILKSPCCSAARVDRRKSIWVDGL*ICSR LSK*VIC*LGTFKFVVQILQ\THTLSN*L\HLNIEKN*GLTG*VSILCKCLFYHSL*PLL*VKCSLRPGVV\THTCNLSTLGGRGGRIT*VQEFETSLGNIVRHRI
223	5720	A	227	1	347	GERLAGRRRKMAVESRV\TREEIGNDS*KPIDREKTCPLSLRAFTTNNGRHHRMDDFSRGNVPYSELQTYTWM DAT\LKDLTSLAQELYPQATLNGHTF\FAVALTHATPPGSRVND
224	5721	A	228	3	225	SCQGERLAGRWRKMAVESRV\TQEEIKKEPEKPIDREKTCPLLRVFTTNNGRHHRMDEF\SRGRWSKAPGKQK

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						GP
225	5722	A	229	1984	2676	
226	5723	A	230	2	590	GCRNSARGKMAVESRVTQEEIKKE PEKPIDREKTCPLLLRVFTTNNGR\HHRNGRVSPRGNVPSTELQIFPLGW MPTLKELTSLVKEVYPEARKKGTH FNFAIVFNRLCKVPGYR*FSFLQS* GGLASTHVWAERGLDDSHPELQSR KFQIGDYLADIA\ITPPNR\APPPSGR MRPYLNSNFTYLFIFYFFPSVM
227	5724	A	231	1	291	
228	5725	A	232	3	320	AKNRLQILKFCLHFKERKTVLP SKH AVPEVIEDFLCNFLIKMGMTRTLDC L/QASEWYELIQKGVTELRTVGNVP DVYTQIMLLENENKNLKKDLKHYK QAAEYVIF
229	5726	A	233	209	461	
230	5727	A	234	104	609	RQPGTRGTRRTRWRLEGAYYLEQV TITEASEDDYEEVTC*F*IPDDNF SIPEGEEDLAKAIQMAQEATDTEIL ERKTVLP SKHAVP*VIEDFL/RCNFL DQNGELTRTLDCFQSEWYELIQKG VTELITVGNVPDVYTQIMLLENENK NL*KDLKHYKQAAEYVIF
231	5728	A	235	222	502	TSLIKHYISNLFTFINSVEYKQ*WFL LWLCVSLKC*LGQA WWAQACNLS TL*GPRWAADHLRSEVRDRTG\QH GETPSL/LKNTKISAW*WVPV
232	5729	A	236	565	779	APGVRD*PGQHGENLSLQK*KLKK LAGHGGIHLFCQLLRPRQKYRLSP EGQDCSE/PMVCTLA WATEQDPVS
233	5730	A	238	656	923	VPVHRGKERGGIQDLDEIATPTLLS KSSSFKTSYCTDFFLFTESCCVTR LECSGMISAHCSLCLPGSSNSAPTSP VSHNKDRLLHL
234	5731	A	240	171	373	AWLCANKTLFLNFYLFETRSC/SLS RLECNAIIAHCSLLLPGPSDPTS SA SQVAGTTRTCHDTQPI
235	5732	A	241	915	1283	QRQGRGLWDNEEGEIGTKYSSFKI DTVEKLFLGGGRSRVKPRGSNKAR DPPSFPSPAWEVGPQLGVPLKSPCG LHLGLAAVPLYDPRGGGPHTPPHTP P/PTPHPPHPHTKHTPPTNTQ
236	5733	A	242	555	767	NKKDLFSLRSGDQKSKVKTSEGPRL /PLRGIRENP/CPPVPAPGGPRHCLAC GGITPVSAIITRISCPLYSN
237	5734	A	243	2	744	GTMAVFFVLLALVAGVLGNEFTIL KSPGSVFRNGNWPPIGERIPNVAA LSMGFSVKEDLSWPLAVGNLFHR PRATVMVMVKGVNKLALPPGSVIS YPLENAVPFILDSVANSIHSLSFSEETP VVLQLAPTEERVYMRKANSLEFY LSITFLQLHNRLFQKNSVLTSLPLTS LNNNNELHLLFF/S*LQPLH*ISNFLS CDKHFTQKMIVLINNHSNLPMLPTK FGNPFLTKSFSPFNLSLKPFA
238	5735	B	244	385	544	MTGSPEDDETGYPLRSPGQERSST

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						EKPMDNAATSGIRSPGIGQFPFRKTTDPX*
239	5736	A	245	1	449	GNEFSILKSPGSVVFNRNGNWPIPIGER IPDVAALSMGFSVKEDLSWPGLAV GNLFHRPRATVMVMVKGVNKLAL PPG\SVISYPL\ENVDLLFLSELQVLH DISSLLSRHK\HLAKGSILPDLYSL\AE RAGFGMEIGKRYGEDSEQFRDASKI
240	5737	A	246	2	1230	GAGRVRARHLLTLRLSPCAGPFRV APQCCGRRGTMAVFFVLLALVAG VLGNEFSILKSP\GSVVFNRNGNWPIPI REVRDPPDVAAI/SPMGFSVKEDLSW PG\LA VGNLFHRPRATVMGDG*RG VNKTWLYPQGSV\SYPLE\NAV PFS LDQCLQIPHFIFLEETSCLFLQLGF PVREVRVVLWL GKANFSV*RTFSVT LARQLR/NIRLVFKENS VSSVSLPLNS LSRNNEVDLLFLSELQVLHDISSLL SRHKHLAK\DHSPDLYFTGSWAGLA DEIG\KALLGEDSEQFRDASKILVD\ ALQKFADDMYSLYGG\NAVVELV TVQSFDTSL\IREGQGTYSLEGKTS GTPASPYNLAYKYNFEYSVVFNMV LWIMI\ALALA\VIITSYNIWNMDPG YDSIIYRMTNQKIRMD
241	5738	A	247	1547	1965	AQGRFQALCSLVAVRAWGWPLSG NSFSCGNSQCVTKVNRSVTTRRTAP MGPTRRMRVWLAASWRMAGRIVG GMEASPGSFRGKPAFERTRSTSVGR HHQRQPLRS*NHRFQDPTKWVAYV VRPTSAARRPAPCGPSKKA
242	5739	A	248	403	734	MAVQAGTQCLVQQLHSGFLQHLW LDHCRPRKMLTEVLLEVAPA*DQA LLAGWEDVCGSREAHGLD\GRPKG RGLVSSSTATSKSAVSALYRGCLTI WTTWARTVLASEPLR
243	5740	A	249	1	552	MVWSSQRCRKHCGAAGPGTVQC LVRPLLTD RMVCAGYLDGKVDPAR PQKNTDTSVSNAGRFTDIWMPVLE EFKAVGIERQNVGPGLNGEAHPGR GRVRSCLREVPWQVSLKEGSRHFC EQLWWGTAGCCLPPTASVSGIKA L/YESELADARRVLDETRERARLQ IEIGKLRAELDEVNKR
244	5741	A	250	63	497	LPDVEKLGRRRGRKMDSVEKGAAR LRIPNPRGRPSRGRPPKLQRNSRGG QGRGVEKPPHLAALILARGGSK\GIP LKNIKHLAGVPLIGWVLRAL\DSG AFQRCACARVGGAAWAGVGRGSR AAGGAGASGATALGRGPSLMPGM C
245	5742	A	251	1	349	GTRAVVCGRRLISVREQIRHFVMRP EINTNHLDKQVQLLAEMCILIDEL DNQAYCETKKNCHLNENIEKGAAL KQTLLLSDLCRHFRFAEKSTLFKEV QTSVIPYFLVGSSSFK
246	5743	A	252	2	423	LRWSL/DSVAQAGVQWGDLSLQA PPPGFTPFSCRLRPSSWDYRCQPRT

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						*RRGFIVLARMVVIS*PCDPPASASQ SAGIIGM/SHRARPGFPT/CQTTQEPG GTTSHGYRIPPP*QDLC*LPQFPERG SGSQRC*DKPGSPSL
247	5744	A	253	891	1564	SPRALAANPWWMVTSVSSRVKQSC TQQGGFVPLAQVHSPHSELYALV SLFFYFLFDICRARILSGSFCILRTL LLLFLRRSLNSVTQAGVQWRDLGS LQAPPPGFTFPSRLSLPSSWDYRRLP PRPANFVFLVETGFHRDETRIVSI S\GPRDPPASASQSAGITGVNHRAW PTFCIFCRDRVSSCWPGWSRSHTPG LKRSSCLSLPKFWDYRHKLPYP
248	5745	A	254	6	338	MEPSCGLGSEALALTQTWAGSHSL KYFHTSVSRPGRGEPRFIYVGYVDD TQLVRLDND/APSPKMVPRAPWIEH EGSKIWDRETHIAKDRQIFRVNLR TLRSYYDQIEAGD
249	5746	A	255	2	424	
250	5747	A	256	25	486	EFHRLRENPPWCLSPADKTNVKA/A WG\KVGAAHVRSMCAEALERMFLS FPTTKTYFPHFDLSHGSAQV*GATG KKVADALTNAVAHVDDMPNALS ALASDLHAHKLARVDPVQLSSS*SHC LLG*PWPAHLPRPSFTPGGCTPSLG QVSWAFC
251	5748	A	257	230	358	FLIILRRSLILSPRLECNLSVPAHCSL/ RTPGFKRFSCLSLSSS
252	5749	A	258	75	188	
253	5750	A	259	340	535	FRFKALFDLFLVEIASCCVAQAGV QWCDLSSVQPPPPG\SSDSPTSASQI AGTTGALQHAWLIF
254	5751	A	260	1618	1962	DRVSLSPRLECSGTILAHCKLR/LP GFTLFSCLSLPSSWDYRRLPPRAN FFVFLV\EMGFHRVSQ/AMGLDLLT SGDPPASGLSKCWGLQGVSNLRPS QASPSFKGIKGPQTLRA
255	5752	A	261	3	395	
256	5753	A	262	152	514	LATLLGPWSCARVPSVPALLTPPPL AGPPPPQPLLQRLCSGPRLLLLSLGL SLLLLVDVCVIGSQNSQLQEELRGL RETFSNF\TASTEGPSRALSTQGRA MWGRKMEVRLEFPVWRKQQ
257	5754	A	263	138	1072	
258	5755	A	264	1	488	
259	5756	A	265	1	2105	FRAASCAPPSWRMELRSGSVGSQA VARRMDGDSRDGGGGKDATGSED YENLPTSASVSTHMTAGAMAGILE HSMYPVDSVKTRMQSLSPSSQSPV \PSIYGALKKIMRTEGFWRPLRGVN VMIMGAGPAHAMYFACYENMKRT LNDVFHHQGNSHLANGIAGSMATL LHDVVMNPAEVVKQRLQMYNSQH RSAISCIRTVWRTEGLGAFYRSYTT QLTMNIPFQSIHFITYEFLQEQVNP RTYNPHSHIISGGLAGALAAAATTP LDVCKTLLNTQENVALSLANISGRL

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						VVPMGPLLPNALERGGDGTAAHRK AVCGDIREVWELDRLLPCDIRDGAF ITMPFHICYAQNREGELLRPAELAD GAAPRELGGQGGGPEDGWGQPRW RRRQGPFGREDYENLPTSASVSTH MTAGAMAGILEHSVMYPVDSVKPR ARPRLLAALRRGRRSGEHRWLRRL LGSRGTRSLKLCTVLPWPFGLAGA AHTCAVSEGVPRRGSPHHAGAER VALARPRALGTWCVAAAPRVISGT WGRQVFSRLVAALYRFDSPWDPL SEGSCTSSPDFGSPSRREAMTFAFSF CLRGGRHMPSLREHYWARMSHER HKDWANVGGTITVLSEPNFLNNTR LARNRTPWARHDNWCHHWQHVSP ESSLDCVRLQGLPWMAAAEVEMK LPAGHMHMPVSFPNRSPLGAGCIN
260	5757	A	266	882	1299	
261	5758	A	267	1	2607	MAFAWWPCLILALLSSLAASGFPRS PFRLGvangievystkinkvtsrf AHNVVTMRAVNRADTAKEVSFDV ELPKTAFITNFTLTIDGVTYPGNVKE KEVAKKQYEKAVSQKTAGLVKA SGRKLEKFTVSVNVAAGSKVTFELT YEELLKRHKGYEMYLKVQPKQL VKHFEIEVDIFEPQGISMLDAEASFIT NDLLGSALTksfsgkkghvsfkpsl DQQRSCPTCTDSSLNGDFTITYDVN RESPGNVQIVNGYFVHFFAPQGLPV VPKNVAFVIDISGSMAGRKLEQKE ALLRILEDmqeedylnfilfsgdvst WKEHLVQATPENLQEARTFVKSM DKGMTNINDGLLRGISMLNKAREE HRIPERSTSIVIMLTDGDANVGESRP EKIQENVRNAIGGKFPLYNLGFGNN LNYNFLENMALENHGFARRIYEDS DADLQLQGFYEEVANPLLTGVEME YPENAILDLTQNTYQHFDGSEIVV AGRLVDEDMNSFKADVKGHGATN DLTFTEEVDMEKEMEKALQERDYIF GNYIERLWAYLTIEQLLEKRKNAH GEEKENLTARALDLKYPHFVTPLT SMVVTKPEDNEDERAIDKPGAS YQPPQNPYYYVDGDPHFHIIPEKD DALCFNIDEAPGTVLRLIQDAVTGL TVNGQITGDKRGSPDSKTRKTYFGK LGIANAQMDFQVEVTEKITCGTG\RA\STFSWLDTVTVTQDGLSMMINR KNMVVSFGDGVTFVVVLHQVWKK HPVHRDFLGFYVVDShrmsAQTHG LLGQFFQPFDFKVSDIRPGSDPTKPD ATLVVKNHQLIVTRGSQKDYRKDA SIGTKVVCWFVHNNGEGLIDGVHT DYIVPNLF
262	5759	A	268	1	1842	
263	5760	A	269	3	377	
264	5761	A	270	1	621	MTKRCLDHRGEWLPAGGGGGHTE GTRCLHHAPVTWVGIEVDIFEPQGI

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						SMLDAEASFITNDLLGSALTCSFSG KKPVWLRGRHTPKGNLDSEVLAGL SPCPIPLAGLTVNGQITGDKRGSPDS KTRKTYFGKLGIANAQMDFQVEVT TEKITLGTGRA\STFSWLDTVTVTQ DG*APLQGLQGGGLQEGDHS GPQP NPGALSEPELV
265	5762	A	271	3	2722	FSDGLCMVALSHLGSALQLGSLCFP RSPFRLLGKRSLPEGVANGIEVYST KINSKVTSRFAHNVVTMRAVNRAD TAKEVSFDVELPKTAFITNFTLTIDG VTYPGNVKEKEVAKKQYEKAVSQ GKTAGLVKASGRKLEKFTVSVNVA AGSKVTFELTYEELLKRHKGKYEM YLKVQPKQLVKHFEIVDIFEPQGIS MLDAEASFITNDLLGSALTCSFSGK KGHVSKPSLDQQRSCPTCTDSSLN GDFTITYDVNRESPGNVQIVNGYFV HFFAPQGLPVVPKNVAFVIDISGSM AGRKLEQTKEALLRILED MKEEDY LNFILFSGDVSTWKEHLVQATPENL QEARTFVKSMEDKGMTNINDGLLR GISMLNKAREEHRIPERSTSIVIMLT DGDANVGESRPEKIQENVRNAIGG KFPLYNLGFGNNLNYNFLENMALE NHGFARRIYEDSDADLQLQGFYEE VANPLLTGVEMEYPENAILDLTQNT YQHFYDGEIVVAGRLVDEDMNSF KADVKGHGATNDLTFTEEVD MKE MEKALQERDYIFGN YIERLWAYLTI EQLEKRKNAHGEEKENLTARALD LSLKYHFVTPLTSMVVT KPEDNEDE RAIADKPGEDAEATPVSPAMSYLTS YQPPQNPYYYVDGDPH/FSIIQIPEK DDALCFNIDEAPGTVLR LIQDAVTG LTVNGQITGDKRGSPDSKTRKTYF GKTGASPM AQMGFP GWEVTTEKIT LLEQARCRAFFSWLDTVTVTQDGH FLASSRRLSMMINRKNMVVSFGDG VTFVVVLHQ/VCWKKHPVPTVDFL GFYVVDSHRMSAQTHGLLGQFFQP FDFKVS DIRPGSDPTKPDATLVVKN HQLIVTRGSQKDYRKDASIGTKVVC WVFNHNGEGLIDGVHTDIYV PNL
266	5763	A	272	1168	1626	RAGRGGEGHKLNSYGGRRARSQG HLLSSALSPFVSAASYQPPQNPYYY VDGDPHFIIQIPEKDDALCFNIDEAP GTG\RLIQDAVTGLTVNGQITGDK RGSPDSKTRKTYFGKLGIANAQMD FQVEVTTEKITCGTG\RA\STFSWLD TVTVT
267	5764	A	273	534	690	FVIFSPCSIAMATKENMTSQRGML KSIHASKMNTL\ANRFP\VNLSIQRV NL
268	5765	A	274	3	946	TTKMAAGTSSYWEGEARRPPDLRK QARQLENELDLKLVSFSLCTSYSH SSTRDGRDRYSSDTTPLLNGSSQD RMFETMAIEIEQLLARLTGVNDKM

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						AEYTNAGVPSL\NAALMHTLQRH RDILQDYTHEFHKTKANFMAIRERE NLMGSVRKDIESYKSGSVNNRRT ELFLKEHDHLRNSDRLEETISIAMP TKENMTS\QRGMLKSIHSMNTLA\ NRFPAVNSLIQRINLRKRDSLILGG VIGICTILLLLYAFHLMGHLQGLLTA TAFTPWSGIRKHRREKLTVLIISLTS RMNARLTVMDSVTWSG
269	5766	A	275	269	476	VMAVLPSGTALKTNWEPGRDLQC NGSSLLSGAPHIVSLLGFRIRAKTG RARC\HACNPNTLGGRGGRI
270	5767	A	276	2	424	
271	5768	A	277	3	452	
272	5769	A	278	3	498	PTLLVPTDSERTHHGSCFLPDKTNV KA\AWGKVG\AHAGEYGAEALERM FLSFPTTKTYFPHFDL\SHGSAQVK GHG\KKVADALTNAVAHVDDMPN \ALSALSDLHAHKL\RVDPFNFKLPS HCLLVTL\AAHLPAEFHPLRWHALP GTSFLGFLSTVADLPNTR
273	5770	A	279	333	538	IFSSLWFFILSIKDFILFYFLFLAQSR SVT\RLCSGTISAHCNLCPLNSSDF RVLRLGNRLRLKIKK
274	5771	A	280	192	607	GRLWGCVSKKSVGCLPHPGCLWA AFLTLDACGLPSSPWMPVGSPLPHG CLWAAFLTLDACGLPSSPWMPVTW FPWGLPKLRDPKPPSNLMTRPVSEIP PVLSPSPSPTPSATRPTHFSLKGPA HRPAHVFPFNPCFVP
275	5772	A	281	17	363	GLESEFLRLGRLRPGEQDSALASAV PGSLAQTLFPFWS/PLW/TMSFPAHA APHPACCHCLSY/PVSCPVSVPSSLP LGCPQLLPSCPNSCYPSPAVPTYCP AGKEEKRRSPSCQACS
276	5773	A	285	96	389	QGPAAENMAAKMFEFIGKFGALV DAGGVVNSALYSVDAGHRAVVFD RFRGVQDIVVGKGTWLPWLQKS/ HFDQRSQPRNVLVFTGSKDLQIGNL H
277	5774	A	286	1	390	FFYFFFLERDFLFLFYIFFAVLLLLP NLECNGAISAHRLRLPG\SSDSPAS ASQVAGITGMQHHAWLSFVFLVKT GFVHLGHAGLKLPTSDDPPTAASDI VGITGMIPPVAGPKQRHFCARSVLV PFI
278	5775	A	287	16	546	QLNGRSIRHEVMSHRKFSAPRHGSL GFLPRKRSSRHRGKVKSPKDDPSK PVHLTAFLGYKAGMTHIVREVDRP GSKVKNKEVVEAVTIVETPPMVVV GIVGYVETPRGLRTFKTVFAEHISDE /CRLPLRQKKAHLMEIHVNGGTVA EKLDWARERLEQQVPVNPVFGQDE MIDVI
279	5776	A	288	1	625	CKFIRVMAHTRLRLPLRRKKAHL MEIQVNEGTVAEKLDWARERLEQQ VPVNVQVFGQDEMIDVIGVTKGKG

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						KGVTSRWHTKKLPRKTHRGLRKVA CKDGLIKNNASTDYDLSDKSINPL GGFVHYGEVTNDFVMLKGCVVGT KKRVLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEKKAFM GPLKKDRIAKEEGA
280	5777	A	289	1	903	
281	5778	A	290	38	482	
282	5779	A	291	1	1131	
283	5780	A	292	1	1329	STHASDGVMShrkfsAPRHG\SLGF LPRKRTSRHRGKVKSFPKDDPSK\IP VHLTAF\LGKAG\MT HIVREVD RP GIHRCNKKERWWRA\THCMRPPP MVVGGHLVGYVETPRGPPGPFKT CLLLEH\SDELPRGVFYKEFGH*NL KKKAFTK\YCKEIGKDEDGKKPAW KKDFQQH*KKLLAQVHPCSLAQTO\ MRLPLARQ\KAHLMENQVNGGT VA\EKL\DWAREKLE\QQ\VPVNPSV LGRMRMID\VIGGDQRAKGYKGGS PSRWHTKKAAPAKTHRG\LRKV LVLGAWHPARVAFSVG/RAAGQK GYPSTALEINK\KIYKIGPGVTL SRA GSLIKEQCLHLNYDLSDKSINPLGGF VHYGEVTNDFVMLKGCVVGTKKR VLT LRKSLLVQTKRRALEKIDLF DTTSKFGHGRFQTMEKKAFMGPL KKDRIAKEEGA
284	5781	A	293	238	326	HTYKSDTRYERHACWGALL/CNYM RQECLDSRFVDRPMPVFR LVSIG TSILYMKAFMHMPFK
285	5782	A	294	2	358	GWGMSLGGAGVEGMEVGTS DLGF FSGQRALSPWVSPVPPGLCAWRKD SPVEQKPQGPSLPLSALPYLWG/AP WPPAGPQTRGLGPFRGTGSPSPIS RAQKDSWPWPVPSTPACFSAPG
286	5783	C	295	56	175	MASXNRQQFFXNTPXKLLKSPHCNI YRLLSAKSQGKFWK*
287	5784	A	296	1178	1515	KKFMKILEHMFEGFFSFLNFFIFSG GRRSALTARGGSEVAANLGLTCNL HPPGFKRFSLRLRSSWDYRRPPR PANFVFSVETGFCYVGQAGLKLLT SSDPPASAFPKC
288	5785	A	297	136	251	IHQEKPPNIFSVKKRHYD*PGQHDP LASASQSAGITGV
289	5786	A	298	118	337	IHQEKPPNIFSVKKRHYD*PGQYQK TLLKIQILAGYSGTCLAKSOLLRR VGREVIQLALKIRAPIWKIECL
290	5787	A	299	160	437	KRDITSLGQYQGNPSLLKIQILAG YSGTCL\KSQLLRRLRHQNRNLG GRG\GSEQRSCHLHSGGHSETVSK KKKKRERQWRQIGTCMP
291	5788	A	300	61	1302	FSGSCVPPRTCGLCWISTGQSGVVS VSSTRLEESEGTQPPSPSSDTGSEGE EDDEGEEHGLGGQNEVGIIPTTLEFL ENHGKNILLSNGNRTVTRVASYNQ GIVVINQPLVPQLLVQVRIDFLNRQ

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						WTSSLVLGVITCAPERLNFASACP SNGQPGCCGAVGSSTTSQAGLSSQI CEKFGPNLDTCEGTILGLRLDSSG GLHLHVNGVDQGVAVPDVPQCH ALVDLYGQCEQVTIVNPEPGAASG KSAGTQGDMEKADMVDGIKESVC WGPPPAASPLKSCEYHALCSRFEQL LLLPEDYFMPPPKRSLCYCESCRKL RGDEAHRRRGEPPREYALPFGWCR FNLRVNPRLEAGTLTKKWHMAYH GSNVAAVRRVLDRGELGAGTASILS CRPLKGEPGVGFEEPGTNC
292	5789	A	301	1	936	
293	5790	A	302	1	1023	
294	5791	A	303	1	867	
295	5792	A	304	1	569	SGRVAMGRRRAPAGGSLGRALMR HQTQSRSHRHTDSWLHTSELNDG YDWGRLNLQSVTEQSSLDLFLATA ELAGTEFVAEKLNIKFPVPAEARTGL LSFEESQRIKKLHEENKQFLVVYRG DQTNQNTTPEELKQAEKDNFLEW RRQLVRLLEEQLILTPFERNLDFW RQLWRVIERSDIVVQIVDA
296	5793	A	306	846	1070	RVGDRSEREIVILKTNFTYFQVFPKA GCGCFSFLFSFFLSFFFLRGETESRSV ARMKCSGVISAHCNLCPLGSS
297	5794	A	307	118	340	KFQTEVSHFFLCNLCSYFIFFLL/CS FLLIHF/LYSLFFFLFCFMFFLFIMIY /LFFVLLIRYSYIKSLLFLMSCN
298	5795	A	308	42	352	TRGPRVPHSGSASSPAQKSGCTG/P* NSALARPALVSFRAMPNSRGW/PQG EQR/PGSPHRSPEGHWKRVHVPPA AQRGPGAGGCHQGTGPEAQAHAHQ VRPPAQGG
299	5796	B	309	796	3180	VAEAPGLVDVPGGHPEPQSCEKLE NTGGKIGHRKKMPYSTPAPCVSPLK LDLWLSVRERTPDGSLTLLHCATS DPQGGQALCPGGSPQHQLAGQLV VHELFSVLQEICDEVNPLLTLSQP LLLGIARNETSAGRASAEFYVQCSL TSEQVRKHLYSGGPEAHSTGIFFV ETQNVRRLPETEMWAEPCPSAKGA IILYNRVDVVLASTPMRICPPAAMPP LLPLRLCRLWPRNPPSRLLGAAAGQ RSRPSTYYELLGVHPGASTEEVKRA FFSKSKELHPDRDPGNPSLHSRFVEL SEAYRVLSREQRRSYDDQLRSGSP PKSPRTTVHDKSAHQTHSSSWTPPN AQYWSQFHSVRPQGPQLRQQQHK QNKQVLGYCLLLMLAGMGLHYIAF RKVKQMHLNFMDEKDRIITAFYNE ARARARSVPALFCSLLPVQEPHFHGP IPTTQAPVSQPDAPGHQRKVVSVID VYTRATCQPREVVVPLTVELMGTV AKQLVPSCVTVQRCGGCCPDDGLE CVPTGQHQRVMQVLGTWNGQG MQILMIRYPSSQLGEMSLEEHSQCE CRPKKKDSAVKPDSPRPLCPRCTQH

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						HQRDPDPTCRRCRCRRRSFLRCQGRG LELNPDTCRFSCSLSTAGSLLQLTDV WWLLGRLKISLVGEQAQPDHSSHE SQPRCTGRVLSICLSAVATATGAEG KRKLQIGVKRVDHCPIKSRKGDV LHMHYTGKLEDGTEFDSSLPQNQPF VFSLGTGQVIKGDQGLGMCEGE KRKLVIPSELGGATLVFEVELLKIER RTEL*
300	5797	A	310	61	674	GCGTLGPLQWDFPEPGCKGMMAPL AEGQSSAHISVWGNLRTFCVSTKKI PVDGASGSPTQVSASLTCSAQAA LDIELGTGLGNNLVSFGRDAKQAG AGLRVKNRAGSPSTRSPEGHWKR VHVPPAAQRGPGGWGLPPRAHGE AQGAHQVRPPA\QGPQPPAGSGAG RQGSRLWLVRPPVGPDPDRPAC HPSRWHPAVAA
301	5798	A	311	89	1166	
302	5799	A	312	1	2094	MGAPAVQSSSGPAGARPRKAGVER RAEPAGPGLPETTRKSPQILGFSLR AVVWDLFPQSKQIVRRKLPQIPQAV LVQADVATLTSRRVLHACGLVPLE MPCIAQYGTAPSPGPRDHLASDP LTPEFIKPTMDLASPEAAPAPTALP SFSTFMDGYTGEFDTFLYQLPGTVQ PCSSASSASSTSSSSATSPASAFKF EDFQVYGCYPGPLSGPVDEALSSSG SDYYGSPCSAPSPSTPSFQPPQLSPW DGSFGHFSPSQTYEGLRAWTEQLPK ASGPPQPPAFFSPPTGLSPSLAQ PLKLFPSQATHQLGEGESYSMTAF PGLAPTSPLHLEGSGILDTPVTSTKAR SGAPGG\SEGRCAVCGENASCQHY GVRTCEGCKGFFKRTVQKNKYIC LANKDCPVDKRRRNRCQFCRFQKC LAVGMVKEVVRTDSLKGRRGRLPS KPKQPPDASPANLLTSLVRAHLDSG PSTAKLDYSKFQELVLPFGKEDAG DVQQFYDLLSGSLEVIRKWAEEKVP GFAELSPADQDLLESFALELFILRL AYRSKPGEGKLIFCSGLVLHRLQCA RGFGDWIDSILAFSRSLHSLLDVDP AFACLSALVLITDRHGLQEP RRVEE LQNRASCLKEHVA AVAGEPQPASC LSRLLGKLPRLTLCTQGLQRIFYLK LEDLVPPPIIDKIFMDTLFP
303	5800	A	313	858	1143	QLVPCCPPTQRTVQKNKYICLAN KDCPVDKRRRNRCQFCRFQKCLAV GMVKEGVWL/RVRPTGARVGLSGV RPPGPPGFCPGGPTGGHVLFPPHL
304	5801	A	314	190	330	ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKKVIFHTNKNQKRIWT
305	5802	A	315	190	324	ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKKVIFHTNKNQKRI
306	5803	A	316	85	310	CAWHVNILIGKRLNTFPYRSGTRQG CMLLPFLFNTILKDLVTALKNQDIK GKQIK/EEIKLSLFTEMITRVDKNQ

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307	5804	A	317	33	494	
308	5805	A	318	1	612	
309	5806	A	319	113	551	LLWRESAVTALWGKVNVDDEVGGK ALGRLLVVYPWTQRFVFESFGDLST PDVVMGNPKVKAHSKKVLRGAFS GGLAHLADNLKGTFAHTEVSLHCD KLHVGSWRTFRLLGNVLVCCCWA HSLLGKEFQPHQLQACLIKKIGWLG VG
310	5807	A	320	221	376	DRVSIPRLESSGAILAHCNFRL/SGFK QFSCLSLPSSCDYRCVLP RRALCSSC
311	5808	A	321	32	452	
312	5809	A	322	72	570	SRRAWVSFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFDD SFG\NLTCASAIMGHPKV\HVGKK VLTSLGDAIEHLDDLKGTFAQLSEL HCDKLHVDPENLKLGNVLETALAI /HFSKQFTPEVQASWQKMGD\GV ASALCFTKHLDFMCMMQSFQR
313	5810	A	323	35	359	
314	5811	B	324	102	431	MIYRDLISHDEMFSDIYKIREIADGL CLEVEGKMVSRTTEGNIDDSLIGGNA SAEGPEGEGTESTVITGV\DIVMNH LQETSFTKEAYKKYIKDYMKSIKGL LEEQRPDR*
315	5812	A	325	132	708	RRRRLPSVAIMIYRDLISHDEMFSDI YKIREIADGL\CLEV\EGKMVSRTTEG NIDDSLIGG\N\SAEGPEG\EGTRST\ VITGV\DIVMNHHLAGNKFSQKEAY KKYIK\DYIEIQFKGETLKEPEDQKR VKPFYDRGLQE\QFKHILG*FSKTYQ FFIG\ENMNP\DG\MVALLDYREGWV *PHI*FSFKDG\LEMEKC
316	5813	A	326	1	5796	
317	5814	A	327	3	467	
318	5815	A	328	73	1593	
319	5816	A	329	57	1358	RRKVAMDLIPNLAVETWLLAVSL VLLYLYGTRTHGLFKRLGIPGPTPLP LLGNVLSYRQGLWKFDTECYKKYG KMWGTSSSLFGPHYPSSEALGGSC VRLLLCVTP**TRT*GCCVSYN*GT YEGQLPVLAITDPDVIRTVLVKECY SVFTNRRICATTSTIKMQTHSVTMW LPPAVLQSQHGVCLFL*QSLGPVGF MKS AISLAEDDEWKIRSLSPFTTS GKLKEKRHHKIH\KMSLTAPCWRK PYPSGT*VCTFNYSIFGAYSMDVITG TSFGVNIDSLNNPQDPFVESTKKFL KFGFLDPLFLSIHLPFLTPVFEALNV SLFPKDTINFLSKSVNRMKKSRLND KQKHLRDLQLMIDSQNSKETESHK ALSDLELAAQSIIFIFAGYETTSSVLS FTLYELATHPDVQQLQKEIDAVLP NKVRG
320	5817	A	330	870	1150	HRLDFLQLMIDSQNSKETESHKALS DLELAAQSIIFIFAGYETTSSVLSFTL YGTGPLHPDVQAGNCKREIDAVLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NK\APPTYGAVGTDGSYL
321	5818	A	331	144	377	RRCCKGISTSCHCIITNEIFIFIFEAE SHSVA\RLCSCGAVLAHCKLCLPGL RHCPASATREAEAREWLETRSRL Q
322	5819	A	332	3	323	DRVSLSLSPRLECNGMISTHCNLHF PGSSDSPDTP/SQVAEITGVHHHAQL IFVFLVETRFHHIGQAGLELLTSSDL PTSASPSAGIIGVRHCAWARITFQRT KCFSI
323	5820	A	333	187	450	NYVSQKRKKLNSPINYKEIEFIVLK LPK\KKPLGPNGF\AEFYQTFKKGM \TPILDHLLQKIDVTLPLYKYKTDFT LTLKPKTIQKTRA
324	5821	C	334	122	292	MMCSMTLSFIFSMRKLCSIRASS WNSPWFRVSGCPSFTEYWWKVL MVYMLRSS*
325	5822	A	335	295	931	VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTCGMPQHVTQ*RPINTS HQYSVKLGHPHPETRGFKELVR\ KDLQNFLKKENKNEKVEIHIMEDL DTNADKQLSFR/EEFIMLMGEA*PG AFPRRKIARGLTEGPGVHHHKPGPG GGAPPKDHSGPRFTVGHGHGHSTW WPRPQATNHGGQATLPLPNHRPRG LLCQTVLAVGLGAGAK
326	5823	A	336	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQ\RFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTF\AQ\SELHCDKLHVD PENFKLLGNV\LVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
327	5824	A	337	3	556	HSLFGTSEVINKLRSPDA\MGHFTEE DKATITSLWGKVNVE\ DAGGETLGR LLVVYPWTQ\RFDFSFGNLSSASAIH GQPPKSRHMGKKVLTSLGDAIKHL\ DDLKGHLLPKPEVNCTCDKAALLD PEELSSFLGEMLLG/VPVFGQSHFRA KEFHPWRLQGFPGISRRWQKMVT\ GVASALVPSRYH
328	5825	A	338	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQ\RFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTF\AQ\SELHCDKLHVD PENFKLLGNV\LVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
329	5826	A	339	38	547	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF DFSFGNLSSA\SAIMGNPKVKAHGK KVLTSLGRCHKSTWDDLKG\TFAQ A*SE\H\CDK\LVH\DPGGTFKLLGK MLLG*PV\LAIPFSAKEFHP*RLQAS WQKQKMAEDGDLELASALVPSRY H
330	5827	A	340	168	330	SSLGLDLVCGDMAKCTKKVRIISKY GTRYGASLRKMVKRIAITQHTKYI CSSRA

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331	5828	A	341	2	355	ARATMVLSPADMTNVKAAWGVKVG AHAGEYGAEALERMFLGLLTTKTY FSHFDLSHGSAQVKGHCMMKVVDAL TNAGINVDNLPNALDTLIDLTPIF CRSLLNFYLISNSLFIIISVH
332	5829	A	342	176	410	AGLLPDP/TITARMNVGVHSEVNP NTRVMNSRGIWLAYIILVGLLHMV LLSIPFFSIPGGWTLTNVIHNLATYV FLHT
333	5830	A	343	469	708	
334	5831	A	344	49	351	ATSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLDGYPWTQR GFDSFGNLNYTSDVMVDPKFMGHG MKVLTYLGDALCDLDDTNGNFAH VSTVMC
335	5832	A	345	665	921	AKKKEKKTGALSARRQPNPTQNT PHPHPPNPPTHHPPPSPPTPHSPPP FLILQKLLIAVTIFDPTYCVISYSW VIMTFNKL
336	5833	A	346	2	341	HEEGFVNPGARFCLPEAAAVRRPPG EATVIMSDQEAKPSTEDLGDKNEGE SIKLP/VLAHVRTETHFNKTTHTLT SLPQSYCQIAVPLNSLTLLFARPTT AAHHTPELPMQ
337	5834	A	347	209	397	VSLWQAMRLPKNTPEEKDRRTAA LQEGLRRPVSVPLTLAENGAFLLWS DMENLSDIYWYASE
338	5835	A	348	87	356	IHFYRVKIFFHILCFYIFIQICHYSFIF YFFCRQG/HLSRLEGSGAILAHCNL CLLGSNDPPTSASRVAGTAGTHHH AWLIFVFFIETGY
339	5836	A	349	3	204	KMEARKQRESMRGREAREKEKG YERSSEGERVVERNIGHKRRRDAK REARWEKIHGAKEARRNRYK
340	5837	A	350	3	341	HERHEIPIKMSHRGPWLMVDFLSY KLSQNGYSWSQFTDVEENTTEAPE RTELDRTPPIAINGNRSWHLADSPA VNGTTGHSSSDARDVIPMAAVQH ALWEASDEFELRHR
341	5838	A	351	67	541	EAPARRALCGRVPSEAQRDGHQAP LLSRRRL*AFFVADGIFKAELNEFL TRELAEDGYSGVEVRVTPTRTEIIL ATRTQNVLGEGRRRIRELTAVVQK RFGFPEGSELYAEKVATRGLCAIA QAESLRYKLLGGLAVRRCAQNQSE DHACLGTNW
342	5839	A	352	3	495	
343	5840	A	353	1	459	EDGYSGVEVRVTPTRTEIILATRTQ NVLGEGRRRIRELTAVVQKRFGEPE GSVELYAEKVATRGLCAIAQAESLR YKLLGGLAVRRACYGVLVIMESA AKGCEGVVSGKLRGQRANS/MKFG KAGGFPGLVNYCALVGPLCAYT GVVGH
344	5841	A	354	1	885	SWSTHASVSAERGGKMAVQISKK GEFVADGIFKAELNEFLTPQLAED GYSGVEVRVTPTRTEIILATRTQ

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						VLGEKGR\RIRELTAV\VQKRFQFP RRASVELYA\EKVGHYRSCVAIAQG RSLCVYKLLRKGFACAGGPCYGV AAGSIMEKWGPKAFCVCWWSGKT SEEQRA*IP*SFVEWP*WIHSGDPV* LTNVDTAVR\HVLLRQGV\LG\IKVK IMLALGTQLGKIGPKKPLPDHVSIV\ EPKDEIL\PTTPIS\EQKGGKPV TALH GPTRSPQPNRVSLAAVFWSLDVAL
345	5842	A	355	1	284	SLFLYTANSRLGPLVSPAFMTHRISC NVTKGLPHDHYACLQEIKSSYKFYR YFETQQQSVQPCLSRTHQKSRLN NVYSAVRRLQVHMKALLNE*VSPA FMPHRJSCNVTKGLPHDHYACLQEI KSSYKFYRYFETQQQSVQPCLSRTH QKSRLNNVYSAVRRLQVHMKAL LNE
346	5843	A	356	1	1404	
347	5844	A	357	1	771	
348	5845	A	358	3	913	
349	5846	C	359	461	667	MRMTMMMMMIHLKLILMMMM KSMEPLLEGAYDPADYEHLPASAEI KELFYISRYTPQLIDLGTN*
350	5847	A	360	76	158	
351	5848	A	361	1	2313	
352	5849	A	362	788	926	PSPPELPEGDFEGFFPQKLQ*SCLPTL QKKKNNNNNNNNNNNNNNNEK
353	5850	A	363	168	447	TGTPGYACNSQNLGGPTGGISRPV *NQPGQKGETPGFLKIPKLTRGGGR ALQFQVLGRVRPENPLNLGGQNFN* PKLCPCTSTWKGIRLPF
354	5851	A	364	637	1258	VLFLRKPTAACLGHALSHRNLGPS AANSPSVLGKPAPSWSHVPATVLP GQGGTPCDMRVSGTVRVGSTVMST TSIPALPHLGSTSVGPPQPGHEKQ MITWCKDRLQLTHSDEFGVGVFFQ TTMYILASKMCTGAQRSGCWALRV PQEDGKNQLIRFYCMYVCIFYFETES HSVVQAGVQWRDLDSL*PPSPEFKR ISCLSFLSSW
355	5852	A	365	217	481	KCSFQM*YRLKNNNNHSHPPFSISL FLISSNIQNNFGSRYN*NHLKMYKT EAQRLTCSMLHKSNNPHLFILNRMFL TRNLLGPHSLVP
356	5853	A	366	1	245	PVPRGGSKLLTHHLAPLTLPKAGDS GVNPRVPPFFLSPPAIWGPCKILGL AKTPVPRFPLGKKFFPSP*FPFFPK NKTL
357	5854	A	367	145	196	
358	5855	A	368	120	173	
359	5856	A	369	138	321	NECLLGSSFFSV/PNSSLLK*KS*ASA VAHTCNPSTLGG*GGWIT*GQEFET SLANMVKPLY
360	5857	A	370	1536	1629	KSQKACNPSTLGG*GGWIT*AQEFT TSLANT
361	5858	A	371	11498	11651	LKNNFKKCTMWA\GMVADTCNPST LGGRGGWIT*GQGFKTSANMMKP

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						CLY
362	5859	A	372	15	272	RLKAATLKMPGSAAKGSEL SERIES FVETLKRCGVPRSSSED TARVTLLM MRWIFNDHRWIPP*ELVDPYIYFPW PCSTLSCWDWS
363	5860	A	373	433	612	QAPLQKPTVRR*K*VREIRGRD*VE E*IEEWYR*RSGRETRRGRESGR*ER GEVDREERKRE*GSRVRRGRERRG RERRGRERGGEESQEGKREKRE RRGREKRGREERKRAKEVFKDGER PRAKVGIVLKRQ
364	5861	A	374	785	1178	ALGCPGCPLLAVSGKDHNSSTQPAT HNSRDRRERRKEERERRGRERGEE IEGKR*RSGRETRRGRESGR*ERGE VDREERKRE*GSRVRRGRERRGRE RRGRERGGEERQEGKREKRRERR GREKRG
365	5862	A	375	1969	2208	GANPIHDLPHDLTTSRPHIFIIFFE MESRSVTQAGVQWHDLGSLKSPPT GLKLFSLSLPSG*NYRCTPSHLANF CIF
366	5863	A	377	171	442	GKKWSFSLQNWVQAY*LSCNRY CSLKDHDFTPSDGGPDIFLHICDVE GEYVPVEGDEVYKMC SIPPKN EKL QAVEVGITHLGPQTQH
367	5864	A	378	3	775	SVHSSAHASERVAEQNGLQGQAMS SVPSPPPQPPTHQA\GVGLLDTPRSR ERSPSPLRGVVPSPLPTRR\TRTFSA TVRASQGPVYKGVCKCFCRSKGH GFITPQLMAAPDIFLHISDVEGEYVP VEGDEVYKMC SIPPKN EKLQA VEVVITHLAP\GTKHETWSGHVISF LGDGGSTPCPVLVGRLCGEEAADT GDDILPHETGLQRGNGPSHVSPGGK GYGGAGVGCGVFP AISTAYGPLQQ PLHHLKSIKSI
368	5865	A	379	7	316	APSPDAMGHFTEEDKATITSLRGKE NVEDAGG*TLGRLLDDYPWTHRIL DS*GKLLSDYAIMGKQDDKEHA EK ELPSLEDALAHWADASASGHWPSD VPCAYR
369	5866	A	380	61	304	ARTWNSVRMASSGMTRRDPLANK VALVTASTDGIGFAIARRLAQDGAH VVVSSRKSQNVQV*VST*LASV*L IYLMCVLP
370	5867	A	381	2	281	
371	5868	A	382	2	558	HSLLERLRLSISFLVQTPIGHSTEED\ KATITSLWGKGEMWKNAGRKKPL GRPPGLSLPQWTPRGSFEQALGNL VSSCPPAPSMGKPPQKSKGTMAKK GA*PSLGKMPIKAPLDD\KGT\FAP A*SELHC DKLH/VLDPENFKLLGN VLVTVLAIHFGKEFTPEVQASWQK MVTAVASALSSRYH
372	5869	A	383	3	368	EFFCGLCVKSEISLHLFCLANFFPSL KPQITSSGEMVPLLPCQS*EWRRKD ESSTLPPPPSSGAECPTWLRPSPSTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PCPCLPHPYVQGSCLCETQSHLTVNP ASSYRISPPPLISSRTRY
373	5870	A	384	179	455	EFGWGGGKSLGLPRAGLD*IGGSLG FIPLLSTPVSHSHAFSVGAILLIFLL ESLAFQWLLLLSSSHFLYFSLFFRQ SSFCFLTEEQKKKK
374	5871	C	385	22	423	MKAAVLTALXFLTGSGARHFWQ QDEPPQSPWDRVKLHELQEKLSPLG XEMRDXRAPMWTXXNASGPLQRR VRXLWPRALRLSRRTAAQTWPSTT XRPPSILSTFSEKQARVRGTSKA CXPLLESXKGXVS*
375	5872	A	386	1	671	SGRIQEVPHGPFMRKAAVLTALV FLTGSGARHFWQDEPPQSPWDRV KDLATVYVDGLTEDSGKDSVTSTFS KLRE*LGPVTQEFWDNLIEKETEG RQEMSKDLAEEVKAKVQPYLDDF QKKWQEEMELYRQKVEPLRAELQE GARQKLHELQEKLSPLGEEMRDRA RAHVDALRTHLAPYSDELQRRLAA RLEALKENG GARLA EYHAKATEHL STLSEK
376	5873	A	388	24	499	HTDTYPHPLIARPQGFPELKNDF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFSTCRSPEACCEL TLQVRGPQKRERFMPVCHLATCL LFPTPLRRFPLDAAIIFSDILVVPQA LGMEVTMVPKGKPSFPESLREEQDL KRLLDPEMV
377	5874	A	389	109	750	HTDTYPHPLIARPQGFPELKNDF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFSTCRSPEACCEL TLQPLRRFPLDAAIIFSDILVVPQAL GMEVTMVPKGKPSFPPELREEQDLE RLRDPEVVASELGYVFQAITLTRQR LAGRVPLIGFAGAPWTLMTYMGFI LTWTQNMWAPLWMLCINTHVCFD RTECIPLPSSTINTDD
378	5875	A	390	1	295	PQTQREPAMVLSPADKTNVKA GKVG AHAGEYGAELERMILFFT TRTYFPRDL SLLSDPV*FPVITEAF ARTYSGVIADLLSNTPHMIQMAAS
379	5876	A	391	112	310	
380	5877	A	392	49	615	RAQRGCSQSCGKMNARGLGSELKD \SFPVTELSASGPLES\HDLRLKGF\ S CVKNELLPSHPLES\EKNFQLQPR LK*NFSTLEETFQGSILLPLKITGGDF QGQCRQV\QRLPFSFQAPNLSTGMV FEGGNDETIWDLEDIL**SHHKSEV HGESHTFDGWEYKPWVYCNS SAGS WKPRAAILFIVFVL
381	5878	A	393	167	1955	LCPHVVEGMWEVPVISLMRALIPF MRASPSRVRRRAATPAAVTCQLSNW SEWTD CFP CQDKK/YTVMTLSAIQT IQGNILSETLIMSAMAGFPNKYRHR SLLQPNKFGGTICSGDIWDQASCSS TTCVRQAQCGQDFQCKETGRCLKR

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						HLVCNGDQDCLDGSDEDDCEDVR AIDEDCSQYEPGPSQKAALGYNILT QEDASQSVYDASYGGQCETVYNG EWRELRYDSTCERLYYGDEKEYFR KPYNFLKYHFEALADTGISSEFYDN ANDLLSKVKKDKSDSFGVTIGIPA GSPLLKFIFTRIFTKVQTAHFKMRK DDIMLDEGMLQSLMELPDQYNYG MYAKFINDYGTHYITSGSMGGIY ILVIDKAKMESLGITSRDITTCFGGS LGIQYEDKINVGGGLSGDHCKKFG RARKAMAVEDIISRVRGGSSGWSG GLAQRNSTITYRSWGRSLKYNPVI DFEMQPIHEVLRHTSLGPLEAKRQN LRRALDQYLMEFNACRCGPCFNNG VPIEGTSCRCQCRLGSLGAACEQT QTE/G*GAKADGSWSCWSSWSVCR AGIQERRRECDNPAPQNGGASCPGR KVQTQAC
382	5879	A	394	94	276	
383	5880	A	395	25	1876	ILQGPACTHLLLQFPEYIALFLQGN VRGLLAEMFAVVFILSLMT*QPGV TAQEKGNQRRPATPAAVTCQLS NWSEWTD CFPCHDKKYRHRNLLQ NKFGGTICSGDIWDQASCSSSTTCV RQAQCGQDFQCKETGRCLKRHLVC NGDQDCLDGSDEDDCEDVRAIDED CSQYEPGPSQKAALGYNILTQEDA QSVYDASYGGQCETVYNGEWRE LRYDSTCERLYYGDEKEYFRKPYN FLKYHFEALADTGISSEFYDNANDL LSKVKKDKSDSFGVTIGIPAGSPLL VGVGVSQSQTSLNELNKYNEKK FIFTRIFTKVQTAHFKMRKDDIML EGMLQSLMELPDQYNYGMYAKFIN DYGTHYITSGSMGGIYIYILVIDKA KMESLGITSRDITTCFGGSLGIQYED KINVGGGLSGDHCKKFGGKTERA RKAMAVEDIISRVRGGSSGWSGGL AQRNSTITYRSWGRSLKYNPVIDF EMQPIHEVLRHTSLGPLEAKRQNL RALDQYLMEFNACRCGPCFNNGVP ILEGTSCRCQCRLGSLGAACEQTQT EGAKADGSWSCWSSWSVCRAQIE RRRECDNPAPQNGGASCPGRKVQT QAC
384	5881	A	396	2	307	QAGV**WDLGSLQLPPLRLKQFS/CI LNPGNLSKEF*STKETKQNFVGHQ SQTSKFAISLIQHINMRSGTKTFM MV*GNKQRSKFPIWTFKIFPDMLPS
385	5882	A	397	374	665	GAQGLSLSPRLECNGAILAHCNLC PGSSNSPGSAS*VAGTIGMHHLARL MFVFLVESGFHHVQGAGLELLTSSD PPASASQSAGIRGISRRAGLDF
386	5883	A	398	202	425	RLGGVEEGWGKGRSLVLHLKCGV QILLMTLTGKTISL*LDPSDTIVNVK ALIHDIERIPDHEMLIFACKQLE
387	5884	A	399	202	418	RLGGVEEGWGKGRSLRLNLRGL

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						HIYMITILDNLISLEDMPNPTI*NVK AMILSNNGIHSHE*RLIFEGMR
388	5885	A	400	144	433	
389	5886	A	401	1	3135	
390	5887	A	402	79	929	PVAQGMLRWTVHLEGGPRRVNHA AVAVGHRVYSFGGYCSGEDYETLR QIDVHIFNAVSLRWTKLPPVAPGEV CHPWASSVVPYMRVGHSSVPSDD TVLLWGGRNDTEGPCNVLYAFDV NTHKWFTPRVSGTVPSARDGHSAC VLRKIMYILGGYEQQADWFSNDIH KL
391	5888	A	403	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGPNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMYTGVASALSSRYH
392	5889	A	404	50	562	APSPDAMGVHFTTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIEHLDDLKGTFAQLSE LHCDKLHVDPENLKLGNVLETAL AIHFGAKILPFKGRLPGRRWQKMY TGVASALCFTKHLDFMCMMSQSFQR
393	5890	A	405	228	420	TPEADALYSHNPGGNLDRHTASKPS ALLQPGPAWQRGSACSLQILPESRV GFPTGPP*ARKVSI
394	5891	A	406	653	940	KWKKINVFFETGSRSAQAARVQWC HLGSLQP*HPRLEPPASASQTAGT TGMHHHAWLS*VSFVKMRLGHIIQ DIRRLMDSINMPHYMHQAPPMCQ
395	5892	A	407	795	1802	CRLHTQQIQRLETASGFLRMKGKNS VQLQEGWERFQDPGNHITRPRFLP SDPHPTLMCLQGPPTGKGPGKSRAT GTAAEGA\DETSYF*NAFQLPLYK LIKIIKKKEK*K*KSCT*KRVRWSKL CPRDWAAARTEAPPTGLESRQVC Q\DPPLPTAACIPP/CWLGSF*KRM ND*QTKITPWG*FPHHPRL/PPSSPS NSSSPSPSSSKLSSSSMASPVKYST ARGTIRSRKKCPISKSEANVNSESSS SDSPSPDATDLPFNGLKKLKKDSL TCFVIVLTVPRPLCFCFFLMVLTVTF FPFFQSIVHPSQSTISGPSKEKGSALS GSDFIL
396	5893	A	408	342	515	
397	5894	A	409	3	333	AAWLLGAATGLTRGPA/PRPSPPR ALTPA*GPLAAFTAARSDAGIRAMC SEILRQEVLDKGFHRDLLIKVKFGE SIEDLHTCRLLIKQDIPAGLYVDPYE LASLRERNITEEKTSWRRLWLPSDN
398	5895	A	410	877	1206	QGGQSSLGTAGPEPDSPGDPGSAAE QSAREGRRAHGSNV*PPPARSTD LG PAPGPHIPATRREAREPGPLPRSGPP SPAPLTGVRARGGEGRGGPAREPG RRPEEQPGGR

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399	5896	A	411	238	326	LHSGPGVVVT*YRKMTSLWAGCSR HACNPSTLGSRGIQITRGQEF
400	5897	C	412	194	474	MWKMHMCMCERHGSTVLATYLRQQ MPQHFFSHSSQYIHLANENYLGSLP FLLKHKFFIKCCIPASSNAHADFR ARRKETAAPQPCRPAAR*
401	5898	A	413	1	88	
402	5899	A	414	65	191	
403	5900	A	415	131	363	EVKMAGFLDNFRWPECECIDWSE RNVVASVVAGILVSEKDWLVTCPY LLPWKLMPVPLN*EWLSRTIYFTAV LYR
404	5901	A	416	146	567	EVKMAGFLDNFRWPECECIDWSE RNAVASVVAGILFFTGWIMIDAA VVYPKPEQLNHAFTCGVFSTLAF FMINAVSKLLQVRGDSYGKAAVL GRTGARVWAFHWGFMLMFGSLMA SMWILFGAYVTPKYLFIIRD
405	5902	A	417	17	369	KLTFGLGLGVPPKPVIPFKNRPIGP PWVPPVIPAPLEAQVGGSPSPEIGAP PGYKGEPPFFLKPKQKFTRCQGPPL SQVPWSFRPKKGLNPGSRAFH*LR RPCSTWATKPNFVS
406	5903	A	418	553	673	RRIEKGQVQWLTPVISVLWEAAAG D*LEASSRLYATPPD
407	5904	A	419	2	427	HVIKVLHDDWIFTPIQGP*SM/CSS KNESRHIGS*RVTG*LLEVLSLL*S FGRLNALNMKSL/TSEVQEE*RKLN KTHRVQRDFDKDRKLA VGQSESPG HPTSEKPPSTSSSAGCMCSLHISRG FQLRRKRQLNGKCCPIQ
408	5905	A	420	82	371	RRHSVACTPHPSQVLKSL*SFGRL NALNMKSLKAKFRKSDVN*IKLIEC KEPSTEN*LLARVKVLVIRLPRNLL QPHRLAVCYAA YISPLAFS
409	5906	A	421	103	430	SFGRNALNMKSLKAKFRKSDTNE WNKNDDRLLQAVENGDAEKVASL LGKKGASATKHDSEGKTAFHLAAA KGHVECLRMITHGVDVTAQDTTG VSHALHLAAKNSHHE
410	5907	A	422	87	283	SFGRNALNMKSLKAKFMKSDTNE WNKNDDRLLQAV*NGDAEKVASL LGKKGASATKHDSEGKTA
411	5908	A	423	2	424	
412	5909	B	424	108	395	VGAHAGEYGAEALERMFLSFPTTR TYFPHFDLSHGFCPLRGHGKEGGR RADQRRGQRGTTCPTSLALSDLHA HKLSGGTRFNFQAPKATGLLG*
413	5910	A	425	2	334	
414	5911	A	426	236	649	
415	5912	A	427	76	322	TNSPCYVVFNSFFS*IIENKKQENK VQQAGIRLYGALLTKCPRLYSKQIH PALLRRLQHGVLDLVYFEDILDKLIG HGPGSV
416	5913	A	428	988	1223	RGERADHLRSGIRDQPGQHGETPSL LITQKLAGLGSACL*SQLLGRLRQE NCLNAGVGGCSEP*SRHCTPAWAT

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						ERDS
417	5914	A	429	57	349	ERESPFAPRLEGKGANLG*WKAPLP GLSPFSGLSLPRTGNYGPPQPPVNF F*F*GETGFPRLTREGLNLRPSENPA LVKPNKVPKHHGVEKPGGK
418	5915	A	430	291	594	SWLFRLGAMAHAYNNSSLGGQSGR IVWAQEFNTQPGQHRGDPGLYK*FF FLISQCDGMHLWSQLLRRLRQKDH LNPRAQGCSEL*LHCCAPAWVTEQ DLSQ
419	5916	A	431	27	361	RGPTVTPQIMAVEDVASTGADPCD LSDGLLHEILTSPLILLGLCIFLL YLIVR*DQPAANGSDDDD*PSPLPR LKRRDFTPDDLRRFYSVQDPRILMD FNCKVFDVTK
420	5917	A	432	196	555	SPSMNPRKKVDLKLIIVGAIGVGKT SLLHQYVHKTFYEEYQTLGASILS KN*SYWVDITLKVTDLGDGTGGQER FRSMVSTFYKGS DGCILTFDVTDL SFEALEFWPGGGLAQNGPNEA
421	5918	A	433	1	685	EIKYHSLPRLECRGEISAH*NLCLPG SSDSPATAS*VAGITGMRHYAQLIFL FLVET*FHHVGQGSRTPDNDPPA SASQGAGDYRRD
422	5919	A	434	56	335	KCSPKILLTSESTSSNPCLIDTNASDF HFLSQVLE*VVSPKGSKEALCCILR HLGYETRESCPWCPSPQFRYITFDMG SYVGPVLHHSCQALS
423	5920	C	435	24	332	MKGRTFISLLFLFSSAYS RGVFRRD AHKSEVAHRFNDLGEENFRALVLIA FAQYLQQRPFEDHVTYYAQLQLFV KPMVKWLTA VQNKNLREMNASCN TXMTTH*
424	5921	A	436	130	599	
425	5922	A	437	1	404	
426	5923	A	438	3	647	FSLLSTPHAFGTMKWVTFISLLFLFS SAYS RGVFRRDAHKSEVAHRFKDL GEENFKALVLIAFAQYLQQCPFEDH VKLVNEVTEFAKTCVADESAENC KSLHTLFGDKLCTVATLRETYGEM ADCFLQHKDDNPRLVRPEVDV MCTAFHDNEETFLKKYLYEIARRHP YFYAPELLFFAKRYKAAFTCCQA ADKAACLLPKLDEL RDEG
427	5924	A	439	323	899	MMRVFLSEKALSSSYLEMYLSTPH AFGTMKWVTFISLLFLFSSAYS RGV FRRDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKL VNE AKQEPERNECFLQHKDDNPRL VRPEVDVMCTAFHDNEETFLKKYL YEIARRHPYFYAPELLFFAKRYKAA FTECCQAADKAACLLPKLDEL R
428	5925	A	440	1	1206	SFSLSTPHAFGTMKWVTFISLLFLF SSAYS RGVFRRDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQQCPFED HVKL VNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE

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						MADCCAKQEPGRNECFLOHKDDNP NLPRLVRPEVDMCTAFHDNEETF LKKYLVEIARRHPYFYAPELLFFAK RYKAAFTECCQAADKAACLLPKLD ELRDEGKASSAKQRLKCASLQK/PR NLGKVGSKCKHPEAKRMPCAEDY LSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRRPCFSALEVDETYVPKE FNAETFTFHADICTLSEKERQIKKQT ALVELVKHKPKATKEQLKAVMDD FAAFVEKCKKADDKETCFAEEGKK LVAASQAALGL
429	5926	A	441	28	1587	
430	5927	A	442	1	1652	GTMKWVTFISLLFLFSSAYSRGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPLEDHVKLVNKDD NPNLPRLVRPEVDMCTAFHDNEE TFLKKYLVEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK LDELDEGKASSAKQRLKCASLQK FGERAFKAWAVARLSQRFPAEFA EVSKLVTDLT KVHTECCHGDLLEC ADDRADLAKYICENQDSISSKLKEC CEKPLLEKSHCIAEVENDEMPADLP SLAADFVESKDVCKNYAEAKDVFL GMFLYEYARRHPDYSVLLRLAK TYETTLEKCCAAADPHECYAKVFD EFKPLVEEPQNLKQNCLEFEQLGE YKFQNALLVRYTKKVPQVSTPTLV EVSRLGKVGSKCKHPEAKRMP AEDYLSVVLNQLCVLHEKTPVSDR VTCCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKKADDKETCFAEE GKKLVAAASQAALGL
431	5928	A	443	1	1515	MKWVTFISLLFLFSSAYSRGVFRD AHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKLNEVTEFA KTCVADESAENCDSLHTLFGDKL CTVATLRETYGEMADCCAKQEPER NECFLOHKDDNP NLPRLVRPEVDV MC/H/YPNAAQNPW* TGDHAFQLW KSMKH TFPKSLMLKHSPSMQIYAH FLRRRDKSRNKLHLLSL*NTSPRQQ KSN*KLLWMISQLL*RSAARLTIRRP ALPRRVKNLLLVKLP*AYSRGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKLNEVTE FAKTCVADESAENCDSLHTLFGD KLCTVATLRETYGEMADCCAKQEP ERNECFLOHKDDNP NLPRLVRPEV DVMCTTKCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSE KERQIKKQTALVELVKHKPKATKE QLKAVMDDFAAFVEKCKKADDKE TCFAEEGKKLVAAASQAALGLTCEA CQEPGGLVVPPTDAPVSPPTLYVED

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						ISEPPLHDFYCSRLDLVFLLDGSSR LSEAEFEVLKAFVVDMMERLRISQK WVRVAVVEYHDGSHAYIGLKDRK RPSELRRIASQVKYAGSQVASTSEV LKYTLFQIFSKIDRPEASRIALLMA SQEPQRMSRNFVRYVQGLKKKKVI VIPVGIGPHANLKQIRLIEKQAPENK AFVLSSVDELEQQRDEIVSYLCDLA PEAPPPTLPPDMAQV
432	5929	A	444	2	1848	RFSLLSTPHAFGTMKWVTFISLLFLF SSAYSRGVFRDDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQCCPFED HVKLVNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE MADCCAKQEPERNECFLOHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELFFAK RYKAAFT\CCQAADKAACLLPKL DELRE*LNQKHVLLMSQLKIVTNH FIPFLETNYAQLQLFVKPMVKWLT VQNKNLREMNASCNTKMTTQTSPD W*DQRLM*CALLFMTMKRHF*KNT YMKLPEDILTFMPRNSFSLKGIKLL LQNVAKLLIKLPACCPKLDEL RDEG KASSAKQRLKASLQKFGERAFAK WAVARLSQRFPAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECKEPLLEKS HCIAEVENDEMPADLPSLAADFVES KDVCKNYAEAKDVFLGMFLYEYA RRHPDYSVLLLLRLAKTYETTLEKC CAAADPHECYAKVFDEFKPLVEEP QNLIKQNCLEFELGEYKFQNALLV RYTKKVPQVSTPTLVEVSRNLGKLP SC**SC\CLLPKLDEL RDEGKASSAK QRLKASLQKFGERAFAWAVARL SQRFPAEFAEVSKLVTDLTKVHTE CCHGDLLECADDRADLAKYICENQ DSISSKLKECKEPLLEKSHCIAEVE NDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VLLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKLPSC
433	5930	A	445	1	3780	MKWVTFISLLFLFSSAYSRGVFRDD AHKSEVAHRFKDLGEENFKALVLIA FAQYLQCCPFEDHVKLVNEVTEFA KTCVADESAENC DKSLHTLFGDKL CTVATLRETYGEMADCCAKQEPER NECFLOH/KCFLQHKDDNP NLPRLV RPEVDVMCTAFHDNEETF LKKYLY EIARRHPYFYAPELFFAKRYKAAF TECCQAADKAACLLPKLDEL RDE\ GKASSAKQRLKASLQKFGERAFAK AWAVARLSQRFPAEFAEVSKLVTD DLTKVHTECCHGDLLECADDRADL AKYICENQDSISSKLKECKEPLLEK

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						SHCIAEVENDEMPADLPSLAADFVE SKDVCKNYAEAKDVFLGMFLYEY ARRHPDYSVLLRLAKTYETTLEK CCAAADPHECYAKVFDEFKPLVEE PQNLIKQNCLEFEQLGEYKFQNAL VRYTKKVPQVSTPTLVEVSRNLGK VGSKCKHPEAKRMPCAEDYLSVV LNQLCVLHEKTPVSDRVTKCCTESL VNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKQTALVEL VKHKPKATKEQLKAVMDDFAAFV EKCKADDKETCFAEEGKKLVAAS QAALGLTPLGPASSLPQSFLKCLE QVRKIQGDGAALQEKLCAATYKLCH PEELVLLGHSLGIPWAPLSSCPSQAL QLAGCLSQLHSGFLYQGLLQALE GISPELGPTLDTLQLDVADFATTIW QQMEELGMAPALQPTQGAMPAFAS AFQRRAGGVLVASHLQSFLEVSYR VLRHLAQP
434	5931	A	446	2	2255	STPHAFGTMKWVTFISLLFLFSSAYS RGVFRDDAHKSEVAHRFKDLGEEN FKALVLIQAQYLQCPFEDHVKL NEVTEFAKTCVADESAENCDKSLH TLFGDKLCTVATLRETYGEMADCC AKQEPERNECGTMKWVTFISLLFLF SSAYSRGVFRDDAHKSEVAHRFKD LGEENFKALVLIQAQYLQCPFED HVKLNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE MADCCAKQEPERNES/CFCNHKKD NPNLPRLWRPEVDVMCTAFHDNE ETFLKKYLYENCPERHPLPFMAPG NSFSFAKRYKAATECCQAADKA ACL/LCPKLDLGRG*KGRLRSKQ LKASLQKFGERAFAKAWAVARLSQ RFPKAEFAEVSKLVTDLTKEVTECC HGDLLCADDRADLAKYICENQDSI SSKLKECCEKPLEKSHCIAEVEND EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSV LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCLE FEQLGEYKFQNALVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPG AKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD KETCFAEEGKKLVAASQAALGL
435	5932	A	447	1	477	FYNRVLLLPRLC*GVIFPHRNHL PGSSDSHALAFRVTGITGTCHHACLI FVLLVETRFLHVGQAGLELLTSSDP PSSASQSSGITGVGHCAPTAHFLP HKVLRSLTKLPSGMSPETIHPRRHA EKSCLFSFSLYFHLTSSCSFIHPFSIL TFKC

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436	5933	C	448	141	390	MAKFSLCPPVKERGEKAHWEXXX XXNKATNSICEVSTFMXXXXXXXXXX XXXXXXXXXXLNHYESDWVISKLIP GCIKMTEAITC*
437	5934	A	450	345	462	NQRSTARGKELLQDTRALKKNS*R VIKYSKQQAQTCEG
438	5935	A	451	1538	1709	SKCKLKQDPSHAGTSLQSLLRRLR QENPLRPGFQGCSEL*SYHCTPARV TEQDPIS
439	5936	A	452	243	353	YSYHIRVHVHTHPHLHAC* ¹ LHTVR YT* ¹ NSTHTHTYF
440	5937	A	453	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
441	5938	A	454	2	797	LIGKFAPRGRPRRQRRGGPARVWSL CFKQVFGTEQDPGILFPASGPPSDFL LRLQTSQTIFSAISCF LGPAQHRFLW LAPSCQPTMSSQIRQNYSTDVEAA VNSLVNLYLQASYTYLSLGFYFDR DDVALEGVSHFFRELAEEKRKGYE RLK\MQ\NQ\RGGRALFQDIKKP\A EDE\WGKTPD\AMKAAM\ALEKKLN QAL\WDLHALG\SARTDPHLCDFL ETHFLDEEVKLIKMGDHLTNLHR LGGPEAGLGEYLFERLTCLKHD
442	5939	A	455	2	331	FFVFCFGKRGRLAVFRVEGKGMNPG * ¹ RNLWLPGLKNFSGTLWRGGNNK PGPPLQPKFGFLKKGFSPGGQGGF KIPNLEIGPNKGPKGWE* ¹ RA* ¹ PPNPS PSNFFNKPWVG
443	5940	A	456	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQALSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFT EVQASWQKMVTGVSALSSRYH
444	5941	A	457	38	533	APSPDAMGHFTEEDKATISLWGK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIK\HDDLKG\TFAQ A* ¹ SEPAPVTKL\HVDP\ENFKAPGEM LLVTR/VLAIPFSAKEFHP* ¹ RLQASW AE/MMGDLQLASALVPSRYH
445	5942	A	460	3	198	GIPGSSFCGLCGDVPKPV* ¹ RADGS C* ¹ DGVAPRLLRPRGFRGGRCGPVLD SLAQQRGAESGCRG
446	5943	A	461	649	1185	ETCLAFMYQRTCSADSKRYIWQLF LEKGPMGYHPLHF* ¹ VFLGFFFFFET VLAVLPQAGSVGGHNHSSIASSNHP RA* ¹ ANPPHLVAGDYKLTAQPGLKF/ VFLLETGFSYVCPGWVSGSLGSNGP PAPAFQRHRAKFVSFVPCHHAAQK GSIPFNELTFINWVMLGGASSLSWEI VNSS
447	5944	A	462	1	298	NKEILARPNGSSPEFPPLWGLRQVD

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						PPESGVQSPASPHGKTLFLLKKPTLT GQGGPNPVFPVLRVVKPQGPNPG GGGFH*PKSCPCPEWGAKLDPVF
448	5945	A	463	179	351	RHVGIKHGDHEATEKFIDEFAKVIA DKHLTLEQVYNANETSLF*HYYP KTPITAAE
449	5946	A	464	1	327	PGVPMQRAEFEPYKRSRCDSPRT PSNTPSAEADWAPGLELHPDYKTW GPEHGCSFLRRGGFDKPVLKNIRE NEITGALLACPDSESSFENLGVSVLR* T*KLLNYYS
450	5947	A	465	261	452	GDLRVTGAPSVSLSP*LGLP*VSRP* VPSPLASGTSKPLARFPPEEAVGFSRP GLCLLISFPL
451	5948	A	466	362	991	PSRHLSWLWGSTGCRNAHVQLAG GAGARAGEERPCFPRPELAGTVSPG DKSLRQFGEKGGGGHERMQGPHHS SKESGGQSHGEDPSLEASPPKPESPA SQVPMKSPVIPGETAHGLP*VSRP* VPSPLASGTSKPLARFPPEEAVGFSRP GLWSAMQAGVCDQGICAIRNSPQT TQGGRRP*ERRCRYMHVTTKEAAF TPSAPRECLPH
452	5949	A	467	24	436	RFIVLVHYISAPGELCRGWGSPKME GWGKRTSCQSLPKAGRSPGSLRSTD EYCGHRLPDNV*ATGGGQGPAPG MGVRNPSPAPRTSPGWRVPSNTAP QLLGCFGGQTGRVPFIQDPSSSSG MRNSPPGRGCLESA
453	5950	A	468	2	424	
454	5951	A	469	3	452	
455	5952	A	470	2	467	PDSSGPHRLRENPPWCLSPADKTNV KAAWGKVGAVGEYGAELERMF LSFPTTKTYFPFDSLHSGSAQVKGH GKKVADALTNAVAHVDDMPNALS ALSDLHAHKLRVDPVNFKLLASHCL LVTLAAHLPAEFTPCGGTASLADKF LGFLKQRC
456	5953	A	471	61	346	VRARVPSPAAAMGCTLSAEDKAAV ERNKKIDRNLRDREKAAKEVKLL VLGAGESGKSAIGKPMIIEEGYIQ DEWKPFKGIVYSNTLQAIIGT*KAA VERNKKIDRNLRDREKAAKEVKL LVLGAGESGKSAIGKPMIIEEGYI QDEWKPFKGIVYSNTLQAIIGT
457	5954	A	472	828	1066	QAQWLTPCNAQHFAFRRANHLRL GV*HQTGQHGKTPSLLKEKYKKKK KVASRSHMSVIPTMWKAEAEELLE PGRQRSQ
458	5955	A	473	180	350	EPMAKGKTESPGPKRCGP*I*WVIS QRGTLRFRGAGLFFMGFLRLGENL LEIPRGA
459	5956	A	474	1689	1856	GRCHITCVKSHGGAADFDTTFILFY FILFYFILFIF*TESCSVTQAGVQRGN LGSL
460	5957	A	475	115	324	SNFQLSRKLYF*FFQGKSKHNEYFII FE*T*ILHFLNLGIVIYNYGTSFRKNR

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						MKRKWVNDKMGQQQKHG
461	5958	A	476	310	633	RFSLGEQECEVCYRLRPTPGWTPGE TAGVAGREPLVCSPPPPASPAPP KVRSDMGPCPCAS*WPSGLTKGP SCFPVASHGGITPGQWPGEETSR KERSSATK
462	5959	A	477	2	293	PAAERSCLRVTTFASACPASMEPKRI REGYLVKKGSVFNTWKPMWVVLIE DGIELYKKNCDNSP*GMIPLRGITLT RPWLDFGRRKCWFTKSSIIQYL
463	5960	A	478	387	511	WDPIFISDIYIILITGYLTTY*NVLH WKKIIFYIALIVL
464	5961	A	479	130	240	KNEQDPRDL*DNDKWPNIHVIGVPE EDKDNGETERVFD
465	5962	A	480	116	423	GIRCPGPRESLLSQFILSMRQAGQ DWQPEAYTLRICQLEVFSTCVSSLL HPVCRSQ*LPMEPEVIPGWNGKPRG HWPVQIFKSFTHTGTPNLAGPGCCCG VR
466	5963	A	481	64	343	QLL**LSSTWEGQLAAKELDEQRGI GC
467	5964	A	482	61	342	QPQDTMGHLTPEEKSAVTDLWGK VNADEADGEALVTLLGVYPWTQR MFESFGDLDTPEADMGNPKVKAHG WKVL*AFIDGPAHPDQLKGNLCT
468	5965	A	483	557	816	SRHFERPWVDHLRLGV*DQPGQHG ETPSLQKIQKLARSGGTHL*SSYLG G*SGKNHLNPGSQGCSEP*SCHCTP GWVTEQNSVSKK
469	5966	A	485	277	322	FFF*VYHVWFLFSFLICRFMPFAKFG NF*PLFLEIFFHPYSFSSL*YEW*SFC YCLRGLLCFHVYPLFLVYFSLFFILV NFC*LFFSSLILFFCHMQSTVELVQ
470	5967	A	486	31	309	FLELGPGKPFGNMYDADDDMQYD EDDDEITPDLLQETCWIVRSYFDKK G*VIQQLDSFD*SIHMTALRIGEYAA PIDLQADAHHASGEGEKP
471	5968	A	487	130	521	KAKFRFTCFSTSSFYN*DLDFKIYPSPI KVAEPS*LSGQCFSSLFFHQDLGFCF VLLFETESCSVTQVEHSGAISAHCN LRLPG*SNSPVSLSAAGTTGTHHY TQLIFVLVAEMGFCHVGQSGLELAS CR
472	5969	A	488	32	452	
473	5970	A	489	38	525	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFAQLAS ELHICDKLHVDPENFKLLGNVLVT VLAIHFGQRIHP*RCRASWAEDG*L GVASALVLQDTTELTC
474	5971	A	490	818	947	VCFLFLFF*DGVSLMLPRLECNGTIS AHRNLCFPGSSDSPVSA
475	5972	A	491	17	416	PPSSNPMGHFT*EDTATITSLWGT NAENAGGKTLLRLLGAYPWTQRLF DSFGNLSSASAIMGNPQGAHGLK VLTLL*DAVKHLDDLMTGTFSHPTL

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						PCYKLHLDSENKLLGYVLAIVMAIHFGKEVIPAV
476	5973	A	492	24	452	APSPDAMG/HSLWGVNVEDAGGETLGRLLVVYPWTQRFDFSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
477	5974	A	493	34	548	APSPDAMGHFTEEDKATITSLWGK/VNVE/DAGGETLGRLLVVYPWTQRFDFSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLG/NMLLVTRFGQSHFRAKNFTPEGCRASWQKQKMAEDGDLQWPVPCSSRIPLKPLGP
478	5975	A	494	527	1022	GWASAFWLKPGSPRGYRCNPHHVILPVSAGLEPLCSLLPSTDTCPASQTGSGRANRATPGCGRPAGVRKGRPACKRSKNFRAACGSGARSRPGHRTPGSSRPPGRQKRAPWASQARRPPA *SRPGGRGGAARPHPRRTGAPAGSARGAQRSERARPQPRDPA
479	5976	A	495	2	379	
480	5977	A	496	3	723	VPRVCLLLQQCLDGTDPGTGLPASDRPPISSPLATSGTIFSAISCFWDLPAFLWLAPSCQPTMSSQIRQNYSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKIREGYERLLARMQNQ/RGGRALFQDIKKPAEDEWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD
481	5978	A	497	1	196	GTSVTKMEAFGLGSRGLWAGGPAPGQFYRITFTPDSFMDPASALYRGPIRTQNPMVTGTSVLGV*IEGGWVIA GHMLGFYVCLDRLRDFYRFRVNLSTVLDASGDAE*HYL*QFYRITFTPDSFMDPASALYRGPIRTQNPMVTGTSVLGV
482	5979	A	498	1	401	GTRKWVTFISLLFLFSSAYSRGVFRDAHKSEVAHRFKDLG*ENFKALV VIAFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESPDN*D*SLHTLFGDKLCTVAILPETYGEMADCCVQLEPER NECFLQLKD
483	5980	A	499	47	411	
484	5981	A	500	316	493	LLVGRALPEGDRHDQHQQGLEQSILKLEKEIQDLENAELQISTKEEAIL* KLKAIER
485	5982	A	501	27	526	LSLTSRMEEAELVKGRQLQAITDKRKIQEEISQKRLKIEEDKLKHQHLKKKALREKWLLDGISSGKEQEEMKKQN QIQDQHQQVLEQSILRLEKEIQDLEKAEQISTKEEAILKKLSIERTTEDI IRSVKVEREERAESIEDIYANIPDLP

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						KSYIPSRLRKEIN
486	5983	A	502	25	208	VSRJEA VSGSHGFSIHKLLTVNVITY DCVSSWCLYVSFQKQDPLVLGQRQ LKSKPAGDLNT*GKVIKCKAAIAW KAGKPLCIEEVEVALPKAHEARIQV SRWFRLELSLA
487	5984	A	503	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
488	5985	A	504	52	562	APSPDAMGHFT*EDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTS LGDAIKHLDDLKGTFAQLS ELHCDKLHVDPENFKLLGNVLVTV LAIHFGKEFTP EVQASWQKMAED\ VTGVASALCFTKHLDFMCMMQSFQ R
489	5986	A	505	801	927	
490	5987	A	506	659	837	RKIKEAGHRGSQLYSQHFGRLRQE DCLSPGGQGCSEPRLHRCVPAWVT G*KKTL PKNKQ
491	5988	A	507	3	203	
492	5989	A	508	23	678	RPRVRMAEVQVLVDGR\GHLALGR LAA/LSVAKQVLLGRKV VVRCEGI NISGNFYRNKLKYLAFLRKRMTN PSRGPYNFRAPSRIFWRTVRGMLP HKTKRGQAALDRLK VFDGMPPPY D/KAPLFL*QKKRMVVPAALKVVR LKPTRKFAYLGRLADEVGWKYQA VTATLEEKRKEKAK\IHYRKKK*L MRLRKQAERNVRRIFANTPEVLKT HGLLV
493	5990	C	509	275	370	MPQGGACSPVLPGLSVVSLLTQSY LVVVPQW*
494	5991	B	510	1	1122	MVFLSGNASDSSNCTQPPAPVNISK AILLGVILGGLILFGVLGNILVILSVA CHRHLSVTHYIYNLAVADLLTS TVLPFSAIFEVLGYWAFGRVFCNIW AAVDVLCCTASIMGLCIISIDRYIGV SYPLRYPTIVTQRRGLMALLCVWA LSLVISIGPLFGWRQPAPEDETICQIN EPPGYVLFSA LGSFYLPAILVMYC RVYVVAKRSGRLKSGLKTDKSDS EQVTLRIHRKNAPAGGSGMASAKT KTHFSVRLKFSREKKA AKTLGIVV GCFVLCWLPFFLVMPIGSFFPDFKPS ETVFKIVFWLGYLNSCINPIIPCSSQ EFKAFQNVLRIQCLRRKQSSKHAL GYTLHPPSQAVEGQHKDM*
495	5992	A	511	928	1311	AMIVPTAVQGRQSKDPVSKEKKE KARKERWLGTVAHSCNPRTLGGQG GWIMRSRDRDHPGQQGETPSLLKM QKLAGRGGGHQSRLGLRLRQENG NPGGGACSEPRWHCCTPAWATE*D

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SISNNNKK
496	5993	A	512	23	288	APSPDAMGHFAEEDKATITSLWGK VNVEDAGGETLGRLLVVNPGTLKL NSSLG*Q*FGGCILSPHHCLGKGRK CFFSIVEMLVILYFM
497	5994	A	513	20	207	LDAGTACAETMACTSRLYGLPRST WPNHPDAILPEGYFSSEI*SRPDCGL RVIYRGLTISSA
498	5995	A	514	228	375	CVALGAMRGMRRLPAGAPKMLMG V**ELDRLGYIAHPQLGKRARAGIV L
499	5996	A	515	417	573	ETPTGLRGGTCL*S*LPRRLRWENC LNPGGRCSEPRSHHCTPAWATEQ DS
500	5997	A	516	173	420	LLLANQLMSLQIRQNYSTDLEAAV NRLGNLDLQAYYTYLYLGFYYDRD DEGLEGVSHFFRELAEDKRDY*RL LTMQNQRGG
501	5998	A	517	3	415	HEGHQYAPNPDAMGHFTEEDKATI TSLWIKVNEENAG*ETLARLLAGYP WTQRIFDRFGNLFASDIMGNSPVQ AHGKNVLTSLLDATKHLDDLKGT AQLSELHCYKLHVDPENFHALANE LATALAMHFR**FTP
502	5999	A	518	3	232	
503	6000	A	519	1	2361	
504	6001	A	520	4806	5788	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPPLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVDFTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLC TH TH TH TL FST YLKNDRDKTIMCKLSLIG*LAESEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYEIAARRHPYFYAPELFF AKRYKAAFTCCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
505	6002	A	521	151	364	VTHDCICYLQQTHF*PKDKNRLKLK RCKKQFHENSNOQRVEVALLISAQ RDLRSKIDTEGKSIQQRKKSSC
506	6003	A	522	925	1168	SQHFGPRWVDHLRSGIGDQPGQH GETPALLKIQKLARCGYMRL*SLRR LRRENHLNPGGGGCSETRLHHCI PAWATEQDS
507	6004	A	523	142	329	THSLFLLWSLSHHSPTVNTTLRNLG ALHRRHGKL*AAETLDVFNLTSSCS LLFNPFYRNFR
508	6005	A	524	108	283	KQNLILSPRLKCNPGISVN*NFNLP G LTRSQA*ASREAGTTGTCYHA**IG* IFIIDG
509	6006	A	525	1	345	GTRAAPLRIQSDWAQALRKDEGEA WLSCHPPGKPSLYGSLTCHGIVLYG IP*ATSSHRFIANDPNIITSHSSRPTVF VPSSFSSILFFLAHPLSISLPFFSLPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FPLNFLPLRS
510	6007	A	526	3	276	HEPRRPQYSSGRRAAWLSYSLFSAG CGASAPRPLVMSDSGSYGKSDVEH LYYRNY*STRI*GYIQTSHI*SG*GM TTDSYYGINIFYKLQ
511	6008	A	527	2297	2435	LKLVSKKRVYNFILILLML*TYFLK DGLFECLWHLTCKKKKLQKNP
512	6009	A	528	123	317	QETKKEQNKENKQIK*RSTRKKHR QGTNKTGERGERQTPPVGNRQTPT LGIHARPRRRATTSPRA
513	6010	A	529	787	1069	FASHFGRLRQADPLRSGVQDQPGQ QGETPSLLKIQKFPRRDGGRL*SQLP RKLRQENCFNRGGGDCSEPRLCPL PAWATERNSVKGKERKEKK
514	6011	A	530	110	369	CWLSCCLEVRSCLYTFLSAYNFKCV LTI*HTFFVFFWSLCVYFFIVLCCL VLVWCLSSLYYGHVYYLYFCYSLFI VLGYGILAV
515	6012	A	531	268	331	QM*TAKCARCEGLGLITLCLDCIVA NTLLLVPNGETSWTNTNHLTLQVW LKDGYIGWGLMALCTGIAPVLAGG KDCCGARRCGNR*QMLRYDFS*AL VVLGAIYWLS
516	6013	A	532	807	1060	SWHFGRLRWADYLRPGAGDQLSQ HGEISSLLKTQKLPGCGDTHL*SQLL GRLRQENHLNLGGGGCSEPRSHHC TSAWVTERDSV
517	6014	A	533	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
518	6015	A	534	38	550	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF VDSFGNLSSA\SAIMGNPKVKAHGK KVL\TSLG\DAIK\HLE*SQGAPFAQA *SEL\CDK\PALLDPGGTFKLPGENV AGLTVFGQSHFRAKEFHP*RLQAS WHKQKMAEDGDLELASALVPSRY H
519	6016	A	535	2	348	ARAGAGRLRRAASALRLLSPRLPVR ELSSLARLYPHRVDDHYENPTNAGS LD*TSKNVGTGLQLAPA*GDVVKL QTLVDEKVKNVDAFRTLGCGLSAI AYSSLATEWVTGKTADE
520	6017	A	536	385	536	RMSAGALFIGYCIYFDHKRRSDPNF KNRL*DGRKKQKLAKERAGLSKLP D
521	6018	A	537	123	705	AAPTALRVRGPPLLRGPCRHRPRSA FVEKMGVGRNSAIAAGVCGALFIGY/ CIYFDPQKTK*TPTFKNRLRERRK\K QNLQQRRELGL\SKLPD\LKDAESCC RKFFL*RNTSLGEELLSFDG*/YEY*E RAVDHLDKLP\IAV\CGQPQQLQV LQQTLP\PPVF\QMLLT\KLPTISQRIV SAQSLAE\DDVGMRNKLCH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
522	6019	A	538	1	430	
523	6020	A	539	42	373	
524	6021	A	540	1	430	QQLQRLVHPDFFSQRSTQTEKDFSEK HSTLVNDAYKTLLAPLSRGLYLV* SS/YGIEIPERTDYEMDRQFLIEIMEI NEKLAEAESEAAMKEIESIVKAKQK EFTDNVSSAFEQDDFEEAKEILT RYFSNIEEKIKLKKIPL
525	6022	A	541	24	452	APSPDAMG/HSLWGVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFT EVQASWQKMVTGVSALSSRYH
526	6023	A	542	38	547	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGK KVLTSGLDAIKHLDDLKGTFAQA *SELHCDKAALLDPENFKLPGGNV AG*PVFGQSHFRAKEFHPWRLQGF GISRRWQKMVTWSWPVPCSSRYH
527	6024	A	543	328	495	NLGANNCSLLGIGLLKGSMSGRLW PKAFSAG*KQGLQNQRKHTALVKIE DVDA*GE
528	6025	A	544	154	340	PGLLKAAIWGAIYLRATYWTYVLA DLHPFADMLHAGYSITSEVEQPVLA VQLTYNPDES*WP
529	6026	A	545	124	323	EVKSVYLVYILSNRFF*CTYMHILV YYVYFIGLTI*LEEHSMLVYQNLVH YFLVFVNVGIYLLYL
530	6027	A	546	314	445	SPILLQFTVVLTRYLFTKIQFIYFFET ESCSIAQARV*WCDLG
531	6028	B	547	1	1011	MDLKFNNRSKYISITVPSKTQTMSP HIKSVDDVVVLGMNLSKFNKLTQF FICVAGVFVYLIYGYLQELIFSVEG FKSCGWYTLVQFAFYSIFGLIELQL IQDKRRRIPGKTYMIAFLTVGTMG LSNTSLGYLNYPTQVIFKCCCLIPV MLGGVFIQKRYNVADVSAACMS LGLIWFTLADSTTAPNFNLRVLYSY SIGFVYILLGLTCTSGLGPAVTFCAK NPVRTYGYAFLSLTGYFGISFVLA LIKIFGALIAVTVTGRKAMTIVLSFI FFAKPFTFQYVWSGLLVVLGIFLNV YSKNMDKIRLPSLYDLINKSVEARK SRTLAQTV*
532	6029	A	548	244	1408	SRHNGMDLTQQAKDIQNITVQETN KNNSEIECSKITMDLKFNNRSKYIS ITVPSKTQTMSPHIKSV*RVVVLGM NLSKFNKLTQFFICVAGVFVYLIY GYLQELIFSVEGFKSCGWYTLVQ FAFYSIFGLIELQLIQDKRRRIPGKTY MIAFLTVGTMGLSNTSLGYLNYPT QVIFKCCCLIPVMLGGVFIQKRYN VADVSAACMSLGLIWFTLADSTTA PNFNLTGVVLISLALCADAIGNVQ EKAMKLNASNSEMVLYSYSIGFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YILLGLTCTSGLGPAVTFCANPVR TYGYAFLFSLTGYFGISFVLALIKIF GALIAVTVTGTRKAMTIVLSFIFFAK PFTFYVWSGLLVVLGIFLMFTAKI WDKIRLPSLV
533	6030	A	549	66	346	IQQLPTFFHIFSIFFLIR*FFYMKGFR* LVLFYICPHVYA*SYFSLLFFCSLTI* FISFSLYFTLFLFFFTLLFICVLAMFI FFELHLSYIP
534	6031	A	550	21	337	GPEAQCPDQPPWLSFQGLPQGT WATHSAPCSPNLTSRSWCPDSEPGR AGGRGRPPTLDHDAPPTPL*PSKP HPCIPQALPSSRTLRLPYATPRQHAA TQCTP
535	6032	A	551	526	771	PPPLGVPGTLQFLRPRAAVLIGSKLL RPGRFCRWIFSPLLLVNISWLGTVV HACNPSTLGDQGGRT*G*EFETSLP TWRNS
536	6033	A	552	305	569	KKPLKGEKGGSLKTRPSFKKPDAKI YLKKS VGFL*TNPEQFKKEIRNTIPLI KGASSSSSKTNLGINLTKVVKDLN NENSRTLLRQS
537	6034	A	553	90	339	EVSALPDLPAVMLAGPTP*PSFPRTP SYFSAPLLLPLSCSFLLPLMPHSC PPSSSPSPSLLLSITPSPAPSPFLLF P
538	6035	A	554	1179	1408	GYPVGKRRRLGERQGPRQPPTLLPCD KEAERGEHIYFYIYI*YIYNIYII YIYNIYIHIYIYIYIYIYIYIYIYI
539	6036	A	555	722	991	SQHFWRPQVNHVSLGVQDQHGQ HSENPVSTKIYIYIQLARCSDRCL* S*LLRRLRHENHLNLGGGGCSELKS CHCTPAWATE*DPVSK
540	6037	A	556	1	362	GTSRQVCREHSFQSVKLSAGARSW CFLSHWDPAGEVSLTDCSEIFLPFLG MAAVYHYFSINIFFKTSFRLILIY** SYFHLYFLYYSILCLFILLFIHYYC YILFISNLFTIIFLFL
541	6038	A	557	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQSELHCDKLHVD PENFKLLGNVLVTVAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
542	6039	A	558	38	497	APSPDAMGHFTEEDKATITSLWGK\ VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIK\HLDDLKGTFQAQ *SELAVDKLACGILENFKAPGEML LVTRFWQSHFRQKNFTPEGCKASW AERWVTW
543	6040	A	559	1	414	FETVSLLLLRLHTGTISTHCNLRLP GSNDSAASAS*VAGTTSVCHHTGLI SVFSIETEFHHVGQTGLELLTSSDPL TSASPGAGIKGGSHCAQSPICFRGN NEMNYQATGIYSKSEIFFCLGYVTM SRCLTSQSGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
544	6041	A	560	178	334	NVCRLPVTNAESDAMINDAIRPINF TGFLTMFA*NLTGADPADVIAAFD VL
545	6042	A	561	322	649	
546	6043	A	562	3	452	
547	6044	A	563	24	587	GIPQTQREPTMVLSPADKTNV\KAA WGKVGAHAGEYGAEALERMFSLF PTTKTYFPFHDLSHGSAQVKGHGK KVADALTNAVAHVDDMPNALSAL SDLHAHKLRVDPVNFKLLSHCLLV TLGA\HLPAEFTPAVHA\SL\DKFLAS VSTGL\TSKYPLSWSPR WPCFLAPW ASQPQLLPFPAPVPPWSLK
548	6045	A	564	3	474	
549	6046	A	565	1099	1243	
550	6047	A	566	425	943	MGRSAPVEISYETMRFMTRNPTN ATLNKFTTELKKYGVTTLVRVCD TYDKAPVEKEGIHVLDWPFDDGAP PPNQIVDDWLNLLKTK\FREGARVC CVA\VHCVGRVGE GAPVL/VLALAL DWNVGMK\YEDAV\QFIRQRRGA FNSKQL\LYLEEYRPMRLRFRDTN GHC\CVQ
551	6048	A	567	1	441	
552	6049	A	568	1	890	MSKSESPKEPEQLRKLFIGGLSFETT DESLRSHFEQWGTLTDCVVMRDPN TKRSRGFGFVTYATVEEVDAAMNA RPHKVDGRVVEPKRAVSREDSQRP DYFEQYGGKIEVIEIMTDRGSGKKRG FAFVTFDDHDSVDKTVIQKYHTVN GHNCEVRKALSKQEMASASSSQRG RSGSGNFGGGRGGGFGGNDNFGRG GNFSGRGGFGGSHGGGGYGGSGDG YNGFGNDGSNFGGGGSYNDFGNY NNQSSNFGPMKGGNFGGRSSGPYG GGGQYFAKPRNQ/GGYGGSSSSSY GSGRRF
553	6050	A	569	579	2102	SPKEPEQLRKLFIGGLSFETTDESLR SHFEQWGTLTDCVVRFGGRD KAVKQ PISLAYLGAVFSECL*K*LIAL*LELC WQRNVLL*F*KLTS*I*G*WETGRTF YKRLV*SFLLPYSKLK*QKLLRSDF VLHKLTLFSGMRDPNTRSRGFGF VTYATVEEVDAAMNARPHKVDGR VVEPKRAVSREVS GFFFFFLNLLG YVLL*T*DSGVF*TYQNFLFEYRLC* SKPMVFLLLDSQRPGAHLT/V*KKI FVGGIKRRHLKEHHLRDYFEQYQK IEVIEIHDLTRSGGKKRGFAFVTFD DHDSVDKIVSKYQIVAFSGSTICM AF*TLIPCCIVVFLVQKYHTVNGH NCEVRKALSKQEMASASSSQRGML VA*LNLKGNFELLQYE*FNA*TSCL KV/ESGSGNFGGGRGGGFGGNDNF GRGGNFSGR/GYVWFIYM*F*LLTIF AMKILQYGNCIQNVTLSPSHT*NLK LFLTGGFGGSRGGGGYGGSGDGYN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GFGNDGKFFRNK
554	6051	A	570	250	381	
555	6052	A	571	249	468	PNQRLKWKS*LMGQGRG*KWKLL VLFYHKA*RMWPA/C\CLDLGLGTG \CTC\CLLVYANWLHLLFLCLCPYP WLS
556	6053	A	572	2	488	QEPAHDLRMYGKI\FVLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTS S\QTNGETGTTCPIVSLYPAPCSDNT HYFVCDGWYYWNDPLNLLYSMT DKGMRMWPAACCLILPR\TSCCCL AYANWLHL\FL\CLCPYPWAILNS LFSWPSLITGILYF
557	6054	A	573	7	412	
558	6055	A	574	3	479	NWELLWLLVLCALLLLVQLLRF LRADGDLTLLWAEWQGRPE/WEL TDMVVWVTGASSGIGEELAYQLSK LGVSLVLSARRVHELERVKRRCLE NGNLKEKDILVPLDLTDTGSHEAA TKAVLQEFGRGFFNGLRTELATYPG IIVSNICPGPVQSN
559	6056	A	575	1	321	
560	6057	A	576	2	1243	GAASAEPGAPEPLLLPACSLGGAGA VRLWAGRRGGAAIPQGSATLVRA VFFPPSWACAAAMNWELLWLL\V LCDV\LLLVQL\RLRADG\DLTL LWAEWQG/RDRPEWELTDMVV\W VTGASSG/ILGEELAYQLSKLGVSL VLSAR\RVHELEKGEKERCLAENGQF LKEKDITLFLPL\DLDTLGS*SRLT KAVLQEV\LRIDILGSTMVGMSQR SL\CMDTSLDVYRKL\ELNYLGTVS LTKCVLPHMIERKQGKIVTVNSILG IISVPLSIGYCAKHALRGFFNGLRT ELATYPGIIVSNICPGPVQSNIVENSL AGEVTKTIGNNGDQSHKMTTSCV RLMLISMANDLKEVWISEQPFLVT YLWQYMP\TWAWWITNKMGGKRIE NFKSGVDADSSYFKIFKTKHD
561	6058	A	577	175	354	
562	6059	A	578	2018	2182	
563	6060	A	579	140	287	MVKRNQCPSLPPN*KMRSQGSTCQ PHCQRWLPSTRSYTHPLKARPSA S
564	6061	A	580	357	760	
565	6062	A	581	182	459	
566	6063	A	582	1	382	
567	6064	A	583	3	406	
568	6065	A	584	173	415	
569	6066	A	585	2	424	
570	6067	B	586	108	395	VGAHAGEYGAEALERMFLSFPTTR TYFPHFDLSHGFCPLRGHGQEGGR RADQRRGARGTTCPTLSALSDLHA HKLSGGTRFNFQAPKATGLLG*
571	6068	A	587	379	579	
572	6069	A	588	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN

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						YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
573	6070	B	589	220	480	MSSQIRQNYSTDVEAAVNSLVNLY LQASYTYLSLGFYFDRDDVALEGV SHFFRELAEEKREGYERLLKMQNQ AWRPRSLPGHQEAS*
574	6071	A	590	142	383	
575	6072	A	591	1	308	
576	6073	B	592	195	326	MMGVLDGVLMEQDCALXLLKDV IATDKEDVAFKDLDVAILVV*
577	6074	A	593	5	1199	PDSLRLILHLFKLSPQFSIMSEPIRVL VTGAAGQIAYSLLYSIGNSVFGKD QPIILVLLDITPMMGVLDGVLMEQV RLCPSPPERCGNGSVFGKDQPIILVL LDITPMMGVLDGVLMEQDCALPL LKDVIAATDKEDVAFKDLDVAILVGS MPRREGMERKDLLEY/ADVKIFKSQ GAALDKYA\QKSGKVIVGGNPANT DCLTASKPAPCIPKENFSCRLDLH NRAKAESGLRLVVTADHGQNGIHW GNHSSTQYPDVNHAKVKLQGKEV GVYEALKDDSWLKGEFVTTVQQR GAAVIKARKLSSAMSAAKAICDHV RDIWFGTPEGEFVSMGVISDGNSYG VPDDLlySFPVVIKNTWKFEGLP INDFSREKMDLTAKELTEEKESAFE FLSSA
578	6075	A	594	46	298	
579	6076	A	595	982	1193	
580	6077	A	596	69	399	VSNYPTVGCCIFLQIRARNPAFQPQT LMDFGSGTGSVTW*VTFFSPILVNF SSRKPYLHHSKINRLNQRENQVVG NL*CFHQRQRRRYMDWQGNLK EMSSKKRRMY
581	6078	A	597	600	887	
582	6079	A	598	813	973	
583	6080	A	599	166	437	ADHLKSGV*DQPGQHGEILSLLKLQ *FPGRGGAHL*SLLGRLKQENHLN PGGGGCSEPRCHWTPVRATVGDS VQKK*KSQDGPRAKLG
584	6081	A	600	3	238	SGDRDHPG*HSETLSLLKIQQ\IAGR GGGRL*SRLRLRLRQENGVSPPGGG ACSEPRSHHCTPAWETERDSVSKK KKKKL
585	6082	A	601	4005	4345	SQHFRPRRADHLRSGVQDQPDQH GETPSLLGGRGGRITKSGDRDHPG* HGETPSLLKMQ/EKLAGRGGGRLW SLLGRLRQENGVSPPGRACSEPRS CHCTPAWLTEQDSVSKK
586	6083	B	602	1	9234	MGAPTLPPAWQPFLKDHRISTFKN WPFLEGCACTPERMAEAGFIHCPT NEPDLAQCFFCFKELEGWEPDDDP EEHKKHSSGCAFLSVKKQFEELTLG EFLKLDREKAKNKIAKETNNKKKEF EETAKKVRRAIEQLAAMD*
587	6084	A	603	1577	2233	SGCLLSPSVGRQNSPVELGGAGLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RAGWAPQERGRAALLISPGPNVR GGPDWLPSVLQMRGLPLWDLGGRP DVGRMSPGGRPGSCWATQLRFHIS LAPLFSWAGRSGSRLNPSTLGGRGG PITRSGDRDHPG*HGETLSLLKIQKI SQACWR/CACSPSYGRLRQENGVPN GGGACREQRS GHCTPAWATEQDSV SKKKKKKSGSTIRLKHILHKII
588	6085	A	604	151	454	FKIGPGAVAHACNPSTLGGRSRI TRSGGRDHPG*HSETPSLLKIQKLA GRGGGCL*SQLLWRLRQENGVPNG GGACSEPRSRHCTPAWVTERDSVS KKK
589	6086	A	605	1362	1647	
590	6087	A	606	10289	10708	SQHFGKLRQEDHLRSGVREQPGQH GKTPYLLKIQKLARRSGACL*SQLL RRLRQENRLNPGGVGCSEPRLHHC TTAWTLQ*DPVSKKLKKKYIERQR YHQHMKHPWSTKIYVCMGDG*HR SVEKQIIQTLCMFVFTHTY
591	6088	A	607	709	980	
592	6089	A	609	234	381	PPWTQFSLSCVCLL/CSRPA/VSAWR QARENESQAKGETAYETITSCENRS H
593	6090	A	610	1	1755	
594	6091	A	611	1128	1321	
595	6092	A	612	650	800	
596	6093	A	613	149	475	
597	6094	A	614	1	801	
598	6095	A	615	1284	1386	
599	6096	A	616	20	3888	
600	6097	A	617	204	411	
601	6098	A	618	1	1468	
602	6099	A	619	48	178	
603	6100	A	620	79	1953	LQVGTASSLLLSRVFGDRGYSPET RKCPKPINVRVTTMDAELEFAIQPN TTGKQLFDQVVKTI RPSRQVWYFAG LHYVD\NKGFTWLKLDKKVSAQ EVRKKNPLQFKFR/APKFYPEDVA\ EELIPGTFQKLFF\QVEGRESLSDE DLLAPLETGRALWGSYACASPRLG DYNK/EKLHKSGVPSASERLIPQRV MDQHKLTRDQWEDRIQVWHAHR GMLKDNAMEYLKIAQDLEMYGIN YFEIKNKKGTDLWLGVDA LGLNIY EKDDKLTPKIGFPWSEIRNISFNDKK FVIKPIDKKAPDFV FYAPRLRINKRI LQLCMGNHELYMRRRKPD TIEVQQ MKAQAREEKHQKQLERQQLETEK KRRETVEREKEQMMREKEELMLRL QDYEEKTKKAERELSEQIQRALQLE EERKRAQEEAERLEADRMAALRAK EELERQAVDQIKSQEQLAAELAEYT AKIALLEEARRRKEDEV EEWQHRA KEAQDDL VKTKEELHLVMTAPPPP PPPVYEPVSYHVQESLQDEGA EPTG YSAELSSEGIRDDRNEEKRITEAEKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ERVQRQLVTLSSSELSQARDENKRTH NDIIHNENMRQGRDKYKTLRQIRQ GNTKQRIDEFEAL
604	6101	A	621	269	361	
605	6102	A	622	210	367	ISQSGDCCSVWLSLQGPPKGCPKP/I PSPGLQPRATPPA*VQQRSTHPMSC SN
606	6103	A	623	1792	1935	
607	6104	A	624	9	326	
608	6105	A	625	250	381	
609	6106	A	626	155	457	NQKELGNTPRYPLEASNWLQPVKD WPVTNQRLKWK*LMGQGRG*KW KLLVLFYHKA*RMWPA/CCLDLGL GTG/CTCCLLVYANWLHLLFLCLC PYPWLS
610	6107	A	627	2	488	QEPADLRMYGKI\FVLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTS S\QTNGETGTTCPIVSLYPAPCSDNT HYFVCDGWYYWNDPLNFLYSMT DKGMRMWPAACCLILPR\TSCTCCSL AYANWLHLLFLCLCPYPWAILNS LFSWPSLITGILYF
611	6108	A	628	2	364	
612	6109	A	629	946	1142	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFA
613	6110	A	630	946	1193	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFA*SAFPIVQGLLFRS WNL
614	6111	A	631	946	1142	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFA
615	6112	C	632	294	710	MVRSRQMCNTNMSVPTDGA VTTS QIPASEQETLVRQESDYSPSTSSSI IYSSQEDVKEFEREETQDKEESVSS LPLNAIEPCVICQGRPKNGCIVHGKT GHLMACFTCAKLLKRNKPCPVCR QPIQMIVLTYFP*
616	6113	C	633	822	1149	MLVLHICLLL TIRGFRAWRSGLKT PQFPSRGLTTAEARRPGPRGSFHS PGQGTGRSYALIRGGTVLLAAKAAGS RSEGSRPPLGLGFLHLSDTQGHTG PRSSQARAV*
617	6114	A	634	5	76	
618	6115	A	635	269	354	
619	6116	A	636	184	299	FFCTFSTDGVSPC*PGWSRSPDLVIH SPRPPKVLGLQA
620	6117	A	637	3	307	ESCSEAQAGVQGAQSWLTATSSSQ VHAILLPQPPK*LGLQVPATTPG*FF VFLVETGFHCVSQDGLKLQTS*SAH LGLPKCWDRHEPLRPAKKQLFKN VP
621	6118	A	638	2	131	SKAALTGSGPGP/IPLCFVSAVLAPFI RPS*SLLAGRLDGGQD
622	6119	A	639	1	822	
623	6120	A	640	1258	1454	LSGIIHYSFFTIRNIKALFSLC*VFQF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFA
624	6121	A	641	248	386	SARLSLPKIWDYRREPLHPARSFFIY SSSSILY*S*LVSITALLF
625	6122	A	642	132	243	LGLQVPATAPG*IFFVFLVETGFHH VSQDGLDLLTS
626	6123	A	643	397	954	
627	6124	A	644	1	1388	
628	6125	A	645	2285	2409	
629	6126	A	646	36	224	
630	6127	A	647	242	933	YGESKDWNQKDLLSALVLTTVNCL PTPIMAKSAEVKLAIFGRAGVGKSA LVVRFLTKRFIWEYDPTLESTYRHO GNHSMMEVSMGGY*DTAGQEDTI QREGHMRWGEGFVLVYDIT*PRKF LKEVLALKEHLDEIKKPKNVTLILV GNKADLDHSRQVSTEEGEKLADEL ACAFYECSACTGEGNITEIFYELCRE VRRRRMVQKTRRRSSTTHVKQTI NEMLTKEISS
631	6128	A	648	596	709	
632	6129	A	650	1	367	
633	6130	A	651	135	307	
634	6131	A	652	170	372	
635	6132	A	653	3	320	
636	6133	A	654	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVSALSSRYH
637	6134	A	655	52	518	APSPDAMG/HFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF DFSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIHLDDLKGTFQQLSE LHCDKLHVDPENLKLGNVLETAL AIQFRRKNSPL*GQASWQKMVTGV ASALSSRYH
638	6135	A	656	123	219	
639	6136	A	661	413	545	
640	6137	A	662	4	350	
641	6138	A	663	1034	1091	
642	6139	A	664	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVSALSSRYH
643	6140	A	665	38	602	APSPDAMG/HFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF DFSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFQQL A*SELHL*QSCNVDPENFKAPGEM LLVTR/VLAIPFAKEFTPEGCRASW AERWVTCSPVALFLQDTTEAQLP MNAELFKDKAFILASNYK
644	6141	A	666	24	452	APSPDAMG/HSLWGKVNVEDAGGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
645	6142	A	667	38	536	APSPDAMGHFTEEDKATITSLWCK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFAQ A*SEL\HC*QAGMWD\PENFKLLGE MLLVTRFGQSHFRQKNFTPEVARL SWAERWVTWSWPSALVPSRYH
646	6143	A	668	132	357	
647	6144	A	669	1	89	
648	6145	A	670	136	594	LNRVAFLPGAAVILIGHLHTHTGPS GVCNVSMRGFSSPAGWTPTGSHRG KERPAGRLMHRRMGWSAVEWTG\ AQGIPCISTCPERTGGDAATRSRPP VLPPPPRPPQRRCRHLVSRAGTPRC ACAGTLTSKRGTHWRSTELLRRSP LRSSQ
649	6146	A	671	400	696	
650	6147	A	672	120	352	
651	6148	A	673	276	401	
652	6149	A	674	139	470	
653	6150	A	675	136	1058	GVVGAAASGAGSRKAGLAGVPGPP GRANRESPPGPVAMGRVIRGQRKG AG\SVFRAHV\KHKRGAARLRAVDF AERHG\YIKG\IVKDIIHDPGRGAPLA KV\VFRDSYRFKKRTEL\FIAAEG\IH TGQF\VYCGKKAQLNIGNVLPVGT\ MPEGTIVC/CALEEKPGDRGK\LAR ASGNY\ATVISHNP\ETKKTRVKLPF RVQRR\SPSANKSLWLVLVAGGWP ECDKPILKAG\RAVPQI*RQKRNCW \PRVTGVWAMNPFEAFLKGGNPPA HRQSPPIRRDAPAGRKVGLIAARR TGRLRGTKTVQEKEN
654	6151	A	676	21	340	
655	6152	A	677	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
656	6153	A	678	38	529	APSPDAMGHFTEEDKATITSLWCK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFAQ DVNLHC*QACMLDPENFQASWGN VL\VTRFWAIPFSGKEFHP*RCQAF LGRKMGDLELASALVPSRYH
657	6154	A	679	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EVQASWQKMVTGVASALSSRYH
658	6155	A	680	3	545	HSLFGTSEVINKLRSPDAMGHFTEE DKATITSLWGKVNVEIDAGGETLGR LLVVYPWTQ/RFFDSFGNLSSASAIH GQPPKSRHMGKKVLTSLGDAIKHL VDDLKGHLLPKPEVKLH\CDKAALL DPEELSSFLGEMLLGDPFLGNPIFGQ KNFTPEVARLSWAERWVTWSWPS ALVPSRYH
659	6156	A	681	1	432	
660	6157	A	682	334	845	AVRVRYVAFRYRAPRAVCLRLWSC RREVIHVPVRGKQGGKVRAKAKIS RSSPRGPCRFPVGPSCTELLRK\GNY AER/MSGAGAPV*LGGRCCLKYLTAE IPEAWLANAAA*QRRPRIIPRHLAS SPIRNDEGS*TKLLGQKLTHAQGGV LPNIQ\AVLLPKKDGESEGRRSK
661	6158	C	683	392	445	MQPAVQRVGNLSRYFPS*
662	6159	A	684	183	481	
663	6160	A	685	253	385	
664	6161	A	686	256	374	
665	6162	C	687	354	416	MKESPGGELPQTGKKPVFLF*
666	6163	A	688	2	171	
667	6164	A	689	320	584	TRLPFDRPRATGCHQPVPSERRSPIS QDRLTHVQLLFTWNPSP\LRPSKFSF EYLL\PPRSCTCGGSHPGPKP*ASR LTAAALLLVAA
668	6165	A	690	33	494	
669	6166	A	691	1	522	PLKRS DGCNDGRPTRPPTRPDITVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVDVGGKALGRLLVVYPWA TQRFESFGDLSTPDAVMGNPKV KAHS\KKVLRGAFSDGLAHL\DNLK GTFAHTEVSLHCDK\LHVDP*RTFR LLGQRAW SVVAGPIHFQKNFNPT SCRLA
670	6167	A	693	241	1104	
671	6168	A	694	95	462	
672	6169	A	695	33	494	
673	6170	A	696	1	523	PLKRS DGCNDGRPTRPPTRPDITVF TSIAHTDTMVHLTPVEKSAVTALW GKVNVDVGGKALGRLLVVYPWA TQRFESFGDLSTPDAVMGNPKV KAHS\KKVLRGAFSDGLAHL\DNLK GTFAHTEVSLHCDK\LHRGSLKNFR LLGQRAW SVVAGPIHFQKNFNPT SCRLA
674	6171	A	697	318	515	
675	6172	A	699	2	648	
676	6173	A	700	137	507	
677	6174	A	701	118	375	VAVVQIIFLPVFI AEKYKDLVPD NSK TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLK\A IRILVQERLTQD
678	6175	A	702	1	969	AATVLT TIGEAPSRSDSAPARPLAA SPVPAPPAPPRFFSPGRGPVDQSEKR WTMFRKLTSLDYHNPAFGNCKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ETEFRNFIVWLEDQKIRHYKIEDRG\NLRNIHSSDWP\FFEKYFKRC*TCPFKIQDRQESYLTGFFGLAVRLEYGDNAEKYKDLVPD\NSKTA*QLQLKIAEPLINLDVNNP\DFKAGVVGF*TWLQIQRH\DG\LP\GQMLKANS\GFVWQERLDHQGCQFA*GQIKQKRGLPV\ALDKHILGFD\TGDAVLNEAAQILRLHIEELRELQTKINEAIVAVQAIILDPKTDHRLGKSLEDEHLRTSASHLL
679	6176	A	703	105	1591	
680	6177	A	704	110	431	
681	6178	A	705	171	1577	GGNRATIQAGQCGNQIGAKFWGR*SVNEHGIRPHRPHTHGSDPAAWT RNPPVYYNESHKVGKYYVPR\AILGGI*EPGEPWDSVR\SGSFLGPPKGEKIFPPFRPDNFVFGQSGAGNN\WAKRPLAQEGAEL\VDS\VLDV\GTEGRQRS CD\CLQGFP*PTSLGRGGTGS\GMGTLLYQQGFKEYPD\RIMN\TF\SVVP\SPKCLD\TVVQPYKATLSVHQLVENTDETYCIDNEALYD\ICFRTLKL\TPTYGDLNHLV\SATMSGV\TCLRFPGQLNADLRKLA\VN\MPFRLHFFMPGFAPLTSRGSQYRAL\TVPELTQQV FDAKNMMAACDPRHGRYL\TVAAVFRGRMSMKEVDEQMLNVQNKNSS YFVEWIPNNVKTA\CDIPPRGLKMAVTFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGE\GMD\EFTEAESNMNDLVSEYQQYQDATAEEEEEDFGEAEAEAA
682	6179	A	706	1	558	
683	6180	A	707	1306	1459	LASMCWCWIESHFCPPGPTGGSRRGPP\HL\WLPGRSSGRSQRRLAESTEAPR
684	6181	A	708	1073	1324	
685	6182	A	709	1	797	
686	6183	A	710	1	3210	MVKGSIQQEELTILNIYAPNTGALRFIKQVLRDLQRDLDSHTIIMGDFHTPLSTLDRSTRQKVNKDIQELNSALHQEDLIDIYRTLHPKSTEYTFFSAPHHTYSKIDHIVGSKALLSKCKRTEIITNCLSDHSAIKLELRIKNLTQNRSTTWKLNNLLNDYWVHNEMKAEIKMFFE TNENKDDTTYQNLWDTFKA\VC\RGKFIALNAHKRKQERSKIDTLTSQ\KEL EKQEQTHSKASRRQEITKIRAE\KEI ETQKTLQ\NINESRSWFFERINKIDRPLARLIKKKREKNQIDA\IKNDKGDIT TDPTEIQTIREYYK\HLYANKLENLEEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQ\SIEKEGILPNSFYEASIIIPKPGRD\TTK\KENFR PISLMNIDAKILNKILAKRIQQH\IKNLIHHDQVG\FIPGMQGW\FNIRKS\INVIQHINRAKDKNHMIISIDA\EA\KAFDKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSQYKINIQA FLYTNNRQTESQIMSELPFTIASKRI KYLGQLTRDVKDLFK/ENHKPLL EIKEDTNKWNIPCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWY YQNRDIDQWNRTEPSEPTPHIYNL IFDKREKNKQWGKDSLNFNKCWE NWLAICRKLKLDPLTPYTKINSRW IKDLNVRPKTIKTLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPSLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGCGEIG TLLHCWWDCKLVQPLWKAVWRFL RDLELEIPFPAIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF
687	6184	A	711	1	2666	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSLDLQRDLDSHTLIMEDFNTF LSTLDRSTRQKVNKNTQELNSALH QADLIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEIITN YLSDHSAIKLELRIKNLTQSRSTTW KLNNLLLNDYVWHNEMKAEIKMF FETNENKDTTYQNLWDAFKAVCRG KFIALNAYKRKQERSKIDTLTSQK ELEKQEQTHSKASRRQEITKIRAE KEIETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNQIDTIKNDKG DITDPTEIQTITRESYKHLIYANKLE NLEEMDTFLDTYTLPRLNQEEVESL NRPITGSEIVAIINSLPTKKSPGPDGF TAEFY/PESYL*QTHRYHTEWAKT ASIPFENWHKTGMPSLTTPIQHSVG SSGQGNQPGEGNKGYSIRKRGSQIV PVCRRHDCLSRKPHRLSPKSP*ADK QLQQLRIQNQCTKITSILIHQQQTN REPNE*PIHNCFKENKIPRNPTYK GCEGPLQGELOTTAQGNKRGHKQ MEEHSMMLGRKNQYRENGHTAQG NLQIQCHPHQATNDFLHRIGKNYFK VHMEPKKSPHRQVNPKEQSWRH HTT*LQTLQGYSNQNSMVLVPKQR YRSMEQNRALRNAAAYQLSDL*Q T*EKQAMGKGFPI**MVLGKLASH M*KAETGSLPYTLYKNQFKMD*RF KR*T*NHKNPRRKPRHYH*GHRG QGLHVQNTKSNGNKSN*QMGSN* TKELLHSCRNYHQSEQATYNMGEN FRNLLI*QRANIQLQ*TQTNLQEK NKQPHQKVGEQHEQTLLKRRHLCS QKTHEMLITGHQRNANQNHYEIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SHTS*NGNH*KVRKQQERQNS
688	6185	A	712	1	4371	
689	6186	A	713	1	1849	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTFIMGDFNTP LSTLDRSRRQEVNKDTQELNSALH QADLIDIYRTLHPKSTEYTFFSATHH TYSKIDHIVGSKAVLSKCKRTEIITN YLSDHSAIKLELRIKKLTQNRSTTW KLNNLLNDYWVHNEMKAEINMF FETNENKDDTTYQNLWDTFKA/EIQA TIREYYK\HLYTNKLENLEEMDKFL DTYTLPRLNQEKVESLNRPTGSEIV AIINSLPTKKSPGPDGFTAIFYQRYK EELVPFLLKLFQSIEKEGILPNSFYEA SIILIPKPGRDTTKKENFRPISLMNID AKILNKILANRIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINRTKD KNHMIISIDAFAFDKIQQPFRLKTL NKLGVVDGTYLKIIRAIYDKPTANIIL NGQKLEAFPLKTGTGTRQGCPSPLLF NIVLEVLAIRAEKEIRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSW VGRINIMKMVILPKDSTWAEVLVG DRRSGRLTEMLVIFLVFQSFHSFLN TLMSPSIFSSWPCFCSSQLVSCLRT CRSVCLSSAAGVSRVASLGNQKKR DLGSENL
690	6187	A	714	1	1825	MVKGSIQQEELTILNTYAAHTGAPR LIKQVLSDLQRDLDSHTIIMGDFNTP LSTLDRSTRQKVNKDTQELKSALH QADLTDIYRTLHHKSTEYTFFSAPH HIYSKIDHILGSKALLSKCKRTEIITN YLSDHSAIKLELWIKNLTQNHSTTW ELNNLLNDYWVHNEMKAEIKMFF ETNENKDDTTYHNLWDTFKA VCRG KFIPLNAHKRKQERSKIDTLTSQKLE LEKQEQTSHKASRRQEITKIRAEK EIETQKTLQKINESRSWFFERINKID RLARLIKKKREKNQIDA KNDKGD ITDPTEIQTIREYCKHLYANKLEN LEEMDKFLDTYTLPRLNQEEVESLN RPITGAIEVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIIIPKPGRDTTKKEN FRPISLMNIDAKILNKKLAKRIQQHI KKLIHHDQVGFIIPGMQGWFNIRKSI NVIQHINRAKDKNHMIISIDAFAF DKIQQPFMLKTLNKLGIKYLGIHLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPKNILI TLQLLLVLPSTLIPLWLPALAGQ
691	6188	A	715	1	3552	
692	6189	B	716	1	3786	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMGDFNNP LSTLDRSMRQKVNKDTQELNSALH QVDLIDIYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIIT NYLSGHSIAKLELKIKNLTQNRSTT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion)
						WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKAGRKKEITKIRAQ LKEIETQKTLKKLMNPGAEIQTIRE YYKHLIYAKKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIITGAEIVAIINS LPTKKSRTRWIHSRILPEASIIIPKP GRDTTKKENFRPISLMNIDAKILNKI LAKRIQQHIKKLIHHDQVGFIPGMQ GWFNIHKSINVIQHINRAKDKNHHIS IDAEKAFDKIQPFMLKTLNKLIGID GTYFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVLEVL ARAIHQEKEIKGIQLGKEEVQLSLFA DEMIVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTRDV KDLFKENCKPLLNEIKEDTNKWKN PCSWVGRINIMKMAILPKVIYRFNAI PTKPPMTFFTELEKTTLKFIWNQKR ARIAKSILSQKNKAGGITLPDFKLYY KATVTKTAWYQYQNRDLQWNR TEPSEITPHIYSYLIFDKPEKNKQWG KDSLNFNKCWENWLPICRKLKLD FLTPYTKINSRWIKDLNVRPKTIKTL KENLGITQDIGMGKDFMSKTPKAM ATKDKIDKWDLIKLSFCTAKETTI RVNRQPTKWEKIFATYSSDKGLISRI YNELKQIYKKKTNNPINKWVKDMN RHFSKEDIYAAKKHMKKCSSSLAIR EMQIKTTMRYHLTPLRMAIIKSGN NSASPTARNKTARNQRTKMIAVTA PRNRAPLELELILYRQNRQSKTHILE TNNTSAELLVPFEEDYLIEIRTVSDG GDGSSEEEIRIPKMSMIDHILPKSIPE ELQNGEGFGYIIMFRPVGSTTWSKE KVSSVESSRFVYRNESIPLSPFEVK VGVYNNEGEGSLSTVIVYSGEDD GYVFLWMVEPQLAPRGTSLSQSFSA SEMEVSWNAIAWNRNTGRVLGYE VLYWTDDSKESMIGKIRVSGNVTT KNITGLKANTIFYFASVRAVNTAGTG PSSPPVNVTTKKSRYLITTAYLEVPE I*
693	6190	A	717	2	3155	
694	6191	B	718	1	3414	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMGDFNNP LSTLDRSMRQKVNKDTQELNSALH QVDLIDYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIT NYLSGHSAIKLELKIKNLTQNRSTT WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKAGRKKEITKIRAQ LKEIETQKTLKKLMNPGAEIQTIRE YYKHLIYAKKLENLEEMDKFLDTYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPRLNQEEVESLNRPIITGAEIVAIINS LPTKKSRTRWIHSRILPEVQGGTEK EGILPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILAKRIQQHI KKLIHHDQVGFIPGMQGWFNHKS NVIQHINRAKDKNHIISIDA EKAFD KIQQPFMLKTLNKL GIDGT YFKIIRA IYDKPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIROEKE IKGIQLGKQEVQLSLFADEMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENCK PLLNEIKEDTNKWKNI PCSWVGRIN IMKMAILPKVIYRFNAIPTKPPMTFF TELEKTTLKFIWNQKRARIKSI LSQ KNKAGGITLPDFKLYYKATVTKTA WYWYQNRDL DQWNRTEPSEITPHI YSYLIFDKPEKNKQWGKDSL FNKW CWENWLPICRKLKLD PFLTPYTKIN SRWIKDLNVRPKTIKTLKENLGITIQ DIGMGKDFMSKTPKAMATKD KIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPINKWVKDMNRHFSKEDI YAAKHKMKCSSLAIREMQIKTT MRYHLTPLRMAIIKKS GNNSASPTA RNKTARNQRTKMIAVTAPRNRAPL ELELILYRQNRQSKTHILETNNTSAE LLVPFEEDYLIEIRTVSDGGDGSSE EIRIPKMSTGGEEMA AVFKNKCR SWSRVVIAYHSSSGNQMG TNPEQD PGQHAIPLEGTLTHTRTHSDWDHLD TAMN*
695	6192	A	719	1	5127	
696	6193	A	720	965	9275	
697	6194	A	721	3	376	
698	6195	A	722	1	380	
699	6196	A	723	104	462	
700	6197	A	724	762	902	
701	6198	A	725	78	747	LRRGRSRETNEEPPPTVQVQGGP QREEKQKTKMAKFVIRPATAADCS DILRLIKELAEYEMEEQVILTEKDL LAEDGFGÆHPFYHCLVAEVPKEHW TSEG\HSIVGFAMY YFTY\DPW\IGQ VICILEDFFVMSDYRGSGIGSEILK\ NLSQ\VAMRCRCSSMHFLG*PEW\N EPS\NFY\KRRGAS\DLSS*RRGW\RL FQGS DKGVIWLKNGPTEGVEGVAC C
702	6199	A	726	149	460	
703	6200	A	727	1	501	
704	6201	A	728	1	391	SPLNKVQLINELNEREVQLGVANK VSWHSEYKDSA WIFLGG LPYDLTK GDHICVFSQ\QRSTIVADNFNGIKIK GRTIRVDHVS NYRAPKDSEEDVDT RQLQEKGC GARTPSPSLSESSEDEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTKKP
705	6202	A	729	18	240	
706	6203	A	730	254	1223	SPLTRVKLINELNEREVQLGVADKV FWHSEYKDSA WIFLGGLPYGLTEG DIICVFSQYGEIVNINLVRD\KKTGK SKGFCFLCYEDQRSTILAVDNFNGI KIKGRTIRVDHVS\NYRAPKDSIEDID DVTRQLQEKGGSGARPPSP\LSSESSE DEKPTKKHKDKK\EKKKKKKEKE KADREVQAEQSSSSPRRKT\VEKED DTGPKKHSSKNSERAQKSEPREGQ KLPKSR\TAYSGGAEDLERELKKEKP KHEHKSSSRREAREEKTRIRDRGRS SDAHSSWYNGRSEGRSYRSR\SRSR DKSHRHKRARRSRERESSNP\SDRW RH
707	6204	A	731	2143	2346	
708	6205	A	732	2016	2206	
709	6206	A	733	90	401	
710	6207	A	734	276	488	
711	6208	A	735	186	537	IWFPLRRRKARQEEKSGLGAPRSPS HNYP\PGYLGCLGKTNTS*TYILDQS NIGKRVA\AILN*ILGGRKLRLEKSL SCQPKVEELYERVAW/IP*KPGCLLL VSVKVRNVFDWCTWVY
712	6209	A	736	3	318	
713	6210	A	737	1	280	REPTMVLSPADKTNVKA\AWGKVG AHAGEYGAEALERMFLSFPTTKTP VNFKLLSHCLLV/TLAAHLP\AEFTPA VHASLDKFLGSVSTVLT\SKYR
714	6211	B	738	34	264	MVLSPADKTNVYFPHFDLSHGSAQ VKGHGKKVADALTNAV\RTVDDMP NALSALSDLHAHKLRVDPVNFKLL STACW*
715	6212	A	739	3	190	EPTMVLSPADKTNVKA\AWGKVGA H/AGEYGAEALERMFLSFPTTKIQIP LSWSLGGHASCP\LG
716	6213	B	740	12	298	MVLSPADKTNVKA\AWDLLPALRPE PRLCQVKGHGKKVADALTNAVAH VDDMPNALSALSDLHAHKLR\LA W*
717	6214	A	741	2	392	QTQREPTMVLSPADKTNVKA\AWG KVG\AH/AGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNAV/AHVGGPVNFKLLSHCLL VTLAAHLP\AEFTPAVNASLDKFLV SVSTVLT\SKYR
718	6215	A	742	623	1235	SNLVELSNTLSWSSGGKVGAHAGE YGAEALERMFLSFPTTKTYFPHFDL SHGSAQVKGHGKKVADALTNAVA HVDDMPNALSALSDLHAHKLRVDP VNFKLL\ASH\CLLVDPGPAHFPAEF TPAVHASLDKSTKYFPHFDLSHGS AQVKGHGKKVADALTNAVAHVDD MPNALSALSDLHAHKLSVDPGNFK LP\SHLPAGDPC
719	6216	A	743	117	403	
720	6217	C	744	62	370	MKSMRKQAPIITAFILTSR\SKGNWIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KLSASVNASLKIPVQCLEILPTTHCS SRDLIFQKFNLLMNQYLIYLGMLSV DTEEDTQLASLFPGEKHSSVSFVCP*
721	6218	A	745	3	1242	AAPQAGLSPVAIAAAIQLHLHSTQC SSPNTCCLPRRTRATIYYSRWYHP LGSVP*SP*PFQEAS/ALTLPACSFY GPLT*FQPKP*GSFPLSQ*MEYTIGL YT*TFHCPGTSRRQIPSSYLNCKDAF LPLL/SNPPQCRPFTGVGLVDVLTGF ETNNKYEIKNSFGQRVYFAAEDTD CCTRNC CGSRPFTLRJIDNMGQEV TLERPLRCSSCCCPCLQEIKSLDEQ CVVGKISKYWTGILREAFDADNFG IQFPLDLVKMKA VMIGACFLIDRN CSPAMEQSWMENYFDEMTEIGFRR SVITNFSSELKEHVLTHCKEANKNLD KMLDEWLTRKNSVEKTLNELMEV KTINEKLTIGKISKYWSGFVNDVFT NADNFGIHPADLDVTVKAAMIGA CFLFAFRLGSELHN
722	6219	A	747	129	1235	EGCAA AVPDSLEAQKRKPSPGGSL DLVSLGSGNSGSQRTVLIMDKQNS QMNASHPETNLPVGYPPQYPPTAFQ GPPGYSGYPGPQVSYP PPPAGHSGP GPAGFPVPNQPVYNQPVYNQPVGA AGVPWMPAPQPPLNCPGLELYLSQI DQILHQIELLEVLTFETNNKYEI KNSFGQRVYFAAEDTDCCTRNC CG PSRPFTLRJIDNMGQEVITLERPLRCS SCC\CPCCLEIEIQAPPGVPIGYVIQ TWHPCLPKFTIQNEKREDVLKISGP CVVCSCCGDVDFEIKSLDEQCVVG KISKHWTGILREAFDADNFGIQFP LDLDVKMKA VMIGACFLIDFMFF\ ESTGQPGNKNSGVWVVGFS
723	6220	A	748	647	797	
724	6221	A	749	2	424	
725	6222	A	750	2	460	ARATHREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALERMLLSF PTTPTYFPHFDLNHGSAHVKGHGK NVDDALTNAVTHVYMPNSLYALS DLHPHNL RMDPVNFMLLSHCLL*T LVVHLPAELTPAVHASLNNVLESER TELTSSTS
726	6223	A	751	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALERMFL/SF PTTKTYFPHFDLSHGSSQVKGHGK VADALTNAVGHVDDMPNALSALS DLHAHKL RVPVNFKLLSHCLLVT LAAHLPAEFTPAVHAFLDKFLASVS TVLT SKYR
727	6224	A	752	1	594	PRLFWSPTQREPTMVLSPADKTN VKA AWGKVG AHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGFAQVK GATGKKVDDIALTKRRGAPLDDMP NALVRPLKRPCTTHKAFGVEPGSTS KLLASHLPCLGEPWAAHLPRPSFNP WRLQRLPWGQSFLGFLVEEPLLEPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KIPVKA WKPSVGHCFAPWGFPAPSSLS
728	6225	A	753	2	386	
729	6226	A	754	33	476	
730	6227	A	755	5	417	
731	6228	A	756	1	412	
732	6229	A	757	2	446	
733	6230	A	758	3	713	
734	6231	A	759	87	236	
735	6232	A	760	181	322	
736	6233	A	761	213	427	
737	6234	A	762	213	422	
738	6235	A	763	1	732	
739	6236	A	764	31	1074	TLILSGFTVKQVYAIDQIFSSRLTITIKMFCGDYVQGTIFPAPNPNPIMDAQMLGGALQGFDCDKDMLINILTQR CNAQRMMIAEAYQSMYGRDLIGDMREQLSDHFQDVMAGLMYPPPLY DAHELWHAMKGVGTDENCLIEILASRTNGEIFQMREAYCLOYSNNLQEDIYSETSGHFRDTLMNLVQGTREEGYSDPAMAAQDAMVLWEACQKQTGHKTM LQMILCNKSYQQLRLVFQEFQNISGQDMVD AINECYDGYFQELLVAIVLCVRDKPAYFAYRLYSAIHDFGFHNKTVIRILIARSEIDLLTIRKRYK ERYGK\SLFHDIRNFASGHYKKSTGLPIC
740	6237	A	765	613	926	
741	6238	C	766	79	405	MIGGTPQMFFISGAKGQWSPSLQPPRAHRSSPWAPSSKSTSGGTAALGSLGSKDYFPRTGDBGVVELRRSDQRR AHLPGCPTVLR TLLPQQRGDRDLQQLRHHELRLS*
742	6239	A	767	1	321	
743	6240	A	768	110	431	
744	6241	B	769	756	1533	MREIVHIQAGQCGNQIGAKFWEPWKASSIELSQCRNSPSKVFRSKEHDGLPVTPPTRR*
745	6242	A	770	20	453	GIPGSTISLFCSEKKLREVERIVKAN DREYNEKFQYADNRIHTSKYNILTF LPINLFEQFQRVANAYFLCLLILQLI PEISSLTWFTTIVPLVLVITMTAVKDATDD\ILQNEKWMNVKVGDIKLEN NQFVAADLLLLSSSEPH
746	6243	A	771	1	1014	
747	6244	A	772	128	2654	LVQD HKAGEHQVGAMARLGNCSLTWAALIILLPGSLEECGHISVSAPIVHLGDPITASCIKQNC SHLDPEPQILWRLGAELQPGGRQQLSDGTQESII TLPHLNHTQAFLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTSSSLICQWEPGPETHLPTSFTLKSFKS RGNCQTQGDSILDCVPKDGQSHCCI PRKHLLLYQNMGIWVQAENALGTS MSPQLCLDPM DVVKLEPPMLRTMD PSPEAAPPQAGCLQLCWEPWQPGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HINQKCELRHKPQRGEASWALVGP LPLEALQYELCGLLPATAYTLQIRCI RWPLPGHWSWDWSPSELRRTTERAP TVRLDTWWRQRQLDPRTVQLFWK PVPLEEDSGRIQGYVVSWRPSGQAG AILPLCNTTELSCTFHLPSEAQEQVAL VAYNSAGTSRPTPVVFSESERGPAIT RLHAMARDPHSLWVGWEPPNPWP QGYVIEWGLGPPSASNSNKTWRME QNGRATGFLLENIRPFQLYEIIIVTP LYQDTMGPSQHVYAYSQEMAPSH APELHLKHIGKTWAQLEWVPEPPEL GKSPLTHYTIFWTNAQNQSFSAILN ASSRGFVLHGLEPASLYHIHLMAAS QAGATNSTVLTMTLTPEGSELHIL GLFGLLLLLTCLCGTAWLCCVAPT RIPSGQVSQTQLTAAWAPGCPQSW RSCPDPRDSGWGRHLK*AVLSPHI LVCRMPSSCPALARHPSQSCWRR MKRSRCPGSPITAQRPVASPLWSRP MCSRGTQEQQFPSPNPSLAPAIRSFM GSCWAAPQAQGGGTISAVTPLSPS WRASPPAPSPMRTSGSRPAPWGPW
748	6245	A	773	123	2486	
749	6246	A	774	128	2573	LVQDHKAGEHQVGAMARLGNCSL TWAALIILLPGSLEECGHISVSAPIV HLGDPITASCIHKQNCSHLDPEPQIL WRLGAELQPGGRQQRSLDGTQESII TLPHLNHTQAFLSCCLNWGNSLQIL DQVELRAGYPPAIPHNLSCLMNLT SSLICQWEPGPETHLPTSFTLKSFKS RGNCQTQGDSILDCVPKDGQSHCCI PRKHLLLYQNMGIWVQAENALGTS MSPQLCLDPM DVVKLEPPMLRTMD PSPEAAPQAGCLQLCWEPWQPGL HINQKCELRHKPQRGEASWALVGP LPLEALQYELCGLLPATAYTLQIRCI RWPLPGHWSWDWSPSELRRTTERAP TVRLDTWWRQRQLDPRTVQLFWK PVPLEEDSGRIQGYVVSWRPSGQAG AILPLCNTTELSCTFHLPSEAQEQVAL VAYNSAGTSRPTPVVFSESERGPAIT RLHAMARDPHSLWVGWEPPNPWP QGYVIEWGLGPPSASNSNKTWRME QNGRATGFLLENIRPFQLYEIIIVTP LYQDTMGPSQHVYAYSQEMAPSH APELHLKHIGKTWAQLEWVPEPPEL GKSPLTHYTIFWTNAQNQSFSAILN ASSRGFVLHGLEPASLYHIHLMAAS QAGATNSTVLTMTLTPEGSELHIL GLFGLLLLLTCLCGTAWLCCVAPT RIPSGQVSQTQLTAAWAPGCPQSW RRMPSSCPALARHPSQSCWRRM KRSRCPGSPITAQRPVASPLWSRPM CSRGTQEQQFPSPNPSLAPAIRSFM SCWAAPQAQGGGTISAVTPLSPSW RASPPAPSPMRTSGSRPAPWGPW
750	6247	A	775	151	273	

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751	6248	A	776	785	920	
752	6249	A	777	332	473	
753	6250	A	778	264	387	
754	6251	A	779	257	354	
755	6252	A	780	101	290	
756	6253	A	781	21	215	
757	6254	A	782	158	955	KMTSSSEQEEDKNNQSATPRQTGP ATTMNSKGQYPTQPTYVPQPPGNP VYPQTLHLPQAPPYTDAPPAYSELY RPSFVHPGAATVPTMSA AFG\ASL YLPMAQ\SVAVGPL\GSTIPMAYYP VGPIYPP\GSTVLGGKGGYDAGARF GAGATAGNIPPPPG\CPPNAAQLA VMQGANVLVTQ\RKGNFFMGGSDG GYTHLVRNQGHLCAREKTSHTLQH FSQCNCFSHINLKLQFRHMLLGCLS GAQTRHFSNLIRNHVMVAVPP
758	6255	A	783	167	342	
759	6256	A	784	368	525	
760	6257	A	785	311	487	
761	6258	A	786	148	298	
762	6259	A	787	164	314	
763	6260	A	788	232	382	
764	6261	A	789	2	390	
765	6262	A	790	3	376	AQKAGLGTIFIMTCSPLLLTLIHCT GSWAQPVLTQPPSVSAAPGQKVTIS CSGSGSNIGNNYVSWYQQLPDPLFH AHK*LLPGSRDSGLEAR*QPRQGS GDHHTLQTKQQQVRGQQLPEPDA
766	6263	A	791	2	353	
767	6264	A	792	2	382	
768	6265	A	793	3	654	
769	6266	A	794	9	885	
770	6267	A	795	1	412	
771	6268	A	796	2	616	WPIDIDIQCGGIPRDNLHDDLPSPP HPSHCPPTPAVSAEGRTRDQSSM TCSPLLLTLIHCTGPWAQSVLTQPP SVSATPGQRTVISCGRSNGDNYV SWYKQLPGTAPQLLIYDNNKRTSGI PDRFSGSKSGTSATLGITGLQTGDE ADYYCGTWDITLSAGVFGGWTKLT VLGQPKAAPSVTLFPPSSEELQANK AT
772	6269	A	797	489	715	
773	6270	A	798	20	371	
774	6271	A	799	181	382	
775	6272	A	800	353	479	
776	6273	A	801	3	368	HEAASSSSASPFQTKIEKMVDLTQV MDDEVFMAFASYATIILSKMMLMS TATAFYILTRKVFANPQHCVTFGKG ENAKKYLRDTRV*RVRRAHLNDL ENIIPFLGIGLLYLSGADPSTAI
777	6274	A	802	246	363	
778	6275	B	804	55	366	MGHFTEEDKATITSLWGKVNVEDA GGETLGRLLVVPWTQRFFDSFGN LSSASAIMGNPKVKAHGKKVLTSL GDAIKHLDDLKGTFAQLPHRLVIVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSSSVK*
779	6276	A	805	129	409	
780	6277	A	806	24	253	
781	6278	A	807	32	433	
782	6279	A	808	15	468	
783	6280	A	809	25	1404	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSA\SAIMGPNPKVKAHGK KVLTSLGDAIKHL\DDLKGTFAQLE *TCTCDKL\H\VDPENFKLLG\NVLV TVL\AIHF\GKEFTPE\VQSFLGRKMV TGVASALSFPDYH
784	6281	A	810	113	387	
785	6282	A	811	1330	1465	SECCGLSRPGHWPFI*WLPSL/CLI DVPT*QRKGGVLRNWWLPG*NLWE LLP/ALAGSGEGHLKNMTGSKLSRM PNRISDSESE/GVNTARIHGEMFWR GDNWACTCCRGARSLAADSADPA TGLTSFPLASASSA\TRASIPKRCLN SWFSTTRP
786	6283	B	812	17	718	MVVVAAAPNPADGTPKVVLLSGQP ASAAGAPAGQALPLMVPAQRGASP EAASGGLPQARKRQRLTHLSPEVPS LPRKLNKRVAAQTARDRKKARMSE LEQQVNQKLLLENQLLREKTHGLV VENQELRQRLGMDALVAEDFCLLQ SDILLGILDNLDPVMFFKCPSPEPAS LEELPEVYPEGPSSLPASLSLVGTS SAKLEAINELIRFDHIYTKPLVLEIPS DTG*
787	6284	A	813	464	714	
788	6285	A	814	349	581	
789	6286	A	815	223	513	DHEEPQAREGDQSVHRPHAERTGQ PGMWRHPRLEDCQPQELL/TKHSTS PSQEKEVHTPH/RPLESCWASLNR DPQHHSSPTPGKTSKSENKEIISQ
790	6287	A	816	384	464	PLPQLLRFAQPKPEAHLTPARPQPK RTCHGLTCRRGVSPGWRRDGPWRT HRSAGATRRPIQETASVPQPEAAPP HRARGSGKMRDGKPGAGNTERRD PQSRTVGLNKKNSTPHQSPQPPADV *TSAGG
791	6288	A	817	1	255	IVMGHSMLPHF*IWSPPPGRAAARL APLSGAGHSGPRLAPWT*AGQLQT QSLVRP*PELGKSELSAPSLVIGSW MDM*PKPGQ
792	6289	B	818	191	1072	MWRSCRLRLRXRGTPSPESAGGWPQ RFYESGANHPVSSPGLRPADRKEEV LFRMFSIHTGEALAIAVATEWDSQQ DTIKYYTMHLTTLCNTSLDNPTQRN KDQLIRAAVKFLD\DTICYRVEEPE TLVELQRNEWDPHIEWAEKRYGVEI SSSTSIMGPSIPAKTREVLSHLASY NTWALQGIDGSRPCCCSRLEEEYQI PEVGGNIEWAHDYELQELRARTAA GTLFIHLCSESTTVKHKLLKE*
793	6290	A	819	1518	1891	

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794	6291	A	820	217	491	
795	6292	A	821	1789	2411	KTYWRKKVEKVVSNNRLVTSPC/C IVTSTYGTANMGENH*KLQALKE TTSTMG/YMASQRKHRGIKPLTSLI IEYLKAKRPEGLRTDKSVKDL/VIL LY\ETALLSSGFQSWKIPRHH*QVS YRMIKL/GLGIDEDGPYLLDDTSAVA VNLKELPPLEGDDDTFTHGKEVGLI LLGLRGWTLPVSVLYNSSDNIFFQG CFPLFLVNI
796	6293	A	822	592	1122	
797	6294	A	823	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
798	6295	A	824	38	531	APSPDAMGHFTEEDKATITSLWGK VNVE/DAGGETLGRLLVVYPWTQR FFD/SFGNLSSASAIMGNPKVKAH GKKVLTSLGRCHKSTWDDLKG/TF AQA*SELHL*QSCNVDPENFKLLG/ NVLVTRFGQSHFRQKNFTPEGCRAS WAE/MMGDLQLASALVPSRYH
799	6296	A	825	1	278	
800	6297	A	826	80	591	RGCKREGLSMSSLIRRVISTAKAPG A\IGPPTVQAVLV\DRTHLHFRDQIG HGPLPSWTSCLPGGVAGRSLNKL KNMGEIPESLPGCDFTNVVKTTCS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRIEIEA\VAIQ GPLTTAFILSGDPCCVWDC
801	6298	A	827	1	396	
802	6299	A	828	1	346	
803	6300	A	829	3	720	RGIPASRWARKAVVLLCASDLLL LLLPPAG/SGRAEGSPGTPDEFTPP RKKKKKDIRDSNDADMARLLEHWE KHDD\NEEGDLPEHKRPSAPVDFSKI DPG\KPESILKMTKKGKTLMMFVT VSGSPTEKETEEITSLWQ\SLFNAN YDVQRFIVGSDRAIFMLRDGSYAW EIKDFLVGQDRCADVTLEGQVYPG KGGGSKEKNKTKQDKGKKKKEGD LKSRSKEENRAGNKREDL
804	6301	A	830	349	567	
805	6302	A	831	1098	1684	
806	6303	A	832	2	441	PCRNRSRVENFVSMWVCSTLWRVRT PPGSG/GLLPASGCHGPAASSYSA SAEPARVRALVYGHGDPKVVET VIPGHTWQLRNVA*PTLRR*FERNT HSSLDDMNISVWLCA*\LKNLELAA VRGSDVRVKMLAAPINPSDINMIQG
807	6304	A	833	3	421	ASMWVCSTLWRVRTPPGSG/GLL PASGCHGPAASSYSASAEPARVRAL VYGHGDPKVVVEGITRELFQRF WIFLQLITAVISSASTVLKNLELAAV RGSDVRVKMLAAPINPSDINMIQGN

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						YGFLPELPAVGGNEGV
808	6305	A	834	2	611	ILQLGRGRAVRVCSTLWRVRTPA\G SGG/GLLPASGCHGPAASSYSASAEP ARVRALVYGHGDPKVVVELKNL ELAAVRGSDVRVKMLAAPINPSDIN MIQGNYGLLPELPAVGGNEGVAAQV GAEGSNVTGLKPGNWVVPAINAGL RTWRNRG*VHPKEALIQVPSDIPLQ SAATLGVPCTAYRMLMDFEQLQP GDSVIQNAS
809	6306	A	835	159	312	
810	6307	A	836	637	974	
811	6308	A	837	240	419	
812	6309	A	838	20	283	
813	6310	A	839	508	715	IPGNFEP SRLGRG*KTQACSPSLWE FWLTQYLPALGAG\HILKNFTTFPVI SCVSKLSTLFGGKMPEN
814	6311	A	840	3	362	
815	6312	A	841	7	479	GAIMGVDIAINKDRRVRKPEKSDQ IYLRLLVKLYRFLARRTNSTFNQVV LKRLFMSRTNRPPLSLSRMIRKMKL PGRENKTAVVVGTTDDVRVQVEVP KLKVCALRVTSRARSRLRAGGKIL TFDQLALD/SPYVRSKGRKFERARG RRASRGYKN
816	6313	A	842	2	723	CAVNSAEQRGAIMVSGHLFITKDRK VR\RKEPKSQDIYLRLLVKLYRFLA RRTNSTFNQVVLKRLFMSPHQGP PLSLSRMIPED*SFPGPQKQRRVAV VGTTITD\DVVRVQVEVPKTERVCTC AVDQAGAPQAAIL\RAGGQDSFTFR PSLALGTSPKGLVGTCSWLFRFPRQ RGPRRWYPAIFGKGPQGTQAQATP KPYV\RSKGPKFERARG\RRASRGY KKLTLDPTLLLKKFLPKKK
817	6314	A	843	1221	2238	EPLIVCVCFCLCPPLFFSFSLGSAEK AVLEQFGFLTGTTEARCYTNHALSY DQAKRVPARWVLAEHIFQKAR*MG DADRKHCKFKPDNIPPTTFSFNFEN YVSGSWSRGHMAPAGNNKFSSKA MAETFYLSNIVPQDFDNNSGYWNRI EMYCRELTERFEDVWVVSGLTLP QTRGDGKKIVSYQVIGEDNVAVPS HLYKVILARRSSVSTEPLALGAFVV PNEAIGFQPQLTEFQVSLQDLEKLS VLVFFPHLDRTSDIRNICSVDTCCLL DFQEFTLYLSTRKIEGARSVLRLEKI MENLKNAEIEPDDYFMSRYEKKLE ELKAKEQSGTQIRKPS
818	6315	A	844	1	306	
819	6316	A	845	216	339	
820	6317	A	846	425	553	
821	6318	A	847	190	334	
822	6319	A	848	241	435	
823	6320	C	849	280	450	MLEKNWCPSLQVPIILNWAQPCGKI LTECCTLGYSLIQGDFTFIRKHAR TRLVKR*

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824	6321	A	850	1	301	
825	6322	A	851	2	3484	
826	6323	B	852	225	326	MAFKDTGKTPVEPEGAIHRIRITLTS RKRSFEK*
827	6324	A	853	348	515	AFKDTGKTPVE\PELAIHRI\IRITLTS\ RNVKSLEK\VSFAVMRGGGGIGRK ATSFTR
828	6325	A	854	42	529	SARSLLDSPHVRSRRTGKSVRKPA RNRPLAFKDT\GKTPVEPEV\AIHRI RITPNKAANVK\SLEKVVCLTLIRRA QKEKNFQS*KGPVS/RLPYPRFLRIH FQGKTPCGLKVFKDVGVRFPWRRI HK\RL\NDLHSPS\EIVKQITFHQYLSP GVEVEVHHLQML
829	6326	A	855	14	345	
830	6327	A	856	1	396	
831	6328	A	857	3	718	RGIPASRWARKAVVLLCASDLLLLL LLPPAG\SGRAEGSPGTP\DEFTPPP RKKKKDIRDSNDADMARLLEH\WE KHDDI\EEGDLPEHKRPSAPVDFSKI DPSKPESILKMTKKGKTLMMFVTV SGSPTEKETEEITSLWQ\SLFNANY DVQRFIVGSDRAIFMLRDGSYAWEI KDFLVGQDRCADVTLEGQVYPGKG GGSKEKNKTKQDKGKKKKEGDLK SRSSKEENRAGNKREDL
832	6329	A	858	80	349	
833	6330	A	859	504	738	
834	6331	A	860	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
835	6332	A	861	38	608	APSPDA\MGHFTTEEDKATITSLWGK\ VNVEDAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAI\MGNP\KVAH GKKVLTSLGDAIKHLDDLKG\TFAQ L\SELH\CDK\LVDPENFKLLGEML LVTVLAIPFRAKEFTPEGCRASWQ KQKMAEDGDLQWPSGPVPPDTTEA SWPMNSEAFKDKAFILASNYK
836	6333	A	863	727	1089	
837	6334	A	864	432	742	
838	6335	A	865	184	352	
839	6336	A	866	204	394	
840	6337	A	867	1	2286	MDLLGRVGSWALQSSCLTDPELW GWEGTPRFLAAAAQFGGPVLKAQ ACSLGAGIAPTELPRPVRWSLLFLA VRSNYQALWPQSPAGLPLVPQPETP RGANIPSPV\HAGDDRGWHMTV EQKFGLFSAEIKEADPLAASEASQP KPCPPEVTPHYIWIDVRACSPTKAV GCSTWGARTVPGVGVAEPKAFGKL GQSAQNPSSA VSAGPRFLVQRFEIA KYCSSDQVEIFSSLLQRSMSLNIGRA KGSMMNRHVAAGIPRFKLLTLGLSLL

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						HADVVPNATIRNVLREKIYSTAFDY FSCPPKFPTQGEKRLREDISIMIKFW TAMFSDKKYLTASQLVPPADIGDLL EQLVEENTGSLSGPAKDFYQREFDF FNKITNVSAIHKPYPKGDERKKACLS ALSEVTVQPGCSLPSNPEAIVLDVD YKSGTPMQSAAKAPYLAKFKVKRC GVSELEKEGLRCRSDSEDECSTQEA DGQKISWQAAIFKLGDDCRQDMLA LQIIDLFKNIFQLVGLDLFVFPYRVV ATAPGCGVIECIPDCTSRDQLGRQT DFGMYDYFTRQYGDSTLAFQQR YNFIRSMMAAYSLLLFLQIKDRHNG NIMLDKKGHIHIDFGFMFESSPGGN LGWEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLA VRPCLGST GDRVQQIESCLGDVQDVAGEA\YM DVVVS LVTIMLDTGLPCFRG/QIKFL KHRFSPNMTEREANFIMKVIQSCF LSNRSRTYNMIQYYQNDIPY
841	6338	A	868	3	164	
842	6339	A	869	1	5340	
843	6340	A	870	649	1028	
844	6341	B	871	1	5823	MCPVDFHGIFQDERRRDAVIALGI FLIESDLQHKDCVVPYLLRLLKGLP KVYWVEESTARKGRGALPVAESFS FCLVTLLSDVAYRDP SLRDEILEVLL QVLHVLLGMCQALEIQDKEYLCKY AIPCLIGISRAFGRYSNMEESLLSKL FPKIPPHSLRVLEELEGVRRRSFNDF RSILPSNLLTVCOEGTLKRKTSSVSS ISQVSPERGMPPPSPGGS AFHYFEA SCLPDGTALEPEYYFSTISSFSVSPL FNGVTYKEFNIPLEMLRELLNLVKK IVEEA VLKSLDAIVASVMEANPSAD LYYTSFSDPLYLTMFKMLRDTLYY MKDLPTS FVKEIHDFVLEQFNTSQG ELQKILHDADRIHNEL SPLKLRCA SAACVDLMVWAVKDEQGAENLCI KLSEKLQSKTSSKVIIAHLPLLICCL QGLGRLCERFPVVVH SVTPSLRDFL VIPSPVLVKLYKYHSQYHTVAGNDI KISVTNEHSESTLNVMMSGKKSQPSM YEQLRDIAIDNICRCLKAGLTVDPVI VEAFLASLSNRLYISQESDKDAHLIP DHTIRALGHIAVALRDT PKVMEPI QILQQKFCQPPSPLDVLHIDQLGCLVI TGNQYIYQEVWNL FQQISVKASSV VYSATKDYKDHGYRHCSLAVINAL ANIAANIQDEHLVDELLMNLEL FV QLGLEGKRASERASEKGPALKASSS AGNLGVLPVIAVLTRLPPIKEAKP RLQKLFRDFWLYSVLMGFAVEGSG LWPEEWYEGVCEIATKSPLLTFPSK EPLRSVLQYNSAMKNDTVTPAELSE LRSTIINLLDPPPEVSALINKLDFAM STYLLSVYRLEYMRVLRSTDPDRFQ VMFCYFEDKAIQDKSGMMQCVIA

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						VADKVFDAFLNMMADKAKTKENE EELERHAQFLLVNFNHIHKRIRVA DKYLSGLVDKFPHLLWSGTVLKT LDILQTLSSLADIHKDQPYDIPD APYRITVPDYEARESIVKDFAA GMILQEAMKWAPTVTKSHLQEYLN KHQNWVSGLSQHTGLAMATESILH FAGYNKQNTTLGATQLSERPACVK KDYSNFMASLNLNRNRYAGEVYGM RFSGTTGQMSDLNKMVMQDLHSA LDRSHPHYTQAMFKLTAMLISSE DCDPQLLHHLWCWGLPMFNEHGM ETALACWEWLLAGKDGVEVPFMR EMAGAWHMTVEQKFGFLSAEIKEA DPLAASEASQPKPCPPEVTPHYI WIDFLVQRFEIAKYCSSDQVEIFSS LLQRSMSLNIGGAKGSMNRHVAAI GPRFKLLTLGLSLLHADVPNATIR NVLR EKIYSTAFDYFSCPPKFPTQ GKRLR EDISIMIKFWTAMFSDKKY LTASQL VPPDNQDTRSNLDITVGS RQATQG WINTYPLSSGMSTISKKS GMSKKTNRGSQLHKYYMKRRTL LLSLLATEIERLITWYNPLSAPE LDDQAGENSVANWRKYISLSEKQW KDNVNLAWSI SPYLAVQLPARFK NTEAIGNEVTRL VRLDPGAVSDV PEAIKFLVTWHTID ADAPELSH VLCWAPTDPTGLSYFS SMYPPH PLTAQYGVKVLRSFPDAI LFYIP QIVQALRYDKMGYVREYILW A ASKSQLLAHQFIWNMKTNIYLDE EGHQKDPDIGDLLDQLVEEITG SLSGPAKDFYQREFDFFNKITN VSAIKP YPKGDERKKACLSAL SEVKVQPGCYLPSNPEAIVLDI DYKSGTPMQSAA KAPYLAKFK VKRCGVSELEKEGLR CRSDSE DECSTQEADGQKISWQAAI FKVGDDCRQDMLALQIIDLFK NIFQLVGLDLFVFPYRVVATA PGCGAIEC IPDCTSRDQLGRQ TDFGMYDYFTR QYGDESTLAF QQARYNFIRSMAY SLLFLQSK DRHNGNIMLDKKGHI IHIDFG FMFESSPGGNLWEP RHQA DG*
845	6342	A	872	1	337	
846	6343	A	873	1	337	
847	6344	A	874	838	929	
848	6345	A	875	21	338	
849	6346	A	876	2	424	
850	6347	A	877	3	452	
851	6348	A	878	3	604	PTLLVPTDSERTHPWLLSPADK VTN VKA\AWGKVG AHAGEYGA EALER MFLSFPTTKTYFPHFDL SHG\SAQV\ KGHG\KKVADALT NAVAHVDDMP NALSALSDLHA HKLARVGP GSTFKL LK/HTCL AGEPWAAHLPAEFQPLA VAT SSLGTFKFPGLLVEAPLLTFQIP V KAGSLGWPLFFCPLGLPSP SPFLH

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						PYPRGL
852	6349	A	879	2	416	EGKPRTSGAEHRSCRGKASMSPNF KLQCHFILIFLTALRGESRYLELREA ADYDPFLLFSANLKRELAGEQPYRR ALRCLDMLSLQGGQFTFTDDRPQLH CAGFFISEP\EESLPFHY\DQ*SIDGK AGNFLKVL MGRIL
853	6350	A	880	1	187	
854	6351	A	881	2	1099	PRVRGRVGEVGRKAQDLRSRQHS SCRGKASMSPNFKLQCHFILIFLTAL RGESRYLELREAADYDPFLLFSANL KRDVAGEQPYRRALRCLDMLSLQG QFTFTADRPQLHCAAFFISEPEEFITI HYDQVSI GLSKGGDF/LWKVFDGWI LKGEKFPASSQ\DHPLPSAERYIDF\C ESGLSRRSIRSSQNV\AMIFFRVHEP GNGISHLTIKTDPNLF SFAMFISSEFQ MGKFNLG*FPHQHRNCSFSIIPV\VI KISDLYPGGHVNGSFS*RKSSVAGCE GIGDFVELLGGTGLDPSKMTPLADL CYPFHGPAQMKVGC DNTVVRMVS SGKHVNRVDFLRIVQLEAVTSWEN PNG\NSIGEFCL SGL
855	6352	A	882	2	645	HGIQAHGQIPSYKTIGGRDDSFHTFF SETGAGKHVPRLLL* NWKPTVMDE VRTGTYCQLFHLEQFITARKIAANN YARGHYTIGKEIIDLVLDRIKRLAD QCTGLQGFLVFHSFGGGTSGGFTSL LMERLSVDYGKKSLEFSIYPAPQV STAVVEPYNSILTHTTLEHSDCAF MEEGEFSEAREDMAALEKDYE EVG VDSVEGE GEEEGEEY
856	6353	A	883	90	1657	EATTSPLRLRHQLGSREAATMRECI SIHVGGAGVQIGNACWELYCLEHGI QPDGQMPK*PKPLGEGDDSFNTFFS ETGAGKHVPRAVFDLEPTVIDEVR TG\TYRQLFHPEQLITGKEDAANNY ARGN\YTIGKEIIDLVLDRIKRLA\DQ CTG\LQGF LVFHS\FGGG\TSGGFTS\ LLM\ERLSVDYWQESPSLEFSIYPAA PRFPQPVVEP\YN\SILPTQHPPWEHS DCA\FM\VDNEAIYDICRRNLDIERP TYTNLNLRL\ISQIVSSITASLRF DGAL NVDLT E FQTNLG\PYPPIHFLATY APCHLC*RKPTHEQLFCSQRSPKCF AFEPTNPDG*NGDPRVHG*IHWLAC LLL\RGDVVPKRCQMLPIAHP SKP KRS\IQFVDWCP\TGFKVGINYQPP\ TVVPGGDLA\KV TREAVCMLSKHH SPFAEAWARPGPTSF DMLCQACPF VHWYLG\EGMEEGEFSK\ARKDMA ALAR KDYE EVG\VDSVKGE GEEEGK GILIHSLFGPCSMSCSQNF SFLTDR R
857	6354	B	884	46	386	XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKA AKL KEYEKDIAAYRAKGKPDAAKKG VVKA EKSKKKK EEEEEDEE DEE

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						EEEDXEDDDEEEDDDDE*
858	6355	A	885	263	484	
859	6356	A	886	146	826	TWKGKDPKKPRGKMSSYAFFVQTC RGGVHKKKHPDASVNFS/ESFSKKCS ERWKTMSA*/R/EKGKFEDMAKA/D KARYEREMKTYIPQGRGRQKRKF DSQLHPRGPPS\AFFLLALEYRPKI K\GEHP\GL\SIGDVAKKLGRDVGIN TAAD\DKQPYEKK\AAKLKEKEYEKD IAAYRAKGPDAACKG\VVKAEEKS KKKKEEEEDEEEG\DEEDEEEEEEDE EDEEDEEEDER
860	6357	A	887	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVGAGHAGEYGAEAL/RMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLP AEFTPAVHAFLDKFLASVS TVLTSKYR
861	6358	A	888	2	435	QTQREPTMVLSPADKTNVKAAWG KVGAGH/AGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNV/EHVDDMPNALSALS DLHAHKLRVDPVNFQAPKATGLLVDP GPAHFPGRVSPRLRLQGFLGTFKLG FC
862	6359	A	889	9	390	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAGHAGEYGAEALERM FLSFPTTKTYFPHFDLSHG\SAQV GPTAKKVAERADQTPWRNVDDMP KRRCPP*SDLH\AHKLARVDPVQLSS S*SHLPCW
863	6360	A	890	2	413	
864	6361	A	891	2	6281	
865	6362	B	892	79	200	XGDYPLGDLTPTTMEEATSGVNESE MAVASGHLNSTGVLE*
866	6363	B	893	209	502	MLLMYNSSDHDVYHMAVEMQRD VLEQIQFLATQLIMQTSSEGISAKS LRGRDSTRKQDASEKDSVPMGSPA FFSLSLWDTSGFGWILNKIIPMTLS*
867	6364	A	894	283	340	
868	6365	B	895	1649	1741	MSFAMTLKKKLEEEAEVKRKATD AAYQARQAVKTPPRRLPTVMVRSP DSASPGGDYPLGDLTPTTMEEATSG VTPGTLPTPVTSPFGIPDILPPGSAP LEAPMTPVTDDSPQKKMLGQKATP PPSPILLSSELLKKGSLPTSRLVNES EMAVASGHLNSTGVLLVGGVLP IHGGEIQQTNPNTVAASPAASESVQ ATIVMMPALPAPSSAPAVSTTESVA PVSQPDNCVPMEAVGDPHTVTVSM DSSEISMIINSIKEECFRSGVAEAPVG SKAPSIDGKEELDLAEKMDIAVSYT AVEAALSFCENDDPQSLPGPWEHP IQQERDKPVPLPAPEMTVKQERLDF EETENKGIHELVDIREPSAEIKVEPA EPEPVISGAIEVAGVVPATSMPEPPEL

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						RSQDLDEELGSTAAGEILEADVAIG KGDETPLTNVKTEASPESMLSPSHG SNPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SLEEPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNATLQSHTLADSIPSSP ASSQFVCSQEDQEAIAQAKIWKKA MLVWRAAANHRYANVFLQPGTR*
869	6366	A	896	3	2926	PGSTISSGTGKHKLLSTGPTWPWSIR EKLCLASSVMRSGDQNWVSVSRAI KPFAEPGRPPDWFSQKHCASQYSEL LETTETPK*VQSQRKRGEKGEVVE TVEDVIVRKLTAERVEELKKVIKET QERYR\RLKRDAELIQAGHMSRL DELCN\DIATKKKLEEEAEVKRKA TDAAYQARQAVKTPPRLPTVMVR SPIDSASPGGDYPLGDLTPTTMEEA TSGVTPGTLPSTPVTSPFGIPDTLPPG SAPLEAPMTPTVDDSPQKKMLGQK ATPPSPLLSELLKKGSLPTSPRLV NESEMAVASGHLNSTGVLEVGGV LPMIHGGEIQTPNTVAASPAASGA PTLSRLLEAGPTQFTTPLASFTN\VA SKPPVKLVPPPVEFFSQATIVMMPA LPAPSSAPAVSTTESVAPESQPDNC VPMEAVGDPHTVTVSMDSSEISMII NSIKEKCFRSGVTEAPVSGKAPSIDG KEELYLAEKMEIAVSYTGEELDFET VGDIHIEDKVDDHPEVLDVAAVE AALSFCENDDPQSLPGPWEHPQQ ERDKPVPLPAPE\MTVKQERLDFEE TENKGIHELVDIREPSAEIKVEPAEP EPVISGAEIVAGVVPATS\MEPPELR SQDLDEELGSTAAGEIVEADVAIGK GDETPLTNVKTEASPESMLSPSHGS NPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SL*EPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNATLQSHTLADSIPSSP ASSQFVCSQEDQEAIAQAKIWKKA MLVWRAAANHRYANVFLQPVTD DIAPGYHSIVQRPMDLSTIKKNIENG LIRSTAEFQRDIMLMFQNAVVMYNS DHDVYHMAVEMQRDVLEQIQQLA ATQLIMQTSVSGINAKSLRGRDSIT RKQDASEKDSVP\MGSPAFLLSLFD GGTQGTPLCPLKPDMMKKVKPQS YPL
870	6367	A	897	150	425	VYHFLVALKIPPSLMVFCCPSPFPS/ PPRLPPHPVLFPLPPSPSPSNP*VLGS PRGLSPPLL*GPPPPKPACFCSFP RDPGKLRWALRG
871	6368	A	898	65	259	
872	6369	A	899	273	962	KRERAVSLGQSGLPVAVRAGPQGGG CTWGADALGGTGACGACSLRSSTP HFLGQSERVPH*QGGVTGIFHHPEHG S*AKK/DPVRPPCA*QKGVAFLPA EA*VSGDQGGPGAVLSP/GRDCPFPS

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						PGP/PGNPQPLAARQGPAPGNSGSL WPWQEPPVDWPSEGTP\GPLLRQQL QSQPKNATGRERHPPQT/AKPFPSCP NTVL*IPEIK*NPWGEQQSRPALGST QDQRICNNH
873	6370	A	900	1	253	KRKVSLCHPGWSAGAPSRLTATSSS LV\KRFSCLSPSSWDYRCAPHLAN L/CRG/RGFTMLARLVLNS*PQMIYQ SRPPKVLGLQV
874	6371	A	901	327	638	LGLQGSTIFHKTLKKDLLQLEKQLN VNRDPGESNNSHNSQIKSFPKIYHFF FFGLLRN*PTNTLDRFVFGFENTHLS VL/QRKTISFNLVCWSHTPSINVCAI YQ
875	6372	A	902	834	1187	RKYETCLSALEIFT*SCSAVGII*FFC LFLGDEVLLCCPGLFTGCHHRWNY SLKLLGSKRSFCLSLSSWNYRHAP PSLGF*KNFKKNFE\KDLAML\PLGLV FNS\YP*VILLWASSNG
876	6373	C	903	150	364	MSILPLQSYINMNAGNLYGQMHNH FPYIVKQKKQVCRTVCTVSLVYHK MCVYMCVCECLXXXXXXXXXXXXX X*
877	6374	A	904	29	372	SYENNHSYAGWSGSRKRFTLFLQIY /CRYITPLYILLYVFEQ*VYYPFKVT* I*MQEIYMDRCITIF/LYIVKQKKQV CRNSVYSITCLPQNVCIGCVYVSUYI HTYIYIYTHHH
878	6375	A	905	1	815	MGNLGQVRRLSLWDYLLGLTHPRG LTTSQPGRSGLSPPAPPQSFQCMCQ NVTPGIMALGMSAVYFQVSGTKEQ PVPGHMPQSILLELWGFQVHHCV GNPRPDFMEHSKDLTSLLDHSC WHGRSHSSKEYLELHRENFLILRS AFPTGLLRAWPRDGISQYLLVELKN NMFRLVAGSAEGAAGPPCPGPRK VAKKKPHLKQAPKNAGPRRWDEG R*GFPSQKQKEEQKKLGA*KRKA RGGRGWPPTGGIK\KSGQKSKLFPW CLRRW
879	6376	A	910	140	512	PARGESRLDPSQWGEPAECAKEPT AVPRGPGLRNRTALTGTQKPPQSRE GARCIIGGSAPSTPPSSARRRWPGG HS*AGRPGRSSRQEPGCCIDRAPGP GLPPASQPPGAAPLRCPTAVGPS
880	6377	A	911	68	675	RSTRTVHIPLLSAQLPGQTP*PLSP WWFFCTPSSQGPPEPREDQPGCAPG PQEAPKPAGNLPPTDSSARAASETG RVLPS/PPTLIFCNLPRRG/FVSV WLMSPFIRL*EATPGPGGQSGDLGG LILHPGQPGHGGQQRGAAGALQR GP/DTSPTPCSRAAAAGMPTA*TLTP *RILPRTAPSPTTPGEQLPRPGNSGR DG
881	6378	A	912	3	3492	GGTVPQGLRTHGTGRGDTVGGDDGE PPQDRTLHLPQPPHLPAPGQGA PAGRGGGAAQ/AGSPTAPCGPGTS

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						GFAEDSREERGHRLPGEPEVPQP*R LHPG/PPGC/MPDVDFS NFSGESSDF DGLAGTSRN/RQAPGNPRSHGDIQA DRVPGWGHRRQAPAGGAEPGKGAEG GAAAAVPAAAGAPGGRDPCRGP PAGG*PQPHEA*G*RTL*P*GAEEAG RDAQPLAAL*QCAAGEGAGRLTLP QPAGGAVSTEAGAAASQHGFL* GIARAVPEDSQRPGVRG*GAEPPEG GE*ETALADFQPGGEGHSGAEPGRG AGEPTGAGGAHPLAAGAGRGCREA ARAGQTLRAAELHGPCVPLCPVLG REGTDPAAVPEE*DGLPTLQGECE AAGPGVRAAEGARPGVLRGQCSE GDFPEPGGEGLPQAGVRADGPGL RAAHTASPAAGRASGCAQAG/RPGP GSPVHGRSSGWCGCMPSAPETTAT A\PRQLHRVSALVGPECHVQPRAGG QLPLQQPRAPQPAVPVQAGGRGLR GRTL VFQQLPGDPGGRPGSPAGS*G RRPTPGL*APRHGRPSAAGKQPAAS LPWKA*CLGECTSRSSPGLQRRPHA AEASPQDPEPGHHAGVPGGCIAGA DQRHRREPHGHLHPPGHPGLGGGP DGLAPGHPCDGD*LRSLRALVQGS GGHDPGGGRGASQEGGRLLLPVCE GQHGR*EATPGPGGQSGDLGGLIL HPGQPGHGGQQRGAAGALQGRG AR/PPTPCSRAAAAGMPTA*TLTP*R ILPRTAPSPTTGLSSSS*PSSRT*LSS AP*PASHL/PGGPQ/IAGPHRQYQGS QGQPSAFVL*QGPVGPQQDGGGLQH VLLGRELPHPGALYPGAAPSTRPAP ACAPRAQGGWEDPERETVPPPRV*E VPGRVLEPGGV*GLEPGGDIIPGGR GVRGPLLGEPA\SCGVPHGKEHPCP PGRPAGQCLHPAQDGHLP HRHRL CQREDGKEAQEGPTAVGHLRGAAP GGCEAGGGRPGGALS IQQPGS*RL ERPGRPAQLCPPGHRRRAEEGATPT SSKN*PQARGRASPPSNASVTEELT QGRGWALPPSNASVTEELTQARGR ASPPSNASVTEELTQARGRASPC LH LRLSKDKLLPRNTTSGSLITSGSL LPISWKPAWGTGT
882	6379	A	913	232	485	TRLRLTPKVCYPYRWSHFDRKFLSRV LMRRSAQKSRDRILNVFHELN/NS VLDMRPMEF*GLRAAS*PQGERRGS LAFIREFHHT
883	6380	A	914	2	1163	
884	6381	A	915	771	1597	GACHLRLTPKVCYPYRWSHFDRKFP SARVLMRRSAQKSS/RDRILNVFHE L\NLKDAISYVAEVAEPLALPGRGC SRLGHWLIQFWT*GQWSFRVSGLLP D/TQGERRGSLAFIRSPSTDNVVNV DFTPRSSTVEASVSYLLYVAMVMQ LPWGRAQPRELRVTDRAVVAPGLG VAWKRGEVQKEGVGVSSHKPSYIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PWPDSLSAGRKVKGRGSSGLGARP DVFAPGPQQPVMVMPPLLLRPW APQLTASSHRRSTLPDVQMLGSPSL TARALERDQ
885	6382	A	916	3	471	DSWLWWLRQRLQQIGGISGSTSTSS MLSRVCGTSRQLAPVLGYLGSRQ KHSPLDLPYDYGALPHINAQIMQL HHSKHHAAYVNNLNVTEEKYQEA LAKGELLEAIKRDGFSDFKVKEL TAASVGGKGSWGGLGFNKERGH LQIAAWPNQDP
886	6383	A	917	54	873	GPRAAQERHSWLWWLRQRLQQIG GISGSTSTSSMLSRVCGTSRQLAP VLGYLGSRQKHSPLDLPYDYGAL EPHINAADHASLHHSKHHA/APYVN NLNVTEEKYQGGLWPRGDVYSPR* ALQPCT*KFNGGGHINHSIFWTN PQAPNGGGETQRGSLGSHQNVDF GS\FDKF\EKLTAAASVGC PKAPGW GWLGFQ*GNRGH/LYQIAACPKSGI PLQGTG/LLFPLLGIDVWEHALLPS SIKNVRPDYLKAIWNVINWENVTE RYMACKK
887	6384	A	918	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFT EVQASWQKMVTGVASALSSRYH
888	6385	A	919	41	601	APSPRRPWGHFTEEDQGLLSTSLWG K\VKCGKNAGRKKPLGKAPLVVL/H PWDPKRSFEQALGNPVLPSA\IMG NPPKSRAHGK\KVLTSLGEMPIKHP G*SSKGTFAQA*SELHCDK\LVDP ENFK\LLG\NVLT\VLAI\PFSAKEFT PGGCRASWAERWVTWSWPVPCSS RIPLSSLAHDCRAFQG
889	6386	A	920	14682	14931	EIGGPRPLPSPLP*ATSTSVLAASGR PERTRHAGIKIVLEDIFTLWRQVET KVRAKIRKMKVTTKVNHRDKINGK RKTAKEQSPLLQESLFATGDVSHNL LRALDVGLLANLSALAELDISNNKI STLEEGIFANLNLSEINLSGNPFEC DCGLAWLPRWAEQQVRVQPEA ATCAGPGSLAGQPLLGIPLLDSGCG EEYVACLDPDNSSGTVAASVSAAHE GLLQPEACSAFCSTGQGLAALSEQ GWCLCGSAQPSSASFACLSLCSGPP PPPAPTCRGPTLLQHVPASPGATLL AAFHIAAPLPTATRWDFGDSPEV DAAGPAASHRYVLPGRYHVM AVL ALGAGSALLGTDVQVEAAPAALEL VCPSSVQSDESLDLSIQNRVGSGL AAYSIVALGEEPARAVHPLCPDTEI FSGNGHCYRLVVEKAAWLQAQEQ CRAWAGATLAMVDSPAVQRFLVS RVTRSLDMWIGFSTVQGVGPAP QGEAFSLESCQNWLPGEHPATAEH

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						CVRLGPTGWCNTDLCALHSYVCE LRPGGPVQDAENLLVGAPSGDLQG PLMPLARQYGLSAPHEPVEVMVFP GLRLSREAFLLTAEFGTQELRRPAQ LRLQVYRLLSTAGTPENGSEPESSP DNRTQLAPACMPGGRWCPGANICL PLDASCHPRPAPMAARQGPGLLGA PYALWREFLFSVPAGPPAQYSVTLH GQDVLMLPGDLVGLQHDAGPGALP HCSPAPGHPPQAPYLSANASSWLP HLPALQEGTWACAPACALRLAATE QLTVLLGLRPNPGLRLPGRYEVRAE VGNGVSRHNLSCSFDVVSVPVAGLR VIYPAPRDGRLYVPTNGSASVLQVD SGASATATARWPGGSVSARFENAC PALVATFVPGCPWETNDTLFSVVAL PWLGEGEHVMDEVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQG VPVRYSPVVEAGSDMVFRWTINDK QSLTFQNVVFNVIYQSAAVFKLSLT ASNHVSNVTVNYNITVERMNRMQ GLRVSTVPAVLSPNATLALTAGVLV DSAVEVAFLWTFGDGEQALHQFQP PYNESFPVPDPSVAQVLVEHNVHT YAAPGEYVLTVLASNAFENRTQQV PVSVRASLPSEAVGVSDGVLVAGRP VTFYPHLLPSGGVLYTWDFGDGSP VLTQSQAANHTYPSRGIYHVRLEV NNTVSGAAAQADVRVFEELRGLSV DMSLAVEQGAPVVVSAAVQTGDNI TWTDFMDGDTVLSGPEATVEHVYL RAQNCTVTVGAASPAGHLARSLHV LVFVLEVLVPEPAACIPTQPDARLT AYVTGNPARYLFDWTFGDGSSNTT MRGCPTVTHNFTSRGTFPLALVLSS RVNRARYFTSICVEPEVGNVTLQPE RQFVQLGDEARLVACAWPPFPYRY TWDFGTEEAVPARVGGPEVTFIYRD PGSYLVTVTASNISAANDSALVEV QEPMLVTSIKVNGSLGLELHYLWD LGDGRLEGPEVTHAYNSTGDFTV RVAGCNEVSRSEAWLNVTVKRRVR GLIVNASCTVVPLNGSMSFSTSLEA GSDVRYSWVLCRCTPISGAENEV GSAQDSIFVYVLQLIEGLQVVGGR YFPTNHTVQLQAVVRDGTNIYSWT AWRDRGPALAGSGKGFSLTALAEAG TYHVQLRATNMLGSAWADCTVDF VEPVGWLMVAASPNAAVNTSVTL SAELAGGSGVVYTWSLLEGLSWET PEPFTTHSFPTGLHLVTMTAGNPL GSANATVEVDVQVPVSGLSIRASEP GGSFVAAGSSVPFWGQLATGTNVS WCWAVPGGSSKRGPVHTMVFPDA GTFNIRLNASNAVSWVSATYNLTV EEPVGLVLWASSKVVPAGQLVHF QILLAAGSAVTFRRQVGGASPEVLP GPRFSHSFPRIGDHVVSQSKNHVS

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						WAQAQVRIVVLEAVSGLQVPNCCE PGIAMGTERNFTARVQRGSRVAYA WYFSLQKVRGDSLFIISGRDVTYTP WPRGCWRSSNRTLVLVQDAVQ YVALRSGPCFTNRLAQFEAATSPSP RRVAYHWDFGDGSPGQDTDKPRA EHSYLRPGDYRVQVNASNLVSFFV AQATVTVQVLACREPEVDVVLPLQ VLMRRSQRNCLDAYVDLRDCVTY QTEYRWEVYRTASCQRPGCPARVA LPGVDVSRPQLVLPRLALPVGHYCF VFVVSFGDTPLARSIQANVTVAPER LVPITEGGSYRVWSDTQDLVLDGSE SYDPNLEDGDQTPLSFQWACVAST QREAGGCALNFGPRGSSTVTIPRER LAAGVEYTFSLTVWKAGRKEEATN QTCWWRPRALPSLFLMQILCNTTA CFSFASFQTCSSSTYSLQATYALVT KATQSPSNTNRSSWLQYTRTHTPVS SALCMPFRPGWKVANRMSILGGG WHDAEDAGAPLVYALLQRCQCG HCKEFCVYKSSLSGYGAVLPPGFRP HFEVGLAVVVQDQLGAAVVALNR SLAITLPEPNGSAMGLTVWLHRLTA SVLPGLLRQADPQHVEYSLALVTV LNEGPSRELVCRSCLKQTLHKLEA MMRILQAETTAGTVTPTAIGDSILNI TGDLIHLASSDV RAPQRSELGAESP LRMVASQAYNLTSALMRILTRSRV LNEEPAFSRAPANLSDVVQLVFLVD SNPFLFGYISNYTVSTKVASMAFQT QAGAPIERLASERAITVKVPNNSD WAARGHRSSANSVVVQPQASVGA VVTLDSSNPVAVLHLQLNYTLLDG RYLSEPEPYLAVYLHSEPRPNERN CSASRRIRPESLQGADHRPYTFFISP GTRDPVGSYRLNLSSHFRWSALEVS VGLYTSLCQYFSEEDVVWRTEGLL PLEETSPRQAVCLTRHLTAFGASLF MPPSHVRFVFPEPTADVNIYVMLTC AVCLVTYMVMAAILHKLDQLDASR GCAIPFCGQGRFKYEILVKTGWGR GSGTTAHSVIMLYGVDSRSGHRHL DGDRAFHRNSLDIFQIATPHSLGSV WKIRVWHDNKGLSPA WFLQHIIVR DLQTARSTFFLVNDWLSVETEANG GLVEKEVLAASHAALLRFRLLVA ELQRGFFDKHIWLSIWRPPRSCFT RIQRATCCVLLICFLGANAVWYG AVGDSAYSTGHVSRLSPLSVDIVA VGLVSSVVVYPVYLAILFLFRMSRS KVLIDISCLDSSVLDSSFLTFSGLHA EVRALLGVLGWAGGPAALAQGL QTLCTSQQAFAGQVKSDLFLDDSK RSGPVVPVFPFPPCPKPPPLSWLPQG ALKGPGHAGIKIVLEDIFTLWRQVE TKVRKIRKMKVTTKVNHRHDKING KRKTAKEQ

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890	6387	B	921	1	714	MVKLSIVLTPRFLSHDQGQLTKELQ QHVKSVTCPCPYLRKVINTLADHR HRGTDGFGSPWLLIITVFLRSYKFAI SLCTSYLCVSFLKTIFFPSQNGHDGST DVQQRARRSNRRRQEGIKIVLEDIF TLWRQVETKVRACKMKVTTKV NRHDKINGKRKTAKEHLRKLMSKE REHGEKERQVSEAEENGKLDMEI HTYISPLLQESLFATGSEWRQRSIVI LQDCPTGPTSQKLK*
891	6388	B	922	1	387	MRVRWLLFWLLFWLLGFISHQST CVINTLADHRHRGTDGFGSPWLLII TVFLRSYKFAISLCTSYLCVSFLKTIFF PSQNGHDGSTDVQQRARRSNCRRO EGIKIVLEDIFTLWRQVETKVRACK KMK*
892	6389	A	923	277	489	
893	6390	A	924	465	634	
894	6391	A	925	1	4652	MGSTGVYKVTPRSCHRFEQAFYTY DTSSPSILTLTAIRHHVLGTITTDKM MDVTVTIKSSIDSEPALVLGPKLSV QELRREQQLAEIEARRQEREKNGNE EGEERMTKPPVQEMVDELQGPFSY DFSYWARVLCFVGTGPAKLKYINY FRSGEKITVTPSSKELLYPPSMEAV VSGESCPGLIEIHGKAGLFLEGQIH PELEGVEIVISEKGASSPLITVFTDDK GAYSVGPLHSDLEYTVTSQKEGYV LTAVEGTIGDFKAYALAGVTLHSQ DVLMLPGDLVGLQHDAGPGALLHC SPAPGHPGPQAPYLSANASSWLPPL PAQLEGTWACPACALRLLAATEQL TVLLGLRPNPGLRLPGRYEVRAEVG NGVSRHNLSCSFDVVSFVAGLRVIY PAPRDGRLYVPTNGSASVLQVDSG ASATATARWPGGSVSARFENACPA LVATFVPCPWEWNTDLFSVVALP WLGEGEHVMDDVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQ VPVVLLAGSSGYLVGKFLESHGSD SGSANSFHLISRNEFKTLPDLTRV PRYSPVVEAGSDMVFRWTINDKQS LTFQNVVFNVIYQSAAVFKLSLTAS NHVSNVTVNYNITVERMNRMQGL RVSTVPAVLSPNATLALTAGVLVDS AVEVAFLWTFGDGEQALHQFQPPY NESFPVPDPSVAQVLVEHNVTHTY AAPAALGGGAVLTRQPSVLLHLCS VPHVAWEPGLKAGPQVSTVLTVL ASNAFENRTQQVPVSVCASLPSVSV CASLTGACWYPRVLIIRSGRVPIVSL ECVSCKAQAVYEVSRSSYVYLEGR CLNCSSGSKRGYTFTLTVLGRSGE EEGCASIPSPNRPLGGSCRLFPLG AVHALTTKVHFECMGWHDADAG APLVYALLQRCRQGHCEFCVYK GSLSGYGAVLPPGFRPQFEVGLAVV VQDQLGAAVVALNRSIAITLPEPNG

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						SAMGLTVWLHGLTASVLPGLLRQA DPQLVIEYSLALVTVLNEYERALDV AAEPKHERQRRQIRKNITETLVSL RVHTVDDIQQIAAALAQC MRKLPE QDIAQGSYIALPLTLLVLLAGYNHD KLIPLLLQLTSRLQGVGALGQAASD NSGPEDAKRQAKKQKTRRTLATSIN TSREPSTDDQLPAHNQTMPQRHAR RSAPPRAYDRKTRQEENPHQTRSH AAAKRRERPPHDLQKQATTRLIPAG PRRRDGTSPRRQTQPPNTRRPAAAG HLARFRAAPGARGARPTARRGR EELDPAHIYAAAPGLPTPPRAGRTPP TPERRDRNTRRRRTREEGEGEFPRV SFLKTIFPSQNGHDGSTDVQQRARR SNCRREQEGIKIVLEDIFTLWRQVET KVRKIRKMKVTTKVNRHDKINGK RKTAKEHLRKL SMKEREHGEKERQ VSEAEENGKLD MN*IH FYMEMFQR AQUALRRRAEDYYRCKITPSARKPLC NRVSLLVFLAFGHSLPGQMDTFFS LRLCASSPAEGDGREEGCLQAFVTP SLLVTVL RKNTFIPTQWGPLIF
895	6392	A	926	3	156	EMFQRAQ/ALRRRAEDYYRCKITPS A\RKLLCNRCTYNLVLP GSEKKYY S HA
896	6393	A	927	183	1518	ASTQSAVGLVSSVVYPVYLAILFL FWMSRSKVAGSPSPAGQQVLDID SCLDSSVLDSSFLTFSGLHAEVINTL ADHQHRTGDFGGSPSVLIITVSLRSY KFAISLCTSYLVWINTLADHRHRTG DFGGSPWLLIITVFLRSYKFAISLCT TYLC\VSFLKTIFPSQNGHDGSTDVQ QRARRSNCRREQEGIKIVLEDIFTLW RQVETKVRKIRKMKVTTKATRLT KIKERRKTAQDHWRL SMKEREHG EKERQVSEAEENGKLD MKEIHTYM EMF\QRAQALRRRAEDYYRCKITLF QRKPLCNVRMAAVEHRHSSGLPY WPYLPATLKNRMGHQPPPTQQH SIIDNSLSLKT PSECLLTPLPPSALPS ADDNLKTPAECLLYPLPPSADDNLK TPPECLLTPLPPSAPPSADDNLKTPP ECVCSLPFHPQRMISRN
897	6394	A	928	123	1040	WRWFTIGTFRILLMFCCLGYEWLSG /GCTTWHSAWV*GSSCHPAICFLCF VAKSDP*RNPGLRKERTPRSQGQ SWFGEDQKSGLSILWADIVHRTG\D\ FGGSPWLLIITVFLRSYKFAISLCTSY LCVSFLKTIFPSQNGHDGSTDVQQR AR\RSNRRRQEGLSICMHTKKRVS SFAGIKIVLEDIFTLWRQVETKVR KIRKMKVTTKVNRHDKINGKKKTA KEHLRKL\GMKERE\HEEKERQVSE AEENGKLD MKEIHTYMEMFQRAQ ALRRRAEDY*QHDKITPSARKAFFA NRVQQWRQW
898	6395	A	929	39	525	TKFVLGT FQILFTASFHPSWWPLA

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						LENPHDSNLSGLFPLIDLDFSP*VLS CWASHTMENCs*LRsKRQITLWCS RMAELVYCLSWKCSHLKRHDFPM GKYQTPTCIDKGNMLYLSKLLGIES QCLGAEMGIPIKAMQSFTTSGRPKN EHSRNFVIIWKVLI
899	6396	A	930	1030	1384	LIALRKMGRNAQAQICIT\SDG*NPS PLKTESTLKT\TQFSLYPWGEKFERT PSLMGQKNFRFTVCQLSQMGAIGFQ/ HIQEWdGERKST\ITKKN*KDGEISW LECMNN\VTCTPDSMKK
900	6397	A	931	1	225	
901	6398	A	932	2	167	
902	6399	A	933	1	3339	PASVHPSVRPTVQRKGLQAGRTSTR GTEARRGAKSAADPCGPGQGTVA AMQSCARAWGLRLGRGVGGRRRL AGGSGPCWAPSRDSSSGGDSAA AGASRLLERLLPRHDDFARRHIGPG DKDQREMLQTLGLASIDELIEKTVP ANIRLKRPLKMEDPVCENEILATLH AISSKNQIWRSYIGMGYYNCSVPQT ILRNLENSGWITQYTPYQPEVSQ RLESLLNYQTMVCDITGLDMANAS LLDEGTAAAEALQCYRHNKRRKF LVDPRICHPTIAVVQTRAKYTGVL TELKLPCEMDFSGKDVSGVLFQYP DTEGKVEDFTELVERAHQSGSLAC CATDLLALCILRPPGEFGVDIALGSS QRFGVPLGYGGPHAAFFAVRESLV RMMPGRMVGVTRDATGKIEVYRL AP*KPREQHRRDKATSNICTAQAL LANMAAMFAIYHGSHGLGHIA\R RVHNATLILSEGLKRAGHLQHDLF FDTLKIQC GCSVKEVLGRAAQROIN FRLFEDGTGLISLDET VNEKDLDDL LWIFGCESSAELVAESMGEECRGIP GSVFKRTSPFLTHQVFNSYHSETNIV RYMKKLENKDISLVHSMIPLGSCTM KLNSSE LAPITWKEFANIHPFVPLD QAQGYQQLFRELEKDLCELTGHDQ VCFQPN SGAQGEYAGLATIRAYLN QKGEHRTVCLIPKSAHGTPASAH MAGMKIQPVEVDKYGNIDAVHLK AMVDKHKENLAAIMITYPSTNGVF EENISDVCDLIHQHGGQVYLDGAN MNAQVGICRPGDFGSDVSHLNLHK TFCIPHGGGGPGMGPVGKHLAPF LPNHPVISLKRNEACPVGTVSAAP WGSSSILPISWAYIKMMGGKGLKQ ATETAILNANYMAKRELETHYRILFR GARGYVGHEFILDTRPFKKSANIEA VDVAKRLQDYGFHAPTMSWPVAG TLMVEPTESEDKAELDRFCDAMISI RQEIADIEEG\RIDP\RVNPLKNVLH TPLTCVTSSHWD RPYSREVA AFPLP FVKPENKFWPTIA\RIDDIYGDQHL\ VCTCPPM\EVYESPFS\EQKRAVFLV LCSLSFKGIDFDGLSPEAFDKQERFH

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						LPTPSLK
903	6400	A	934	2	287	
904	6401	A	935	36	427	
905	6402	A	936	247	1183	CCWESVPDPQLRQISGIALFCSFKE PPLLLGVLHPNTKLRQGRKGCLKIN LLGPES\MAHIGGCDVYWGQQMGR VVKLENG*NRRLPGFGSGPLAKPE DDEPCVWGDPLGIRGRGPKWGLLF VGR\LTRGLF*R*NPWETVKVKLLL SSETPI*GGRNMSFVNDLTVTPGW KEDLISP\NPKQQNGQRRKLPAFWV MGGHKMTGR\LEV*YCDPGK*KFY WTQLRFPNGVQPV*QK\TSLVAET SMARIRRVYVSGPDERR\ADLFVEN MPGFDPNIRPSSSGGYWVGMSTIRP *PGSSMLDFLSERPWD
906	6403	A	937	179	516	VFSVLRAEDKICELLFCLKIKLFSA\S FLVFRNQLPRKND\FYSEPPSENPP ETGESVCLQLKSGAHL\CRVCGCLG PKTCSRCHKAYYCSKEHQ\TLDWRL GHKQACAQPGG
907	6404	A	938	41	274	KRGTERKTHFGGCSIQFSDIASGKNI LPGLCFLTHKR\WFCSL*RQGWVSR WSHE*GCTRCWRLGKFLWVADRFL GSG
908	6405	A	939	3	1111	CAPRQPAPRMAAAGARPVELGF AE SAPA\WRLRSE\QFPSKVGGRAWLG AAGLPGPQALACELCGRPLSFLQV YAPLAPGR\PD\A\FHRCIFLCCREQP VCCAGLARFLGIRLPRKN\DFYSYEP PSENPPPETGESVCLQLKSGAHL\CR VCG\C*GPKTCSRCHKAILLAAREH QTLADWEIGDIRQ\ACAQPDHL\DH NFQDHNFPFFQEF\EIVETEDEIMP* GVWKKEDYSRDY*GALG*STLKGR TWISM\AKHE\SRED\KFFQKF*NFRL ALGTEQDS*YAGRG\IAPWISGENIP QEKDIPDCPCGAKKILEFQVMPQLL NYLKADRLGKSIDWGILAAFTCAES CSLGTGYTEEFVWKQDVTDTTP
909	6406	A	941	3458	4042	AGMIRRPSPWPSIRPPAVFTNSCTS LQEPSSGGTGRVQVPSIYQASISTQIC VKGPD*GRNGKGNLSFGKAGIFHFP WCPKCPRPSSSPISMGLLSPEVDSVE R\PTTFRFPLAPIYKECV*NGAG/AQ APDPRQKRGWPCHWNLMGVGRMP RVSPHLEAWGPKHPDDRYTKGTA ICPRNHLPCDPRISAIGQPQG
910	6407	A	942	226	401	TSGDHWNI\AVAPHENS\DLLLVQGH DYKYRYFGLIVCVL*QAI\VTPEEPQS IVPRLRTR
911	6408	C	943	211	282	MFYPPFNPRYFSVGFIAMNRHTD*
912	6409	A	944	1390	1698	HLFPHIKAGR*YGRPCREGILQ*KE* ETTGRHTCVLQGL\FQEVVVQVRN VFLHEALQLVKFAMQIFEV\LEKFP EPIVKHDL\QNT\EC\FFRHMEKEHS SKK

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913	6410	A	945	27	412	IAEGNWCVYMPDIIWVFPQAEAE DCHSDTVRADDDEENESPAETDLQ AQLQMFRAQWMFELAPGVSSSNL ENRPCRAARGSLQKTSADTKGKQ EQAKEEKLSIIDIVTNYIFFFWHMEIF TGHSK
914	6411	A	946	24	1489	GGSSAAASGVSSRADAPVLAQSPAS AGNGRPSTPRVPGSRRHPSAPRSGP LPREDGCRTPGPQLPLHGA\LLRPR TLLSSAAEDKARSRH\PDQHPSSG GRCKGGTESPSSAAGRPASMAEAE\ EDCHSDTVRADDDEENESPAETDV QALIPMIQAQWKLEAPRVSSSNLE NRPCRAARGSLQKTSADTKGKQEQ AKEEKARELFLQAVEEEQNGALYE AIKFYRRAMQLVPDI\EFKITF\TRSP DGDGVGNSYIEDNDDDSKMADLLS YFQQQLTFQESVLKLCQ\PELESSQI HISVLPMEVLMYIFRWVGSSDLDLT SL\EQSLSLVCQRIPNILCPETPENMPV LALL*KFWGR\SC\IKLVSVTSPGRE DVF*ERP\RV\FDGVYISKTTYIRQG EQSLDGFYRA\WH\QVEYYRYIRFFP DGHVMMLTTPEEPQSIVPRL\TRE YQGLDAIPTGV\TIRLSPRHRTIRTQSI WLLITKEKRKEKPL
915	6412	A	947	17	499	DRVLLCN/PRLECNGMITAHCSKPKP GSK*SSCSLPSSWDYKHEPPYRAN LKNFFVETGSLYVAQAGFELLDSSN PPCFSLPKCWDYRPP*ATTPS/FKND SHFNFLNRF/SHFVVF*VLRNLNC NNIP*GLKVGEIQSPKAETKLGVER GGKNYIRFSK
916	6413	A	948	9	296	RPSHQCRLLPPRASLGLSELCPEDQ QSYIP*LGHSAECR*S/TSGGSCPLS SVSSQASRAS/GPTSLTTAAPTSPRT GASALTEQYWSNRFLNHFAE
917	6414	C	949	114	383	MQMVGVWGGGLGGIKQDKVLLSSE GPRSRDGGGTWRPTLKTSTVRXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXSALL*
918	6415	A	950	1896	2251	IGTPLCRMEIDPFLEEAVPWSSVSSQ ASRASWPTSLTTAAPTSPRTGASAL TEVGRPKT*DHKISSVSTK/TSSHCP GPEHTTSAVPVSRASSCPVTVTTKL SKHPLQLARRVGFTLLY
919	6416	A	951	141	439	
920	6417	A	952	278	1177	RHPLAFFKASRAGPQRPLDGTLGPE DSRASSPMIQNSRPSLLQPQDVGDT VETLMLHPVIKAFLCGSISGTCSTLL LQ\PLDLLKTHLQTLQPSDHGSRV GMLAVLFKGV\TERLLDLWKGMS PSIVR\VSLGVGIYFGHSLLF*SSISW RRPIQTALEV\NHAGGSGSRVAG VCMSPITVIKTRYESGKYGY\KSIYA ALRSIYHSEHGRGLFCGLTATILRD APLSGIYLMFY\NQTKNIVPHDQVDA TLIPITNFSCGDICWYSGPHWVTSTC

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						GMFIQNSYGRLLFHLKVSMDWPST
921	6418	A	953	109	376	SLTRAKSHLGQQFPTSRTSQEENWS P*RGSRTPPTPHLPCQNLRPMSMT/F *QVNFKQFRGAFLSG*KSSVAIRTIQ QSNMALMGTYAL
922	6419	C	955	123	329	MISRAPLPQLSELHCDKLHVDPENX KLLGNVLVTVLAIHFGKEFTPEVQA SWQKMVTAVASALSSRYH*
923	6420	A	956	41	565	APSPRRPWGHFTEED\KAT\TSLWG K\VNVE\DAGG/EKTPGKGPLVVLPP WTPEVPLTSFGNLS\SASAHHGQTP KVQGTMAKKVLTSLG\DA\TKHL\D DSQGAPFAQA*SELALVDKPMWD PENFKASWGNVLVTRFGQSHFRA KNFTPEGCRVSLGRKMGDLELASA LVPSRYH
924	6421	A	957	1	1000	STRAPSPGPFSSKLAGAYKSWCRR DPRTHSAGAQAARSVPICPAPT ASATMSHHWGYGKHNGPEHWHK DFPIAKGERQSPVDIDHTAKYDPS LKPLSVSYDQATSLRILNNGHAFN VEFDDS\QDKAVLKGGPLDGTYRL ISVFTFWGSF*WDKVSEAYCGIKK KYAAE\LTGHWNTKYGDFGKAVQ EPDGLAVLGIFLKVGSAKPGKQV DVLDSIKTKGKSADFTNFDPRGLLP ESLADYWTYPGSLTTPPLECVTWI VLNF\PFVS\SS\EQVFEIP*TLTFNGG GVNPEELMVDNWRPA\QPLKNR\QI KASFQIRWSHSLYSK
925	6422	A	958	3	402	EELTMAGIFV*PTIPVSL/SLFCH*V LTLNSGISPAGSPVLIFSTPEPKR*TS QGESRFHTFYLLKGLNR*I*HPSSS SSSSSSSSSSSSSSSSSSSSSSSSSQ NRFLKPLQHSPLPPLKPLTYAPNL
926	6423	A	959	1666	2187	NFPSSASPPPTDSFL\GLSSEAPSEHR SPSCALDPIFFQTL**SFSFSSLNFI NMLKFVPLNKTTPPLTLAFPYLKQL ASLPIQSCFFF*DKILLCHLGWSAVA QL*LTATSTSWAQVMFPRSWAYRH APPHT/LASCFYFCRDR/SLTIFPRLV SNSWAQVILPPRPPKMLGIQA
927	6424	A	960	3	695	TQLLRPAVFVGAASGIRRLWSA SSGHWCAPAAGRAHAPVRLVRGL GAASTAAPQDAQTGPQPMPRACI MRHLPYFCRGQVVRGFGRLQASL GIP\TANFPEQVVDNLPADISTGIYY GWASVGS\GDVHKMVM SIGWNPY YKNTKKSMETHIMHTFKEDFYGEIL NGAIGDYLRPDDNFDLSQLISAIQG DFEEAKK*LDLPEHLKLKEDNFFQ VSKSKIMNGH
928	6425	A	961	60	569	STDLEELPTLGWF*KQELIILSCPFVS LTYRERLPANFFKFQFRNVEYSSGR NKTFLCYVVEAQGGQVQASRG YLEDEHAAAHAEEAFFNTILPAFDP ALRYNVTWYVSSSPCAACADRIKT LSKTKNLRLLILVGRLFMWEEPEIQ

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						AALKKLKEAGCKLRIMNLV
929	6426	A	962	62	858	QLRWDSGARAWPRPACLSPLPQRL LSHSPSMAQKEEA VATEAASQNG EDLENL\DDPQKLKELIELPPFEIVTG ERLPANFFKFQFRNVEYSS\GRKTL \LCYVV*STGARGGKVQASWG\YLE DE\HAACPLQKESFSFNTILPAFRPK PLAVTNVT\WGYVSSSPCAACADR\ IVKTLSTKTLNRLLLVGRFLMWEE PEIQAALKKLKEA\GCKLRIMKPD FRILSWE\NFVEQEEGESKAFQPWE DIQENFLYYEEKLADILK
930	6427	A	963	409	747	VILQAQSGSPMGP*SLRAFPAESERC QKQERLEPEEGRTCAAGLRGGPRR WWPLSSWTGDLRPSARN*ILPAA PMMEERKDPAPAQPPTS\TLPQFV SPEVLCSPPIENSHT
931	6428	A	964	1092	2338	RCYCSI*PCFHLFQLSFQILDPPVLGT TFL
932	6429	A	965	146	180	
933	6430	A	966	2	921	
934	6431	A	967	1	621	
935	6432	A	968	2	152	
936	6433	A	969	157	1203	NNSGVMPEMPEDMEQEEVNIP**G GFWVTGCHWGFLGRAVHKEFQQN NL\WHA VGCGRARRPKFEQVNL\ DSNAVHHIHD FQPHVIVHCAAERR PDV\VENQPDAA SQLNVDASG\NLG KGKAAAVWEHFSILHLGSGFCILM GT\NPPYREEDIPASLNLYGQTK\ DGRKGCPWRNHLGA AVLRIPLYG EVEK\LEKKCCCELLMFE*KCQFQQQ SQAQWQIHWQARGSPPHMSKDVA PLCARQ\LAERMLDP\SIKGTFWHS GNEQMTKYEGMCQLPDA\FNLPS SHL/RDPITDSPVLGAQRPRNAQLD CSKLETLGIGQRTPFRIKESLWPF LIDKRWRQTVFH
937	6434	A	970	1	508	NSNRQNGPPKKGERERASN/C/YPG APAAQAE/APLVPLSRQNKSTVETS NLKMLISFPKTLRGPEGWWHQG INPGSGAATLGPGS/SPQRPQS/IAAS CSMARRTFFAVSSNSFFLL/CFLCM GSSSGSQPSSSLKQKKHWAKSGSFS VGQWMKPASAIRSGVQRSPRRAS S
938	6435	A	971	21	351	VVSITKAPAYREVSVHNSCLRSNEG GKQPSHTKCLCNSNLLTQFKTKPI E/CWPEKTYMGSSSGSQPSSSLKQK KHWAKSGSFSVGQWMKPASAIRSG VQ\RSPPRRASS
939	6436	A	972	1	1011	
940	6437	A	973	2	94	
941	6438	A	974	661	2244	QYFKNPVGSTAVFEMDRLFISSGTA EMTSRGF\QRS\CNPP\CSSMTGRR ANQIHHLTPDFS\LRELLAPPK\KAGT WADCVSPPCGERDRCEGWADRHR

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						A\CSSPAKSPTASSQVI*KGFKATAF FSRGRSGQHVAPRLHLGLSNHTAV GKREYLARRFLSLYSVSSSTRSFTPF PQ*LRMAFVLSF*IVVCAIL*INNSN KIRKPCC*TVEEPGTLSPFSHHTQV MHLPKKKKTKKHNNKKTVL*GGT GVTDKEPAAQIQAPGKVPQDCD SLNNMRSRHHCGRLCHANKAVSS SKRDTAFLPHFSPGKPGNQNSKNE PPKKRERERSSHCH/YPAAAPAAQAEA PLVPLSRQNRSTVETSNLKMILISFPK TLRGPQEGWWHQINPGSGAATL GPGSSGQRPQSM/AASCSMARRTFF AVSSNSFFLLLVSFALFLALSLASSF KKFNQRVNSSLNCFLD/TERKAQPG RNCFLCSSMGSSSGSQSSSLKQKK HWAKSGSFSVGQWMKPASAIRLRG CRRSPRRASS
942	6439	C	975	597	683	MWFHVCLLVVIFFYFLVHMKYLKC KFLG*
943	6440	A	976	224	290	MPPIPMPIAPVPFPGPGFPP/VYFVP PLPLP/LLFPF*PLPFP*PEVSAKPVTL WSRKRQRSKGEKEGRGRGTGK
944	6441	A	977	3	1815	HFVPSPEAAAAESTACGVTAKML SVRVAAVVVRALPRRAG/LVSRNA LGSSFIAARNFHASNTHLQKTGTAE MSSILE\ERILG\ADTSVDLE*NLGVS *SIGDGIAPRTWG*RVNQAEMV\EF SSRLKGYVL*TEPDNVGVVVFGN DKLIKEGDIVKRTGAIVDVP/VGEE LLGRVVDALG\NAIDGKGPIGFQRR VGEVGL\KAPGIIPR\SVREPMQTGI KAVDSLVPGRGQRELIIGDRQTGK TSIAIDTIINQKRFDGSDKKKLYC IYVAIGQKRSTVAQLVKRLTRCKM PWKYTIVVS\AT\ASDAAPLQYLAPY SGCSMGEYFR\DNKGHA\LIYDDLI QNKAVA*PVKMSLLRRPPGREAY PGDVLYLHSRLLERAAMNDAFGG GSLTALQVIET\QAGDVSATIQTDV NSI/TLPEQIFLETWFNKG\IRPAIN VGLSVSRAGSPPTNPGAMKPGSQV PWKLELASSIREVACFLPPVSVSD/L DAATSTNLLESVA VPS*LEFAESQG PVFSPWLIEGTSCLLSYAGCKGDIFD KLEPSKITKLRNAFLSHVVSQHQL VGALCRADGKISEQS\DAKLKEIVT/ NFLAGFEA
945	6442	A	978	532	878	SYHFGRRPRQADHLRSGVQDQPGQH EETPSLLKRQK\LAGHGGIYL*PQLL GWLQENCLNLGGGGCSELGLHHC IPAWATEQDCLKKQNETKKESYS** GTSCLIAFLFKSDQK
946	6443	C	979	36	236	MGPTIPDXSXFWRKPITWMPTWE GTSNVGPQLSSSKSLHSXRGHPIPI PTGQAGPRDSGPGASP*
947	6444	C	980	26	160	MRFQSTGLGAPHCALNKCVSCLNX XXXXXXFLLRGPKLNPFKGG*

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948	6445	A	981	1	523	FFPKGFFLGYPRVFPFPFLNPGPGQ I*FSPP*K/RKLRAP*KKASSSSSVK TGNTFIESTVGCAKPCALEPHHSAP/ PQQPAPSGPGPPGEPG*ERLCASHK AFISHKQSH*SPQ*PCQAGVTL SRLQ TTNSPRP/PVRRGCGGLEPRP*VS/PS QPTACSENSQGSQSPKRTLS
949	6446	A	982	145	1315	CLPPPGLGPAPSLSSSCWGPPMPRT IRGIPPGSICRLCFCPAAGLLSLVAL QRPASSPTRHSALLCLRWA*PTSPS LPQSLGSRACLHSPLP*QAGSPCHA HTCGHLGPPVV*VPLPCPRSHSHSS CLFPAGSQCP*QAPAGVSISCQASSS ASSCGPGPQGYGQTPGPIPETPRDR\ PCHPTPPKSKLQARGPWRAWVG*R TADGSCGKKP*/CGPTIPDKSSPLA GLSSFPWFWAETHHPGMP*RGKR DPRKCGNPQPPSPKLKSPPTAHGD HPAP*FPTGKGWTPKDSWTPGPP* SRRPRPLN*WTAA*PWGQNPWAWT PAHPRKKP*RPRGCLSLSVSACGK WAPSPTSQGCCGRCDAVPKQQGL AHPTVLLNKCVCVSLN
950	6447	A	983	1	682	PPLFFQAAGKMADIQTERAYQKIQP TIFQNOGRGSCCGETGKIEKLPR/Y YKEHSGGLQRHPKEAY*GPPTLT KCPF/TGKCVHFEGGILSGVVTK/M KMQRITIVARR/DYLH/YIR/KYNRLP RKRHKNMVS\HLSPCFQGTSRFG\DI VTGGAKCRPSEARQWRFNVLKGH QGLARHQRSSFQKFLRLGHRGRSPT MEIRLVPASPGKKKKKSFVPTGGAV DSIGGRGV
951	6448	A	984	1	465	
952	6449	A	985	1585	2239	
953	6450	A	986	9	2580	SLPPKKCELRLHNCWGLFSPPARQ SGSVAAVVAASAVSGVSGPSPPLT CASSLSRSPRARTRPVAVCVSPTTP RLPPRSSLRADMSGDHLHND SQIEA DFRLMDSLKHKD\KQKDENARAR GHKEEKDRIEESKHSNSEHKDSEKK HKEKEKTKHKDGSSEKHKDKHKD RDKEKRKEEKVRASGDAKIKKEKE NGFSSPPQIKDET*DDG\YFVPPKEDI KPLKRPRDEDDADNK/PHKKIKTED TKKEKKRKLEEEEDGKLKPKNKD KDKKVPEPDNKKKKPKKEEQKW KWWEEERYPEGIKWKFLHKGPFV APPYEPLPENVKFYDGVKVMKLS KABEVATFFAKMLDHEYTTKEIFRK NFFKDWKEMTNEEKNIITNLSKCD FTQMSQYFKAQTEARKQMSKEEKL KIKEENEKLLKEYGFCIMDNHKERI ANFKIEPPGLFRGRGNHPKMGMLK RRIMPEDIINCSKDAKVSPPPGHK WKEVRHDNKVTWLVSWTENIQGSI KYIMLNPSSRIKGEKDWQKYETAR RLKKCVDKIRNQYREDWKSKEMK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VRQRAVALYFIDKLALRAGNEKEE GETADTVGCCSLRVEHINLHPELDG QEYVVEFDLFGKDSIRYYNKVPVE KRVFKNLQLFMENKQPEDDLFDRL NTGILNKHLDLMEGLTAKVFR/T YNASITLQQQLKELTAPDENIPAKIL SYNRANRAVAILCNHQRAPPKTFEK SMMNLQTKIDAKKEQLADARRDL KSAKADAKVMKDAKTKKVVESK KKAQVRLEEQLMKLEVQATDREEN KQIALGTSKLNYLDPRITVAWCKK WGVPIEKIYNKTQREKFAWGHLT WLDEDYEF
954	6451	C	987	65	235	MQFRVKYHICSTLLSLKTKICITCIIP SHLFPASTIPSWGCFHLIYHIAQKHV ING*
955	6452	A	988	16	148	SPAEGGCVCVCVCVCVCVCVCVCV CVCVCVCVCVCVCVCVCVCVCVQVG ACVCN/CVCVCVCVCVCVCVCVCV CVCVCVCVCRWVLAACATCVL
956	6453	A	989	287	504	LPRNFKTIYLDSEMVLESSKRGVCV SVCVCVCVCVCLCVCVCVCVCVCV /C*YLDLNHGKCTHPVSFSVRIFLA
957	6454	C	991	201	488	MGSRPRFCLFTTNTLCPDVTSSVC SPKTTXRLKXTFMPCSRKPKQAVL TSSEMALAACSXFSRSPDDFTQYQV AELVWDSLQPLGQXRSHCSLR*
958	6455	B	992	53	302	MTSALTQGLERIPDQLGYLVLSEGA GLASSGDLENDEHAASAMSELVST ACGLRLHRGMNVHFKRLSVVFGEH TLLETRVLTEX*
959	6456	B	993	277	573	TSALTQGLERIPDQLGYLSSGDLEN DEQAASAISELVSTACGFRHLHRGMN VPFKRLSVVFGEHTLLVTVSGQRVF V*
960	6457	A	994	134	1271	NPGPVQVGVEGGQEEGPSSKKQAK TRQVCLASITEAPGPKIRFSEPLRPP AGCRHQMGSPTSGSASSPQTPFCPG/ PPSPA VCV/PPKTTGGETHQGA*RA HSMPCSRKTAGCAEQLQRWHWL PAHHSPGPQMTALHLHLSVPGSRA GLGFAPAPGSAQKSSG*RCKS*EAC *RDGRPDTLHLQTQVSGLTWPQVF SFPSQVPSRPPPPYMVLNTDLPÉPPS APTLAPRLPWPSTSHLCYPKGPVLP LWPLPSDPSSPPFVSARPA/ALPAAP EHPPTDPSPAFSSPSLPFSPPLPRAD RR*GWSAGPPGG/EPHRLGSRDAEP PAGPLAHASSLTIAVFGAGGAPYQI GSFRLQAPVTCLQPLRSSFCLRHWP LAPPLA
961	6458	A	995	1	422	
962	6459	A	996	3	760	TSRGRVGTQAGEPRDLRPPPCSSPL RVAVVCLEQPERGAWEAHNIPQP NGDSA VRSFGVTGTHVKLPGPAPD/ NPNVYDFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGVRNKRIKPGPERF

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						QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLPSVHV\NLDIQDNH EEATLG/ARFLICE\VCQCIQHTEDM ENEIDELLQEFEEKSGRTFLAHTVCF ILFSFLDICF
963	6460	A	997	425	591	EYLKQWNVVFVDIKNHLC/MHLHA HIHTQV*THTQTHTRHTHTHTHTP CHCLVHTA
964	6461	C	998	120	368	MGTAHKPGYPQISTTVCIYVPDFAIL SPVLSFCRLIYLHTRMLQATELLQ ALQNSTTKGNRRERARDNSKMRH DGRAWRC*
965	6462	A	999	2	393	ARGKKPNLRAFLPLPRAWPEPQTL QQPRWP*TVQLPVAIGDKALALGR RKSGPGPGFVVLRTVPHALSHVRS FRSLLPLSLTLCVSFSFCLSVFSP PCSDGANPWQSQSWKQEDGSSSPW EVSA
966	6463	C	1000	1247	1716	MLRPRLRCFFSSSQTACSSDLNRSV GSSQARPQGSPSSFSASCRKCSSLVH KEGPQLLVVGQVPSFYGPSTCPFHT AAADSAWPCRSRASFKVLSHDFHR PLVLLAAQRLPPARFPLGRLGARSH TAGGAERAGVGAAQQLQRRPRWP GRRARAPRP*
967	6464	A	1001	3	630	FCPRGQEFGEKNLLSPRRPWGHFT EEDQGLLSTSLGQG*ILEDAGRKK PLGKAPLVV\YPMGPQGFL*TGFGQ PCPSCPLPIMGQPPKVQGHMAKK\V LTSLGEMPIKH\LDLDPQGHLCPSLSE LHCDK\LVDPENFKLLGKCAGD\V FGNPFQRRIHPWRLQASWQKMAED GDCKWPVPCPPDTTEASWPMNSEA FKDKAFILASNYK
968	6465	A	1002	41	625	APSPDAHGVISQRRTKAT\TSLGQ G*ILEDAGGRKPLGKAPLVLPKW DPKRSFEQALGNPVPLPSA\IMGQPP KVQGHMAKEGA*PSLGEMPIKH\LD DPQRAPFAPA*SELH\CDKL\HVDPE NFKLLGNVLVTVLAIHFGKEFTP/E RLQASWAEDG\DI*SGQCPVLQIPLK PLGP*IQKLSKDKAFILASNYK
969	6466	A	1003	106	1315	KQSGRAPGKVVSRAFPGLNPCPGW K\LLTQ\VGAVLGRGLGDGLGAALG PGNRTHIWLFRGLHGKSGTWWD HLSEENVPIKQLVSDDEKAQLASK LWPLKDEPWPI\HPWETGSFKV\GL FDLKAGHVGLLWTKDGQKHVVT LQVQD\CHVLKYTSKENCNGKIGNP VC*EGKT\VSFRKATSILEFY\REL LPPK\QTVK\IFNITDNAAIKPGTPLY AASLFVQGGYVDVTAKT\GKGFQ SCSLKRWG\FKGQPAYRIGQTENPT GRPGA\VA\TGDIRVWPGTKMPGK MGKHIHGQNMGLK\WVRINTKPPIN YVNGSVTDIKNCLVKVK\DSKLP\A AYKDLGKNLFPYIIFLMGDGRGNL PERFCID*KPCCQPRWRFPINICPNIL

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						WDVGRTLTIFL
970	6467	A	1004	218	530	KFEGCLPPRDETRIPIWARRCAYVV *SKEVSL*HCNTVTPG\GKPNK\TRVI WGK\VT\RAHGKPVAMVRAQIPEG NLSCLRPFGR\IRSDGCYPSRILNLT EKS
971	6468	A	1005	2	269	FESEDEGEFDDWEDDYDYPEEEQ LSGAGYR\ADKMFLRTREPALDGGF QMHYEKT\PFQDLAFIEELFSLMVVN RLTEELGCDEIIDRE
972	6469	A	1006	1	456	AELSELYEESDLQMDVMPGEGDL PKWEEATGTRAAIPWVPATGAQQ LEEEGPMEE\EEAQPMAAPEGKRSL ANGPNAGEQPGQSPGRRTSRAEDE A\EFDDWEDDYDF\PREEPVKGAR LRFLPPS*KTPPSFWENRNTPLWGG LKIFY
973	6470	A	1007	563	771	WSMVSLCSTAAVAPVCSRIPERTRR ATASVTHFCGDLG*SPVKPLSLGYR SNLGGPEEGREGGRKARRK
974	6471	A	1008	300	391	AVCTMSEMAELSELYEESDLQMD VMPGEGDLPQMEVSGSGRELSLRPS RSGAQQLLEEGPMEEEEEAPMAAP EGKRSLANGPNAGEQPGQ\VAGAD FSESEDEGEFDD\WEDDY\DYPRRR SQLQWCPVTRVSAALEEA\DKMFL\ RTREPALDGRVSRCH\YEKTPFGSV SLLSEELFFT*LVCQSV*PEEL\GCDA WRG
975	6472	A	1011	100	270	LRSSAVTVLVSLIHSPSSFHHPSVD T*PHCLESPPGFKAIFIRGLFTEACF CRIA
976	6473	A	1012	13	670	RQRPKARASIP\HQPPQEACQPPAA ALTRPQRP/PSALSHPAKPHSVSSA GSSYKNNPFASSISKHGVS\SSSSSG GTPVQSSVSGSLVPGIQPPSVGQATS RPVPSSAGKKMPGFPEVDSGSPSRR SK\GDSSGGTQGVAKLLTSPSLKPSA VSSVT\RLPPCQKERVGLCCWPAPL *WLHPTNPAAQSC\GP*ARTPRGLG AAGVSLAQRKSLSTYRA
977	6474	A	1013	3	578	GIPWWTHASEAVQTEIPVVGPREW QSC*PRR/RLKPSAVSSVTSSTLSK GASGTVLLAGSSLMASPYKSSSPKL SGAMSSNSLGIITPVPIV\QCSPSAL TPLPKQGS\PRMPSSQALPPGPSTRP WPQSSGWLALQPAPCSASPTRCGA HPYPAESAR*SPDGQCAHAHRVPLP SPPLGALPLPRVLVSLP
978	6475	C	1014	426	653	MVTWGGGSHQRRERKEGPGTRVFM GREALES\PCSASHCRPLLGFELSNT NLLLWLF\CYLRLLCKQTGNPSCK KYI*
979	6476	A	1015	1286	2318	RTVPFYPMHLMVMMKTEPKIGVCK NP\IIVESTKV\FS\KELHCHVPREKL APT\VT\PLGVLSISQGGQCRSPSCGS/ GPEFCPL*AHSLGMGRHWDHPGSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LQPEGAPEQWGALRYSDQMPGDQ ADSPTGVPTALPPEPVNTVPPTTAQ RKPQPRAAPLTTV* RQSCKAQSTGQ SAPPEQQGPGSLHGRHIRSAEKRSA ENSRSSRRTPSSRKGA VSVHPGRPA RSDS\PRPKWQALPLKRSQFPWYSR PFPVKLRSTWKRVRKIRTQVFHAL* FP*GSSNQTSRETPK* QKSPNAEC SR AQTSHETPASSYSCTLLLATACKHTI TVKVGGHSAQCFQNSNSAVQL
980	6477	A	1016	315	480	
981	6478	A	1017	1	1845	
982	6479	A	1018	1	447	
983	6480	A	1019	218	544	SGFSLSLRGSISFSL/CFKVGMCV TY PRCYC*SVPV*KPLIKPGWVSELKPK MNWASCSRTLASFLLQAARSHPW T PMKMETMEQSKLRSQPCPKAAGAV DPRAVVHGT
984	6481	A	1020	198	562	LKCGKQWSDPITSPQTESQLLGSSQ QQLHQQRHLQGP*K*NRDSPLCFSL SSCPIPKTYTNRHILLP/SSSKSLCKF L*PA*ISPQKMGFSFLSQSVCKFSKL LCSASLIKLFNSIQVTS
985	6482	A	1021	72	270	
986	6483	A	1022	545	812	
987	6484	A	1023	477	750	
988	6485	B	1024	537	867	XEQAAPCSALSLPMASCLRGHGEA RADPWSSTRPIDLKFKGPFTDVVTT NLKLRNPSDRKVCVKVKTTPHRY CVRPQQWNLLTPGSTVTVSVMLQP FDYDPNEKSKHKFM*
989	6486	A	1025	822	1750	SSAEPSPSSPAPSQQTAAGAPPLC AVSPMASASGAMAKHEQILVLDPP TDLKFKGDG*VFIRPEQYYTV*KWC KRSKRHGFRP\FTDVVTTNLKLRN PSDRKVCVKVKTAPRRYCVRPNS GIIDPGSTVTVSVMLQPFDYDPNEK SKHKFMVQTIFAPPNTSDMEAVV/W KEAKPDELMDSKLRCAVFEMPEN DKLNDMEPSKAVPLNASKQD\GPM PKPHSVSL\NDTETRKLMEECKRLQ G\EMMKLSEENRHLRDEGLRLRKV AHSDKPGSTSTASFRDNVTSPLPSLL VVIAAIFIGFFLGKFI
990	6487	A	1026	184	282	VIASQNIFVLSSVTGPKDRSGRQPLV FLKSPG*THPS*SVSRNLFSA*PGD FRKTKGCRPDL SFGPVTLLRTKIFW LAIT*D* CFLGYIKMGHIVEHCQQ
991	6488	A	1027	445	992	HCCGRNCLQRRWGWKRVRSLLAGI VFVSPFFKLELQKPLPSEQITIGLML LPFPHFFFCFVFCFLFVCLFF*DRV MLCHPGWSA VVRSQTVTSASRVQ AHCLSLPSSWDYRHPPCLAFSR/DR GFTILARLVLELMTS*ATPSLFCCFI ADSVQQYAPSLYILRNTNPRLLAK IFVA
992	6489	A	1028	33	476	HEDHAGPEPPRSYIPPYNATVVQKL

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						LDQGALLMGKTNLDEFAMGSGSTD GVFGPVKNPWSYSKYREKRKQNP HSENEEDSWLITGGSSRGSAAVSA FTCYAALGSDTGGSTRNPAAHCG V/GFKPSYGLVSRHGLIPLVNSMDV PG
993	6490	A	1031	187	1611	RAWERQERQRSGCSWLTRGVRRG GEGRTTRRKMASKEMFEDTVEERV INEEYKIWKKNTPFLYDLVMTHAL QWPSLTVQW/LSLKVTKEGKDMP LHWLGLGTHTSD*SRILVVARVHI PNDDSQFDA\SHCDSDKGEFGFGS VTGKIECEIKIN\HEGEV\NRARIYM PQNPSHPLLTKTPSCLMVLVFDYTK HPAKPDPSGECNPDL\RLRGHHKEG YGLSWNSNLSGHLLSASDDHTVCL WDINAGPKEGKIVDAKAIFTGHS VEDVAWHLLHESLFG\SVADDQKL MDM/WDTRSQYHLPRPSSLGWD\A HTA\EVNCLSFNPYSEFILATGS\A KTVA\ALWDLRLRLNLHTFESHKDA EIFQ\VHWSPHNETIFGFKCTCRR\LN VWDLKIGKEQSPEDAENGPPENLL IHEGH\QVKISDFSWDPPMKPWVICS WSEDN\IMQIWQNGLKIFYNDERVR CHDHPKLEGKGS
994	6491	A	1032	3	551	FLLAPVEVSEGSFAEIWGQITGVGLF LCLGESPAWGLSKRDLMSVKA CGPKAHFCLGYKAGGLPGTQRGAT QALL*KFEGVYARRMKPDSNLGRR CAYVV*SKEVSL*HCNTVTPG\GKP NKT\RVIWGKSKLGAHGKQWAWF VPKFKAIFPA*RPFGHR\VRSDGCYP SRILNLTEKSN
995	6492	A	1034	20	867	ALERRVRKSGDCCTDSGTMNIFDR K\ITFDALLKFSHITPSTQQA/HMKK VYASFA\LCYFGAAAGAYVNMVT HFIQAGL\LSALG\SLILMIWLMATP HSHETEQRKLGTSLLGFCIPYRKL LGPALGSFVIAVKRQASLPTAFMGH SNGSFPAFTLSALLC/RRPSYFLG\G IL\MSALSLVAFCLPLG\NVFFWIPF WVFQ\NLYVGLVVMCGFVLFDT QLINEKAEQGDQDYNL/WHC\IDLFL DF\ITVFQKNSMKDPGP*MKKDKKK RRRNEVTIQPFPI
996	6493	A	1035	153	546	PAQETGRPRSKAHVASTWRAFPPE DQVLLAGAP/LWEDEAHFWAKCG VEAL\TTLEVTRPACLEGK\VHGSL\A RAWKSDEGQTPK\AKQGERRKK KTGSG*/RRPDSSYNRRFCQTLPTF GKKEGPQWPTS
997	6494	A	1038	1	433	
998	6495	A	1039	101	1898	SAAMIGGLFIYNHKGEVLISRVRD DIGRNAVDAFRVNVIHARQQVRSP VHQHLLRTSFFHV/IRRSNIWLGSS PRQN/VSTVAMVFEFLYKMCVMA AYFGKISSEENIKNNFVVHYMELLD

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						EILEFGYPQEFRD/SGALKTFNITQQG IQGVQAS/AQKEGSSQFTSQVTGQIG WRREGIKYRRNELFLDVLESVNLL MSPQGQVLSAHVSGP/VWVMKNYL SGMPECKFGMNDKIVIEKQKGTA/ G*NQARAGKQSIADDLHLSTQCVR LS/KFDSERSISFIPDGEFELMRYRT TKDIILPFRVIPLVREVGRKLEVKV VIKS NFKPSL\LG\QKIEVRIQPLNT\ SGVQVICMKGKAKYKAGENSFVW KIK\RMAGMKNTHIIEIGFLPNKEK KKGGCPPLFPRNFGFKFAPSGLKVG \YK\VLNPKLNYSDHDVIKWVR*I GR\SGIYENSACKATRQLAQLPQPPF LQQVQVPLLQTTHQVSPSPPCFAC PSPLQSPPEVLGLGQSNITKWDRWK QPLGSPGQSGSEGSCSPHPVCSWP NAQALSSVTQSPGGFPFLPHPCGHS SGVGGVLVAPHLRAPPKASEWIPGLS PYSALG
999	6496	A	1040	255	662	TGEGYAGTEATDITHPQLRNQQWV PRCKPFPICDLKIQPERNYLFFLR/QR VSLCHPGWSAVV*SRLTATSAFPGS SYSPAFSLPSSWDYRCAPRPANFCI FSRD/RGFTMLARMVLIS*PVIHPP WPA\KVLGLQA
1000	6497	A	1041	2	297	TLILPQHVNCPGGINAWNTITSYIDN QICQGQKNLCNNTGDPMECPENG CVPDGPGL/VLRDSGSHSIRLHSA/ LGDPAKQSQDFMNYIGLTIDLRSI
1001	6498	B	1042	1	786	MAPHPGSLTTLVPWAAALLLALG VERALALPEICTQCPGQSVQNLKVA FYCKTTRELMMLHARCCLNQKGTIL GILPQHVNCPGGINAWNTITSYIDN QICQGQKNLCNNTGDPMECPENG CVPDGPGLLQCVCADGFHGYKCM RQGCLSAAPQALAGKWPPKNCHL PSFVDGQPQGQKEPCNNYPSIYTFV PVCQGICGIKMLKTELLHLKYWDIG PGNRNSYKFAAGNVKFAVTLNSL LIPQKAKRNYHMTQQFRS*
1002	6499	A	1043	137	1021	GRAEAGSLASQCVALASGSPVLLG GPAVLISLTLDPAPQPMHPMSRE RAKFVKSLYCKTDTKS*CLHARC CLNQKGT/LWGLDLQNCSL\EDPG QNFSIRHITTVIIDLQANPLTGDLAN TFRGFTQLQTLILPQHVNCPGGINA WNTITSYIDNQICQGIQKNLCNNT GDPRKCVPEKGILCYLNGPKVFWQ CVCA\DGFGHGIQSVLPPGLVPHCL MFLREFWEPTHSIRL\HSAFGGPSA* KAKDFHGTIYIGSLPFDLKINLELSLA PVRGALLPRKGIFRPVGFRKLG
1003	6500	B	1044	203	308	XRPLFAPVRARAVEAAGPGSGRAA EHSGPTGTAGCA*
1004	6501	A	1045	78	308	
1005	6502	C	1046	35	259	MQFSTHRGQKYERTPDTSGARVIER PYLTVIIHNNLEGRLEKESGKPYKF

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						AFYVILRCHFTDNFTTAALFVTR*
1006	6503	A	1047	162	1341	PPFQLIMGEIKVSPDYNWFRGTVPL KKIIVDDDDSKIWSLYDAGPRSIRCP LIFLPPVKWNCKMSFSRQILALTWM GLTGLIAFAVIPVYCDHLEFCDGFR KLLDHLQLDKVHLFGRFFGKGLWP MRFTGIPLQIS*SPIPLILCNSLMDTS IFNQTWDCKQLLA*CPAFMLQKNSS LG\IFHPGPGGPYGWAGCHLDFHG* DRA*ESFGVQELNLAFAQGLTLELSK FLCGNLH*NSGTYL*TIYGMCLDPG GGAFLKLLKKKWKLYPNGPKKL HLKTGGNFPYLCRSAEGNLMVQIH LLQFHGTYKAAIDPSMVRPRSLRC RKAALASARRSSSVSSSPVNDLTP VCSLYSQWAFSTRSDRPFFQVPSG LTRGPHWGLGKVGLDGHL
1007	6504	A	1048	321	888	VELSVHPPIPADPRSLLAGAMPWKL PISLPAE\PPCSLSCCLLPATQHPLH PALPAVDGAKKNPVFSGRLPPP/PT QRTSASGISALYA*DREV*AQISELW AMRG*VQKVGTVQISRAGQLAAV TSVGNMSVYPLALMTPPPSPPLPP PPPPVGRWSVGLRDLSPA VPSSEV CLWRSVLCLIPGY
1008	6505	C	1049	137	320	MLKSSFTCFPTEKGPKFLEDNLKTK XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXLV*
1009	6506	A	1050	231	477	GVYFIFFIGLVVFCVLFDDGRFTVA QAGVQWCDLGSLQPP\PP\GSNDSP WPQLPE*LGITGACHHARLIFILLE TGFRPC
1010	6507	C	1052	60	523	MAEAGFIHCPTENEPDLAQCFEFCF ELEGWEPDDDPMPQRKPTIRRNLR KLRRKCAVPSSSWLHGLRPLRXLP PRVAAPLPGFIPWCHQPSGPLSNV LGKEINIFKLDVSTVLLFCLESGRG VLPVQRVLLVQLLALSLSPPFFGGPF WRFE*
1011	6508	A	1053	61	208	IFETGQRKSQEQNWSYSVTQA/GVQ WCDLGSPQPRPPGLK*FSLSYMGS
1012	6509	A	1054	198	1011	QTHGLQQPSQHLP/TSTLRTVTAST/ SMRSRHIHCGRICHANKAVSSSKR DTAFLPHFSPGKPGNQNSKNEPPK KRERERSHCYPAAAPAAQAEAPLVP LSRQNKSTVETSNLKMILISFPKTLR GPQEGWWHQINPGSGAATLGPGS SERPQSIEASCSMARRTFAVSSNSF FLLLVSFAILFLALSLSFKNSPRVNS SNCFLTERKAQPDECFLCSSMGSSS GSQPSSSLKQKKHWAKSGSFSVGQ WMKPASAIRSGVQRSPRRASS
1013	6510	A	1055	1077	1457	ARRPEPPHPAHRGGGTPAQGGAG SPGASSDTSRLLEAPPQSIACWRSCC NAASWWTRSRGTCSRQTQR*GWP* CWRAQRGCAPALAAPQFLLAAHHG QRSAAASTTPGLHAGLRRSRPPRP PRP

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1014	6511	A	1056	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRITATSAVPL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIGVSHHTWPQEVFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFYFHRDEGSLCCPGWS* TPELK
1015	6512	A	1057	166	409	WSDVVGTRHLSAASFNSHAFWNLE EELTLVKGQALPSRGLDCPGRPAPP AACPGPKWRACLWV*FPNQNPISPG RNFNLKT
1016	6513	A	1058	10	604	ARPPKKPTSPTATTTTR*GARPATPP PRRPTAPIRWCTPSTAPPRACI*AT AP*QPQAPHQQTAAALFWASPPPSH QAPWIPPFLQPPS/LPPPPHSPRGP PGAQQGGAPAEKPWRPWTAR*D WTPPGAGLELGGSPGLWGHRRARE GGAGEGRGFEDRTGRFYKRIFVGR GDSKLPGRGFSRFSFGKFFLCF
1017	6514	B	1059	167	355	MASGSNWLSGVNVVLMAYGSLV FVLLFIFVKRQIMRFAMKSRRGPHV PVGHNAKPRSHFILK*
1018	6515	A	1060	67	458	
1019	6516	A	1061	164	528	
1020	6517	A	1062	203	364	
1021	6518	A	1063	103	1019	GNGRGAPGDPCAVASAEPGLTSQD SGVNPNSARGREAMASGSNWLSG VNVPLVMAYGSL/DVCTAIYFCEEA NHALCNEISKGTSCPCGTQCPQGT* K*EIDIRLSRVQDIKYEPQLLADDD ARLLTTGKPRGNQSCVNYLVIGM\ KALGLPFRTS\EIPFHS\EGRHSPFP* WGKNFRSYLL\DLRNTSTAFQGCTA KHLIDTLFGMAMETARYGDKGVF WPRMKYLRVQEALSELATAVKARI GELFSDIH/HVQAAKDLTQSPEVSPT TIQVTYLPSSQSKRAKHF\ELKSF KIDNYNTLAESTL
1022	6519	A	1064	1027	1365	PEVNRLYCLFKNKI*KALLSFQTYIC IYVLDVLIREKMFVKMCQVVVCVC IYMCVCVCIH*CVCVCIIYHTHTHT C/VCDW*AIQ**TCPHYFFLILDQCC PNCTFPLMVTML
1023	6520	A	1065	675	819	HRLDRAHP*RAEGNCLLPVYLSY/G PLIA*TGQGTSSPCLCSL/*PRSAITHT PSQPGDPRQPQTVHSGELNPRVYTK
1024	6521	A	1066	3	603	VDDFVQPARRRWEMLGVLPSVFLG LRRFVHPAKGMKQTRGDSFAFQSG

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						SPGVCFEGQEAEGSLSYGVGLIAAG FVLLSPPSQC/HD SLATQVLVCGVA LLWPSSGRAGTVQ*PAPENRSASP FCLPGHIQVPVPVFTVPRSAITHTPSS NLGTPRQPQTVPLRGAESPGQPCPM SLRKLPQARPLVLYTCSCHPAVDEC FR
1025	6522	B	1067	46	1983	MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLIFYAPWCGHCKQF APEYEKIANILKDKDPPIPVAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEFDEVVNDADIIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKG RPYDNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVIIIIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTELAKFL KVSQGQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSA IKDFVLKYALPL VGHRKVSND AKRYTRRPLVVVYYS VDFSFDYRAATQFWR SKVLEVAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFKKGKLPVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDV LIEFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEEL*
1026	6523	A	1068	1	849	
1027	6524	A	1069	74	2705	KKLDFFRSLPVFQADFSHWQLFRVL FLLHPPLVISMDSWFLVLLGSGLIC VSANNATTVAPSVGITRLINSSTAEP VKEEAKTSNPTSSLTSLSVAPTFSN ITLGPTYLT TVNSSDS DNGTTRTA\S TNSIGITISPNGTWLPDNQFTDARTE PWPGNSSTAATTPETFPSPGNSDSK DRRDETPHIAVMVALSSLLVIVFIIIV LYML/RGFKKYKQAGSHSNSFRLS NGPH*GMWEPQSVPLLA RSP\STNR \KYPTPGPWDKLEEEINRRMADDNK LFREEFDALPACPIQATCEAASKEE NKEK\NRYVNILPYDHSRVHLTPVE GVPDSYINASFISGYQEKNFIAA QGPKKETVND FWRMIWEQNTATIV MVTTLKERKECKCAQYWPDQGCW TYGNIRVSVEDTVLV DYTVRKFCI QQVGDMTNRKPQRLITQFHFTSWP DFGVPTPIGMLKFLKKVKACNPQY AGAIVVHCSAGVGR TSTFVVIDAM LDMMHTERKVDVYG FESRIRTQR* QMVQTD MQYVFIYQALLEHYLYG DTELEVTSLETHLQKMYNTIPTNT

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						NGL*EEFKKLTSIKI\QNDKMRTGNL PANMKNRVLQIIP*EFTRVIIPVKR GEENTDYVNASFIDGYRQKDSYIAS QGPFS\HTMRDFWRMIWSGKSCSIV MLTELEERGQEKCAQYWPSDGLVS YGDITVELKKEEECESFTVRDLLVT NTRENKSRQIRQFHFGWPEVGIPS DGKGMISIAAVQ\KQQQSGNHPA TVH\CSPPGGKERTGTFCALSNVLA RVKA\EGILDVF\QTV\KSLR*\QRPQI GSRQLEQY*VLAYKVVPGVILDAIP QINAQLQSKAANKGPVDPGGLPFNI LVIFLFC
1028	6525	A	1075	734	1151	YRRGPGGLRWAEMSGDFPPIPLPVR GIHPIPLRASQ/PVL*GGQQMGMTGP ISQ/PGETEFQTGLSACPKPHRVPGP SSCTTEKPSQRLHEQMVRGG*SSMG GAGNGVGMESGTVQGTSPSGSWR PAGTGVGARNCWYLP
1029	6526	A	1076	118	399	
1030	6527	A	1077	1	214	LLMRVSLPSEVFFCVVFETESRFVT QAGVQWHDG*QPPPPRFK*FSCL SPPSSWDYRHVPPCLANFCIF
1031	6528	A	1078	2	152	ETESLYVTQAGV\QWHDLSLQPPP PRFK*FSCLSLPSLTTFDTSLKSME
1032	6529	A	1079	2	426	
1033	6530	A	1080	1	1716	
1034	6531	A	1081	2	886	VGGRGEALDGGGSGAPPSVSQTES RAGTMSA YPKSYNPFDDGDEAG ARPAPWRDARDLAPDGPADAPDRQ QYLRQEVLRRAAATAASTSRSLAL MYESEKVGVDSSSEELARQGVLEA HREDGGTRLDDQLKISQKHINSI*ER VLGGLVN/YTFKSKPVEAPPPEQNG TLTSQPNRLKEAISTSKEQEAQYQ ASHPNLRKLDDTDPGPPEAWASAP GVLMLTPKNPHLRA\YHQKIDSNL DELSMGLGRLKDIALGMQTEIEEQ DDILDRLTTKVDKLDVNIKSTERK VRQL
1035	6532	A	1082	1549	1712	SNL*FFFFEMESRSVA\RL\ECSGVIS A\HCNLC L PGSSNSPT\SAS*VAGITG A\THHSRLLFVFLG\ETGFHHVG\QA GL\DSLTLMIQPALASPKCLGLQAVS PPMPSPYSSSFFCPLNILTPHVLYPG LNPPSSFCSDL
1036	6533	A	1083	2	336	
1037	6534	A	1084	218	1080	PSSRMNH\LPEDMENALTGSQSSIAS LRNIHSINPTQLMAR\IESYEGREKK GIS\DVREDFCLFVTFD\LLFVTLW D**EFKC*MGGHLRNTFRRRRLQY *LTISSIFLILFLPGQFFRF*KCLILAY A\VCRLRHWWGQ*RLTTAMTSALL LAKVILLKLSSQGAFGYVLPFI\SFIL A\W\ETWFL\DFKVLPEAAEENR/L SLIVQDASERAAL\PGWSFWMGQF YSPPGIRRDLEGSLKEKQGQLRKP

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						LFRNYEYYFLFKCGKTLTESHRGKK RQAVESPCRQ
1038	6535	A	1085	3	400	
1039	6536	B	1086	333	436	XTPVFSYGDEIGLDAAALPGQPHEG LLLRFPYAA*
1040	6537	A	1087	127	2041	RGVWGGHVPGGSREEWSGEDQGG KRRGDAVAENCAEAREAGESVLGP RVQVGVEPPSDRKLRRVAGSAGTM SQDTEVDMKEVELNELEPEKQPMN AASGAAMSLAGAENGLVKEIFPQ KKKGGGSAEDEAEAAAAAKFTG\L SKEELLKVAGSPGWVVRTRWALLL FWLG\WL\GMLA\GAVVHVRAPR\C RKL\PAQKW\WHTGAL\YRIGEPLRP FQGQRRGANLAGSLKGRLDY\SSSL KVKGVLVGPPIHKNQKDDVAQTDLL Q\DPNFGSKEDFRSLL\HSVKTKNL RGILD\TPNYRG*ELRWFTSQVDT\ VATKVKDALEFWLQAGVDGFQVR DIENLKDASSILGLSWQN\SPKGFSE \DRLLIAGTNSSDLQQLSLESNKD LLLTSSYLSDSGSTGEHTKSLVTQY LNATGNRWCSWSLSQAR\LLTSFL PAQL\RLRYQLMLFTL\PGTPVFQAT GNEV\GLGCSCPLLQPMGGSQFML WDEVPAFP\DPGGC*VANMDCGR GQSE\DPGSL\LSL\RRLN\DQRSKE APPYCHG\DF\HAF\PLGPWTLSPH QLGTQNETFSG*CLNLGDVGLS\AG\ LQASDLPASAKP\PAKADLLLSTQ PG\REEG\SPLELERLKLEPHE\GLLL RFPYAA
1041	6538	A	1088	652	905	HLLPPLTPTTTQWGRDLLSPISQM RKLRRHKVKKKTRT/WPGVVDHPL\ NLSTLGGGAWRIA*GQEFETSLGNI ARPCLYKKKFK
1042	6539	A	1089	3	591	
1043	6540	A	1090	266	1905	LGGHTWGTAAAGVWSDWPGRSW AELTSENSAGLSPSWGSPQDEVPGA WPMLQGAVEPMQIDVDPQEDPQN APDVNYVVENPSLDLEEFAASYGL MRIERLQFIADHCPTLRVEALKMA LSFVQRTFNVDMYEEIHRKLSEAT RSSLRELQNA\DAIPESGVEPPAL\D TAWV*\VTRKKALLKL\EKLD\TDLK NYKGNSIKESIRRGHDDL\GDH\LD CGDLSNALK\CYFRPRDYWTSKH VINMCLN\VIKQGRFTLQ\NSHVL YVSKAESTPEIAEQRGERSQTQAIL TKLKCAAGLAELAARKYKQAAKC LLASFDHCDPELLSPSNV\AIYGG FCALVTF\DRQELQRNV\SSSSFQV VLGSWEQV\RDIIKFYESKYAS\C LRRLEMDKDNLLDMYLAPHVRTL YTQICN\RALIQYFSPYVSPDMHRM AAAFNTTGGPPWKNELIKFILEGLI SARVD\SHSKIL\YARDV\DQRR\TF* ESLCLMG\KEFQRRAKA\MMLRAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VLRNQIHVSYPYPTQRKDARGELTPA NSQSRMSTNM
1044	6541	A	1094	2	397	SQDHVRGFLEKESAIVSRPLNPFTA KALSGTSPGDSDDVQPGPSVGPPSK DKDKVLPSFWIPSLTPEAKATKLEK PS/RLECVEKLIRKDMVDPVTGDKL TDRDIIVLQRGGTGFAAGSVKLQAE KSRPVMQA
1045	6542	B	1095	30	310	MTRHGKNCTAGAVYTYHEKKKDT AASGYGTQNIIRLSRDAVKDFDCCSL PRSCCHAYEKQRGTRREEQKELQR AASQDHVRGFLEKESAI*
1046	6543	A	1096	29	449	
1047	6544	A	1097	2	1069	IETRCTPRCRNSARGESLVRMTRHG R\NCTAGAVYTYHEKKKDTAASGY GTQNIIRLSRDAVKDFDCCCLSLQP CHDPVVTDPGYLYEREAIL\YIL\H QKK\EIARQMKGLTRKAGGGTRPPK EQKELQR\AASQDHVRGFLEKESA IVSRPLNPFTAK\ALSGTSPGDSDDV \QPGPSVGPPSKDKDKVLPSFWIPFA TPRAKATK\LEKPSRTVTCPHVKG PLR\MSEPERPVHFHNR*NSS\VEPR GASITPQASAYVCA\VTR\DSLKRQ PPVAVLRPSGAVVTLECV\KLIRKD MVDPVTGDKLTDRDIIVLASGAVT GFAGSGVK\LQAEKSRPVMQALRC AGGPNKPGGLP
1048	6545	A	1098	5	576	SRVVEFAKMAENSGRAGKIIRDDSG VKGAVSHEQVIAGLQTTFRNRQRG LASQS\AAELGDWKLNEATALVIDT TGREVDET\RKCYRMVWKEFLVEA NLSKEVACPAFGRTTKEQ\QKII*DT *HSSFQAKGKELK*ISGKKHNI/RVL MGEDEKPSQPKENS\EGGLGLKASIS AGVWVSPRDQGLCIFFLP
1049	6546	A	1099	534	1004	RMSAGALFIWGTAIYFDRKKTEVT PNFQEPGFRERRKKQKLAQGEKLG FPK\LPDLKDAEAVQKFFL*RTSL GEEL\LAQ\GEYKGV\VDHLTKPELP VCGQPTASLLQVL/QQANFFPPPV\F QMLLD*SSPTISQRIVSAQSLAE\DD VGMRNKCLH
1050	6547	A	1100	91	942	GLLVGVGAAAVMPGIVELPTLEEL KVDEVKISSAVLKAA\AHHYGA\QC DKPNKE\FMLCRWEEKDP\RRCLE\ EGKLVNK\CALDFFKA**NRHCAE/P LFLQEYWGLCIDYTRPSKLPSTVR KQAGKSFDEC\VLDKL\GWVRP*PG ENCQKVTKVKTDRLPENPYHISRP RPDPSP\EIRGEILQPATHGS\RFYFW TKLKMGPVAHTRSCAQTITDENAH AGLHPTDSGVLSGIHQHLTKKLTID DLAVILYHFLSIKIFKGEAPPLQHYP QSHQTTLCSPPQNG
1051	6548	A	1101	140	812	GDFGDRAGAGRETEEIFHSSQQLKI RPWAGAGRAAEPKDWRIWGTGEW GSRQIPSPVPSPRSNPFLPQAGAG

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						HFVQNPKYPTSPPLQRSLEELPLSP TVFKLLHPDPPCKAPLTLQPVAPK *I*ESPPLPPMLDPRDFPSPAPHPANE LKKRRGNPRQWFFLSEPRLSHLQN GTGWGWKGKDGRRRTGMELGLI PEAPVPISGPPFIHSHSQPPCYTGL
1052	6549	A	1102	228	860	STAQGNLLTVFIQPRASMSGGKYV DSEGHLYTVPIREQGNIYKPNKA MADELSEKQVYDAHTKEIDL VNP RPLNIFNG*PWSKIDFKDVIAEPEGT HRF*RAF GKASFHLSL* RKYWFLP LCWSALFGHPRWALIWHGFTSANS LLFLAHL/WAVVPCIK/SFLI*GFQCI SR/VSYSLRSTTGLVTPLFEAVGKI FQQLSASNLQKEI
1053	6550	A	1103	825	920	
1054	6551	A	1104	222	1244	RWEKKMALLCYNRGCGQRFPET NSDDACTYHPGVVPVFDALKGWSC CKRRTTDFSDFLSIGGCTKGRHNSE KA\PEPVKPEVKT\GTKELCELKPK FQEHIISSPLSQ*KQLKRSPDEPMT NLGIKNIWPLKQALDKLKLSSGNE ENKKEEDNDEIKIGTSCKNGGCSKT YQGLESLEEV CVYHSGVPIFHEGMK YWSCRRKTSDFNTFLAQEGCTKG KHMWTKKDAGKKVPCRHD LHQT GGEVTISVYAKNSLPELSRVEANST LLNVHIVFEGEKEFDQNVKLWGV DVKRSYVTMTATKIEITMRKA EPM QWASLELPAKKQEKQKDDTTD
1055	6552	A	1105	87	313	ISQERG*RRDKERLAQREIK/RRRER EK/ER*EERIDKKREAKREKR/ERER KIPEEREERKKGIFVFIWFNPMSVP H
1056	6553	A	1106	37	404	PQLSRCRSECMYVNPTVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1057	6554	A	1107	19	919	AVWWNSEFLAGRRVLVTGAGK/G WAAGKGGQRPAAAGRGQGTPLSP LPAGIGRGTVQALHATGARVVAIVS RTQADLDSL VRECPIEPVCVDLGD WEATERALGSGVPVDLLVNNAAV ALLAQPFLAEVTKEAF\DRVCPSASRS FEVNLRAVIQVSQIVARGF/I*ARGV PGAIR/VNVSSQCSQRAVTNHSVYL LPTKGVP LDM LDQG*WAL\ELGPH KLSRCRSELNASKP/TTVGD*RSMG PGPPWSDPHK\AKIMLNRIPLGKFA EVEHVVN\ILFLLSDRSGMTTGS\T LPVEGGFWAC
1058	6555	B	1111	28	384	MKAAVLT LAVLFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK

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						*
1059	6556	A	1112	44	1009	GGIREGGPPRPFRMKA AVLTLAVLF LTGSQA\RHFWQGG*SPPRAAWDR VK\DLATRVPTVTLKEQRTETYVS QFEGRLRGENS*TLKLLADNWGQR* PSTFQPSCAKQLGPALTQEFWYNLE KETEGFRQEMSKDL\EEVKAKVQP/ YTLDDFQERSWQEE\MELYRQKVIE PLARKNFQEG\ARPESLHELARRSL PLGEAVSRPRARPMWDALRTHLAP YSDEMMPALGRAPLGALRENGGAR MGQYHA\QATEHLSTLSEKAKPALE DLRQGLLPVLESFKVSFLSALEEYT KKLNTQLRRPPPPYPVLRINVSKV EKKKKK
1060	6557	A	1113	62	393	IPAKQPTPTS LKTPTEECDQ HENTAS SPSPMTPPCT/PSTNQPSKLPVSHSP NP*KPPAPKLLREMDLTFPPHFPPSV APTMKPLSSATTPMPRRISLSGSHSR RWDPFVG
1061	6558	A	1114	3	450	QTQREPTMVLSPADKTNVKA AWG KVG AHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNAVAHVDDMPNALSALSDLH AHKLRVDPVNFKLLSHCLLVTLAA HLP AEFTP AVHASLDKFLASVSTVL TSKYR
1062	6559	A	1115	9	675	NSARATDSERTHHGARLLPDKTNV KA\A WGKVGAHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGSAQG* RAHGK\KVA\DALTNAVA\HVD\DM PQTALSALSGPATAHKLRVDPVQL SSS*SHLPCWWTLGRPTSPSEFNPW RLHAFPGTKFPGLLVEAPLLEPSKLP LKLGSRLRVGHAFAPLGLPPRALLP FPGTRNPVGLLNKILNWGGKKKKK KKIF
1063	6560	B	1116	61	348	ESALTQLLKAGGSLKKFLFHPGDTV PSTARIGYEQALGVIAAGAGAI VH EKHPGKL AGYISSLLTLAGFATAMA AVVLCVNSFIWQTEPFLYIDT*
1064	6561	A	1117	2	256	CLSCAFWAGSVVIAAGAGAI VHEK HPGKL AGYISSLLTLTG FATAMAAV VLCVNSFIWQTEPFLYIDTVCDRSD PVFPTTAIVL
1065	6562	A	1118	3	270	AVVLCVNSFIWQT/EPFLYIDTVCDR S/DALFLAVCVLKVIVSLVSLGVGL RNL CGSSQPLNEEGSEKRL LGENS VPPSPSREQTSTAIVL
1066	6563	A	1119	1	642	
1067	6564	A	1120	46	998	AIVPSWDLKDTISLLSPVLCIFSPS SQTSLLYVFSLAGRMTQNTVIVNGV AMASRPTQPTHVNVHIHQESALTQL LKAG\GSLKKFLFHPGDTV PSTARIG YEQLAL\GV TQIFAGALRGVILGVC *SWGPGTVLRASGCAFWAGSVVIA AGAGAI VHEKHPGKL AGYISSLLTL

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						A\GFATAMAAVVLCVNSFIWQTEPF LYIDTVCDRSDPVFPTTGYRWDAA KSRRNQWQKEECRAYM\QMLRKLF \TAIRALFLAVCVLKVIVSLVSLGVG LRNLGQSSQPLNE/EKGSEKRLLG ENS\VPPS\PSREQTSTAIVL
1068	6565	A	1121	504	1026	KIKRKKKRPHIPVLRIPGLLNIPCL WHEWVTLSPSKRFAFAVGGN GGESGWLGGTRP/PSPRGMHLPGSS SSESEPHRNCPCGSAQPCGHQAGS EDPQNTGPVAS/EL*PPACWRLCGQ PGPLAGAPAAPLAGHPRPPWRQVGP GTSGSSQSWVSSCDHGGQHSGQHQS SWQ
1069	6566	A	1122	461	548	KNLEQKNAMIHSAGEHHQGAERRS TWELEGPRVTSLTLLV*RAWSSGP APSPT*PPSCTPPRRSS*APAGPSDAS PSRRPRA/SPASQAAPKDKLPETPR RRIEKEP\PGPFAPGIFE/GGFTVSGG REQETPFAGTSGCY/RTPPHFCWL GSPPRSTSSKAGGPSSSPSPTEAES STARPAKSRTMPTSGWHIGSTRPPR RRPSPR*RTSCTAHRRTSCSFSGTMP ARSRGLHSEIRRLQQHCTDLTYELT VKCSEQTGDGTSKSELKKRCELE AQLKVKENENAELLKELGAEKRDD SQCWRTSPRSREKKYLGA
1070	6567	A	1123	148	197	DPLGFL*QKRNQQEDD
1071	6568	A	1124	1333	2383	RMKKEHVLHCQFSAWYFFRGVTI KSVILPLPQNVKDYLLDDGTLVVSG RDDPPTHSQPDSDEAEIQWSDDE NT\ATLTAPEFP*SLPLKVQGSYQIP LGGQVSFPKV*FGS\APRD\AYWIA MNSSLKCKTSLDIFLLFKSSDFITRD FTQPFHCTDDSPDP\CIEYELVLEK WCEMIPGG\EFRCFVKENKLIGISQR DYTYYYDHISKQKIEIRRCIQDFFK\ KHIPVQIL*MKDLVFDIYRDSRG\K VWLIDF\NPFGEVTDSSLFTWEEL\AS ENNFKRRFLVKVDAQEQDSPSFSVA QTSEVTVQPQLICSYRL\PKDFVDL STGEDAHKLIDFLKLRNQPEGR
1072	6569	A	1125	162	413	GADGQINQQTLDDESGDECLDECP GPPRRGKGPPQREVQPASQASPPGT HQ*GSDGSSCTPSPV\SIGSPGLGPPI WRPHKPG
1073	6570	A	1126	2	228	GGPRNKEPYPQGPKNRAQSPKNLV HSLTSM*SSP/LPFKPSKSTIIDNCPLT HQ*NPLKP*PLFPPSPNIPPGFKKP
1074	6571	A	1127	302	488	SPICLTPKSSLTHSSDDYKYSVWQR AVAHTCNPSTLGAEAG/WVT*AEFF KTSLHNIVRPCLY
1075	6572	A	1128	66	703	RRRLPSVAIMILPGPSSSHDEMFS DIYK\IRGDRGRGLCLEGGGRGWVS RTE\GTID\DSLIGG\NA\SAESPRGAK GTERHK*STGV\DIVMNHHLPGNKF SQKEASKKVHQRITMKS\KKGKP*K NRRPRKSKTFL*QGAAEQIKHILAN

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						FKKLQF/YFIGENMNPRAWVLLLDY*RDGVPP\YMIFFKDGLMEKMLTNVAIILDLSPCHP
1076	6573	A	1129	1	1006	LLLLGHASTSTGGGKASKMATT KRVLYVGGLAEEVDDKVLHAAFIP\WGDITDI\QIPLDYETGEK\HRGFAF VEFELAEDAAAAIDNMNESELFGR IRVNLAKPMR\IKESLARPACSDND WLKKF\SGKTL*ED*RGRVRASQS RDPG/TGRAHLLKRRRSNPQVY\WD IKIGNKPAG\RIQMLLRSDVVPMTAE NFRCLCTHEKGFGFKGSSFHRIIPQF MCQGVGDFTNHNG/TLGGKSIYGEE VSM MENFILKAYGDQGLS/MLAC GDPNTNGSQF\FLTC*\KTDWLGWA SHVVFGVHRKALGCLCGQIEAQG SKDGKPKQKVIIAGLWGSTC
1077	6574	A	1130	1	574	DTRFLERLRLSISFLVQTPIGHSTEED QGLLSTSLWGK\VKCGKNAGRKKP LGKAPLVVLPWPDPKRFL*KSFGQT LSLCPLPHPWGKPPKSQRHHGKER LTFPWGDAHKA PLDDPQRAFFAQ *VNLH\CDKPAMWDPENFQAPGEM LLVTVL\AIPFSGKEFHPWRLQGFLG RKMGDLELASALVPSRYH
1078	6575	A	1131	200	740	HGSMRLLIPLALWLGAVGVGVVSQ I*ENSPGGQLQVALEEFHKHP\PVQW AFQH/TAVLESAVDTFPFAGIFVRL E\FKLQQVTSCPEEGTWKKPRVQKSR PQWDG NRKLPWPCIQTWAL EDKSS WARLVPPPPIKTQVL AGGW RSTQE DPSCLRVQRAC*RTPPSFYFGQF AF SKIALPRS
1079	6576	A	1132	79	933	EW PSSIDL VNELQVGISEKVSFLNR KIKPQVPLWYRLDGKVILTA AAGQ IGQAAALAFAREGAKVIATDINESK LQELEKYPGYSK/PRVLDVTKKKQI *SSLPMKLRDFDVLFNVAGFCPSARE LVLGL*GRKDWGLLR*ISMWRSTY LMDSRAFLPKML/RFRNLGNIINMS CCGLPSVKG VVEQDVCTA QPKASR GLASTKSVGCRFHSRQHGSGANLC VARGTVDTPISYKKEYNATRK S*TT ARE*FP*RDKKPGKIPQLPEEISHAL RRJSASDIESAYVTW
1080	6577	A	1133	1601	1778	MEQIRASGKLYKSLYQKREIYIMC STTYIYT*Y/HSTAYTYICLYVHIYIY MYRQYYVF
1081	6578	C	1134	58	394	MAEKPKLHYSNIRGRMESIRWLLA AAGVEFEKFIKSAEDLDKLRNDGY LMXQQVPMVEIDGMKLVQTRAILN YIASKYNLYGKXLKGESPFNLREQD AKXCLDPRGNPKIX*
1082	6579	A	1135	133	985	RNLRGIAILAGKPQVQFFHSRGARM ESTRWLLAAAGVEFEKFMK/SLA EDLDKFR/NDGYFDVSSKCPMV*DL MGLKLVQTRAILNLHLPANYNL/H YGGKDIKGREPLI*YCILGRY*PDFG

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						VEIV/LLLSCPYCSTLREQDCQALPW IKEKN*KNRPTFPCPLEKVLKRAHG TKTYLVGKKS*ARAGPFHLVELSS TTVEELDFQSLSPSFPLPERPLETPES RQPCPHSERKFPYSPGQPQKPSW DEE/SL*EGRQKDFSGFLINGSPWE GPRNLAINPMVS
1083	6580	B	1140	866	942	MDRHCPKLSGAPFGPPAPILGLTDP EFSHEPKLHHARILHRAPPTRDHP VGVISRLPRAGRGRAEGSPGPDLF*
1084	6581	A	1141	405	536	KSAPRPGVVAHTCNPSTLAGRG/G WIT*GQEFENSLANIVKCCFY
1085	6582	A	1142	49	365	TPDKPIRSHETLPIHEK*PRGKTGPPP DSDDPPPGSPSPQHVGNSSQKINSKLP ISSGDHSPNPYHW*CPLPSVLGIP/PV RRDPLCGPESPQEEGGQQRNESFDIF
1086	6583	A	1143	3	452	
1087	6584	A	1144	9	486	NSARATDSERTHHGACLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPTTK\TYFPHFDLSHG\SAQG* RAHGK\KVA\DALTKRRGATWDDM /PQTALSALSDLHVAHKL\RVGPGSTF KLL\SQLPCLGEPWAAHLPAEFQPL AVARLPWNKVSWGFC
1088	6585	A	1145	1890	2027	KCLCPPR/RCPQPLTPYPC*GVKCPP SEIKYKP*MCPIGCPKPSIQ
1089	6586	A	1146	1	903	
1090	6587	A	1147	1	1131	
1091	6588	A	1148	1	1376	WALPAGFDGVMShrKFSAPRHGSL GFLPRKRSSRHGKVKSFPKDDPSK PVHLTAFLGYTPCLAHIVREVDRPG SKVnkKEVVEAVTIVETPPMVVVGI VGYVETPRGLRTFKTVFAEHISDEC KRRFYKNWHKSKKKSFTKYCKKW QDEDGKKQLEKDFSSMKKYCQVIR VIAHTQMRLLPLRQKK\AHLMEIQ VN\GGTCARESWDWPPREGLKQQ VPV\NQVF\GQDENDRTSSGVTQGP KGLQRGSPSR\WHTQESCPKDPPE GLRK\VACIGAMAIPARVALPLWQR AGQEKATHH\RTINKKIL*DLAQQ YLIKGGKL/VSKNNASH*PMTLSDK S\NPLGGFVHYGK*TNDVTFKSL VWLGPKKRVLTLRK\SLVQTKAA GLWRRITLKFIDTTSKFHGRFQTM EEKKAFMGPLKKDRIAKEERSLMP GTDFAWWGLNKSYFPLKKKK
1092	6589	A	1149	3	497	PTLLVPTDSERTHPWLLSPADK\TN VKA\AWG\KVGHAHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGSAQV *GPRARKVADAL\TNVAQRGT DIA QRACPPLSDLHVAHKL\RVGPGSTFK LLKATC/HCLGEPWAAHLPAEFQPL AVARLPWQGSFLGFLKQRC
1093	6590	A	1150	26	508	NSTDERTHPWLLSPADKDQRQGP AWG\KVGHAHVSRMCAEALERM LSFPTTKTYFPHFDLSHGFSQV*GP

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						RARKVADALVNAVAQRGTIDIAQR AVPPLSDLHAHKL\RVGPGSTSKLL KPLACLVDPGPPTSPAEFHPLRLQG FPGDKFPGLSVGKFKI
1094	6591	A	1151	3	520	AKKHGHRGSSLTVFGGPHRLRENPP WCSSPADKTNV\KAAWGKVGAAH VRSMCAEALER\MFLSFPTTKTYFP HFDLSHGFCPG*RATAKKVA\DALT KRRGATWDDMPQTALSGPEATLH AHKAFGVEPGSTLKL\SHLPCW*P LARPPSPAEDPWVERLPWDKFP WVSC
1095	6592	A	1152	232	783	TCNPQTSSNGSQNSKLGRISRKWR MRRCFCFSITRW\LECTSPRSRGRW KTDDVLLKLENMGVSELGQRI*LER FTKDTARFKDEL\DIMKFICKDFWTT VFKKQIDNLR\TNHQGIYVLAQGNKF RLLTQMSAGKQYLEHAS*V/Y*HLP CGLIRGGLSNL\GKISIVTAEVSSMP ACKFQVMIQKL
1096	6593	B	1153	28	249	MFLSFPTTKTYFPHFDLSHGSAARLR ATARRWRRADQRRGHVDDMPNAL SALS\DLHAHKL\RVDPVNF\KLLSHCL L*
1097	6594	A	1154	3	511	DKTNV\KAAWGKVGAAHPGEVWCGP LERMFLSFPTTKTYFPHFDLSHGSA QVKGHGKNVADAL\TNAV\AHVDD MPNAL\SALS\DLHAHKL\RVDPVNF\K LLSHCLLVTLAAHLPAEFTP\AVARP SLGQVSWAFL*SNRCWTFQISLPAE FTP\AVHASL\DKFLASVSTVLT\SKYG
1098	6595	A	1155	2	247	PADKTNV\KAAWGKVGAAH\AGEYG AE\ALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGK\KVADALTQ\GELGG EVGGQGHQQA\VA
1099	6596	B	1156	74	195	MFLSFPTTKTYFPHFDLSHGSAQVK GHGK\KVADALTNAVXT*
1100	6597	A	1157	3	224	
1101	6598	A	1158	3	136	
1102	6599	A	1159	1	371	TQREPTMVLSPADKTNV\KAA\WGM FLSFPTTKTYFPHFDLSHGSAQVKG HGK\KVADALTNAV\ASVDDMPNAL SALS\DLHAHKL\RVDPVNF\KLLSHCL LVTLAAHLPAEFTLAVHAFLGQFP GFF
1103	6600	C	1160	1	156	MVRRPW\RGCS\CPSPPGXPPRRRVHP CGAXLPGQV\SXFC\EQRAELQIXLRL EL*
1104	6601	A	1161	1	577	AAWGKVGAAHAGEYGAEALERMFL SFPTTKTYFPHFDLSHGSAQVKGHG K\KVADALTNAV\AHVDDMPNALSA LSDLHAHKL\RVDPVNF\KPPRPTSRT ST*ATALPRLRATARRWPTR*PTPW PRGRHAQRAVRPERPARAQASGGP GQLQ\LLSHCLLVTLAAHLPAEFTP AVHASL\DKFLASVSTVLT\SKYR
1105	6602	A	1162	1	680	ERTTMVLSPADKTNV\KAAWGKVG

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						AHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHG/GRMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKL RVPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLT SKYR
1106	6603	A	1163	2	1758	TMVLS P/ADKT/NVKAAWGKVGAAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKL/RSRTST*ATALPQVKGYGQEGGRRVDQRRGARGRHAQRAVRPERPALRNKLWVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLT SKYR
1107	6604	A	1164	121	521	SFNKFFKKAKAVSQKKIPATKLRDKGLQTKYSCLYYYFYLRHGLALSPRLACSGTITAHCILKHRGSSDPP*ASHVLKLQYFCTS**LGITGACHHASLLLKFFVETDLTVLPRLVSNFWPSSCPSLLKCWD
1108	6605	A	1165	407	548	VPFTKWHQKIEAGQAWWLMPVIPA VWEAEVAGGSLEIRSS*PAWATW
1109	6606	A	1166	25	628	EFHRLRENPPWCLSPADKTNVK/APAWGKVGAAHAGEYG\SEALER\MVLFPPPTPKPYFPHFDLSHGSAQV*GPRARKVADALTNVAQRGTDIAQRAVPPLSDLHAHKLARVGPSTFKLLKATC/HCLGEPWAAHLP/AEFQPLAVATSSLGTFKPGFLVEAPLLTFQITFKGWKLWLAIVFLPFGLPSPSPSFLHPYPRGL
1110	6607	A	1167	2	121	TFVRLGTLSTPLWGSYDFFFPS*FSLFLFYSVHFMPALF
1111	6608	A	1168	3	582	AKREL RFLVYLHGDDHQDSDEFCR\SQALRENTYPFLAMIMLKDRRMTVVGRLGLIQPDDLINQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLRADQEKERKKREERERKRRKEEEVQQQKLAEEERRQNLQEEKERKLECLPPEPSPDDPESVKIIFKL PNDSRVERRFHFSQSLTVRTT
1112	6609	A	1169	30	130	QILLSPCLPPP*YLNKRWPEDNTCLLKTCLKRT
1113	6610	A	1170	2	1412	GIAGPTISCRGGGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNWNIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVS RPQPRGLLGWGYLIMLPFRFTYYTILDIFRFAPRFIR\PEP\RSR\VT*PRLGTIVSIYGT PFEEKYGRAHPVFYQGTYSQALNDAKREL RFLVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPEGYRVSQALRENTYFLAMIMLKDRRE*PVVGRLEGLIQPDDLINQLTFIMDANQTYLVG/SERLEREERNQTQVLRQQQDEAYLASLR

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						ADQEKERKKREERERKRRKEEEVQ\QQKLAEEERRRQNLQEEKERKLEC LPP\EPSPDDP*KVSKIIFKLPNDSRVERRIPLFHRS�TVIHDFLFSKESPEKFQIEANFPRRVLPICIPSEE\WPNPPTLQEVAGLSHTEVLFVQDLTDE
1114	6611	A	1171	232	427	STKISHTKKTARINKTKGGRGQAW WLSPIIPTLWEIKVGGFEPRRSRLQ *AVFMP\CTPSWATQ
1115	6612	A	1172	232	427	STSISHTKKTARINKTKGGRGQAW WLSPIIPTLWEIKVGGFEPRRSRLQ *AVFMP\CTPSWATQ
1116	6613	A	1173	77	1775	GRKVVMDLIPNLAVETWLLAVSL\ VLLYLYGTRTHGLFKKLGAGGTPL PFLVNALYFRKGYWTFDMECYKK YRKVWGIYDC*QPLAITDPDMNK TVLVKECYSVFTNR\RPFGP\VGFMK NAISIAEDEEWKRIRSLLSPTFTSGK LQGDGPLSLPQYGDVLRNLRREA \ETGKPVTLKDVFGAYSMDVITSSSF GVSIDSLNNPQDPFVGKHQGSF*GF NPLDPFVLLQLKVFPFLTPILEGIKY SLCFPRKSY*VFLNKIC*NRLKEGRL KETQKHRVDFLQLMIDSHKNSKDS E\HKALSDLELMAQSIIFAGYETT SSVLSFIIYELATHPDVQQKEQNEID TILPNK\APPTYDVLQLEYLDMVV NETLKLFPVAMRLERVCKKDVEIN GMFIPKGVGVMIPIPSYVLHHDPKYW REPEKFLPERFSKKNKDNDPIYITP FGSGPRNCIGMRFALNMKALIR VLQNFSPKPKETQIPLEI/DAVGGL LLTEKPIVLKAESRDETVSGLNFPK DILVCSLRKLPQKHQRPSNYFTNR PLKRRRGFIPNVAAIK
1117	6614	A	1174	3	403	
1118	6615	A	1175	2	465	
1119	6616	A	1176	1	1112	AGEFPGQLHSRASFTARS GSAAAL RMRPVRLMKVFVTRKIPRPRCVA LARAADCEVEQWDSDEPIPAKELER \GVAGAHGL\CLLSDHVDKRILDA AGANLK\VISTMSVGIDHLALDEIK\ KRGIRVGYTPLSLT\DTTAE LAVS\ LFLPT\CGRWPEAF\REVKNGGWTS WKPLWLCGYGLTQSTVGIIGLGP* AQAIARRLKPFQVQRFLYTGRQPR PEEAA\EF\QAEFVSTPEAGWPNLILI VVACSLTPATEGLCKKDFQKMKE TAVFINISRGD\VVNQGRPCTRALAS GKIAAAGTGM*TSPELPYKPPFSL TLERIVVILPHIG\SATPQEPGNTMFL VWAVNNLLDGLRGEP\MPSELKL
1120	6617	A	1177	518	780	EVLPSGPGLLALVLR LGSEFKLPHH EVSVGT/HPCQTSGAPARHRSTRDP VFPLSRGHNNPVPSWKHRAALTRH QTFLYCERGLPACIH
1121	6618	A	1178	117	1166	ITMATGQKLMRAVRVFKFGGPEVL KLRSDIAVPIPKDHQVLIKVHACG\

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						NPVETYIRSGTYSRKPLLPTPG\SD VA\GVI*A\VGDNASAFKKGDRVFT RQARSSGG/YMAEYGFFAGRTTLFY KLPKGTGTFKQGSLSDFPYFYCFIR GL\IHS\ACV\KAGESVLVHGASGGV GLAACQIA\RAYGLEVLGTAGTEEG QKICFCKNGAHEV\FNHREVNIDK IKKYVGE\KGIDINEMLANVNLSK DL\SLLSHG\GRVIV\GSRGTIEINPR DTMGQRSPSIIGVTLFSSAKE\EFQQ YAAAL\QAGMGIGWGGPVIRSQYPL ERVAEAHEDIIHG\SGATGKMDSSL MDD
1122	6619	A	1179	264	647	NLGTCPFPVPALQCLLLVETVSRGS LLPVSPLLFQLLYPSPPA\PSYSINSL LPP*PCPASLPFYDSLVI*RPAPF*SH PSPSTPRTEGGV\PSQSHPPCCPQAP APPPSLPASLSQRHLLPPLSHHSC
1123	6620	A	1180	1	575	NFALEAKNSARAISVVQTPIGHSTE EDQGLLSTSLWGK\VKCGKNAGRK KPLGKAPLVVL/HPWDPKGSFEQAL GNPVPPALCPSWGNPPKSRAHGK\K VLTSLGEMPIKHPG*SSKGTFAQPD VNCTCDK\LHVDPENFKLLG\NVLV TVLGNPIFGKEFTPEGCRASWAERW VTWSWPVPCSSRIPLKPLGP
1124	6621	A	1182	265	714	HFTYKYTAGTTIKSKNICITPKSYSC TFLVINTLTTPLSNHYSGFSLRLVLI VLEFFLFWRWSLALSPRLECSGMIS AHCNLCLLD*SDPASASQVAGITG TRHQA CLIFVFLVETGYPHVG*ARL ELLTSGDPSPWPVKVLGLQT
1125	6622	A	1183	84	1009	HSMMM KIPWGSIPVLM LLLLGLID ISQAQLSCTGPPAIPGIPGTPGPAD GQPGDPRG*KERKGFQGLAGDHGE FGEKGRPRGFLGNPGKKFGPKG\W MGPKVGPGAPGTPQAPKGDSDGYK ATQKIAFSATRTINVP/LRRSQTVIRF GPR*FTNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVSRG\NLCVNLMRG RERAQ\KVVTFC\DYCLTNTFPGPPP VGMGPQLKKAPKGGGGGEKKT\VF LQA\TDKN\SLTGAWEGA\NISFSRV PGFFPDMGGPDLWAGFTSTPGSPCP ATLTIPPTTI
1126	6623	A	1184	115	361	GWRGLPHCVGRNCCSVLLMGS/C CL*GPHAL*KPSCSVRCCWPEAPLH SKTDPRLSAA*PPFC*VR*MRYGLR TVCAQILSV
1127	6624	A	1185	3	734	GGSRERARSPESRRLPSRRSAPHRP PPQPCEQDNSPRKIQFTVPLLEPHLD PEAAEQ\RRRRPHPAT\LVLTSD\QS SP\ETAEDRIPNPHLKSTL\AMSPRQR KKMTRITPTMKELQMMVEHSPGGN RQQGEEP*RGPLESTGLQESRPPGI PDTEVECKCWAPFGTAKK\TAECIP KTHEGSKEPSTKEPSTH\IPPL\DSK GANCGSERGGGILGSRLQFGNAWT

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						PDLFLIPSLLGKISCF
1128	6625	A	1186	1	1359	GGPRDVNCRRLRAAETPPAWHL CMRSGAPTPPAAAMESETEPEPVT LVKSPNHRHRDLELSG\DRGWSVG HLKAHLRVYPERPHPEDQRLIYSG KLLLDHQCLRDLLPKQEKRVHLHL VCNVKSP/SQKLPEINAKVA*IPQRE PVGSNARGQYPEDSSSDGFKGKGKF FR\NLSFPWGWENIFKGLEACPSRH FQGLG\PGFLPVYTPYGV/WLQLSW FQQIYARQYYMQYLAATAASGAFV PPPSAQEIPVVSAPAPAPIHNQFPA\ ENQPANSGMLAPSSGLFNPG\ANQN FAG*IAQGGPIVEEDDEINRDWLD WTYSAATFSVFLSILYFYSSLSRFLM VMGATVVMYLHHVG\WFFRPRPV PNFPNDCAPPDVVNSDPH\NNLRE GTD\PELKDP\NHLPP\DRDVTRMGE AGPGPFLYGGTAWVCSFKDFSLASS FFPEGPPSPSAN
1129	6626	A	1187	314	1614	
1130	6627	A	1188	128	1910	RVVDRGRRWDSPLLGGGTWPGR SSLRFASASSDSDSDGLYRASLHPS PGRAALGLCLYLTKTSCCAAIGTLY WGNIAKQEAAYSLGENFFMSETE NSCSPFMSSLLQTEDTKKLQSKNL FILLIKPTNPKMSVNVNPPRCQTQ FYRLQDAPRLIAQG*GAKGNGNPR PVI/MSNMVDVGKGLIGPPNVSPPN IPIELGAQTQFDVKNDRIYVNG\SH GGELSCQDML\DGFFH*KNFVLCPEC GGFLETDLHVNP\KQTIGNS/CGK ACGYRGM\LDTHHKLCTFILKNPPE NSDSGTGKKEKEKKNRKGKDKEN GSVSSSETPPPPPPNEINPPHTMEE EEDDDWGEDTTEEAQRRRMDEISD HAKVLTLSDDLERTIEERVNTLFFLF LNKIKEEGVIDSSDKEIVAEERLDV KAMGPLVLTEVLFNEKIREQIKKY RRHFLRFCHNNKKAQRYLLHGLEC VVAMHQA\QLISK\PHILKEMYDAD L\LEEGFFISWSEKASKKYVSKELAK EIRVKAEPFIKW\KEAEEESSGEEEE DEDENIEVVYS\KAASVPNV\EFVKS DNKDDDD\IDIDAH\KGWMQPSLTV
1131	6628	A	1189	132	362	RRVDWKIQKISIGSSE*KLFNESHGI FLGLQRIDEELTGKSRKSQLVRVSK NYRSVIRACMEEMHQVAIAAKDPA NGRQFSSQVSILSAMELIWNLCILF IEVAPAGPL
1132	6629	A	1190	97	355	AFSYNCPSKISCQRKSQHFHLGGLY VILLFLFQKGQGVCCQSHPERPEGNP RRHQGQKERSCVGKTLL*LPEQDFV PEKVSAFPWWSLCHHPVSVPKGA RRLSAESSRKTTGGQSETSSRTEGEK LRRQNASPRTYGGTRDTFPGMSVG H
1133	6630	A	1191	137	474	

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1134	6631	A	1192	307	583	
1135	6632	B	1193	1	969	MRPYSQTVFSTQYRWVEQHLGPQF VERIILTRDKTVVLGDLIDDKDTV RGVHKSMCPGVTAASWGRAKDAM SICGCWLRELWDTSSRENSAAVKT GREADKPEVTKQTQFSTRKDEQAC SGYPYSDCWLAIELLHSAEPQAPRS RSDANASRSGPLRAGCETRLRLGV SCSACKPKPSVLRRCLLSARPPLCGP LHASFLPGVDSKSGKTAPRTDCTQS TALTGSGGAGDTLRIDEELTGKSRK SHTQVFICTSPLLKYHHCVGKEYR WVEQHLGPQFVERIILTRDKTVVLG DLIDDKDTVGRWTRYWPQSSLA CPD*
1136	6633	A	1194	834	1834	PSWCCRAGWMKPDKMLSKEADAS PASAGICRDHGGPDEDNAHS*SWE HPDTRDGAASGSTGTRNVERYLQ DSTFATSPHL\ESLLKIMLGDEAALL EQKELLSNWHFLVTRLLYSNPTV KPIDLHYAQSLLDLFLG/E*EQPSN PWTSCWQPLSLTS\NVIKECSIALS NWWFVAHLTDLLDHCKLLQSHNL YFGSNMREFLLLEYASGLFAHPSLW QVGVDFDYDYPELGRVSLGAAHLS GYL*TPRQKARKVLRICEAAADD* TSSQHL*DLSHESPSATIAWVLASF WSIRVKGCRLCPRSCQTGSSGITVSE AAFLIWISLATWGQP
1137	6634	A	1195	32	393	
1138	6635	A	1196	102	888	RNLQETAIMEAKPKLHYFNARRRM ESTRWLLAAAG\VEFEKFIKIWQ KIWDKFKEMMGYFDVVSQQVPN/VV *D*WGWLKVQTRAIQLTFASKLQP SYGGKDIKGRRALDL/DVF*EGFSQ ILGLKLFPFPLPVMSPHEEKRCPSLA LGSKRKIKKIGYLPFPFEKSLKEPMG QDYPCWANKLEPGLDIHL\VGTFY YVEELGLLGLISSFPLEGPWKTRI QLTCPTVEEVSLQPRAAPREAPPRD EKPLEEAKEDFPGF
1139	6636	A	1199	46	399	PGSKYDKTAILVSHLNFLNLLIKQP NPTQISPQGMFKRGGAR/PLLKTGPF LPTWKGDSFCYGKHSNSGWFEAKG FRRLPSFKNERKRNIGSPPPRLVVIS SESPHAPFGTKSIPED
1140	6637	A	1200	37	454	PGSKYDKTVILVSHLNFLNLLIKQP NPTQISPQGRPPPPQCRVTEWTTAS TQTQAGLKLKDSDDFQVSRMKEKE T**GAHHQDL*LFPQKAPMPHL*QN PFLKTDSRRNQVRSRTFPTSITFQNV GRSLPNTIYSGKK
1141	6638	A	1201	298	523	LLKVQSRQKHWAVGLRTLTVVGA VLIRVPPLREPLLAPPILVGASSRENI SR*VTGCSPTHSSSTPLATSPRQRA
1142	6639	A	1202	80	589	IFLNLLIKQPNPTQISPQGRPPPHVQ GD*VYNYGPTPASQPERRALKRGI* RKGEGGPRERVWAGAPGLPTPF

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						PENQGEKACG/GGRCLSPISSLQGP FPADWWEIPILA*SPDLHRDWGPAPP PPTSSNRPTPTVLRQERSGL\PPSP GHLGKLVFFQLAWDSFL
1143	6640	A	1203	2	661	FVEADRGLAVGSLRPLNLRGARA AFRFAAGRESRGKGTGERRTRVA VAGKVTSVPFVVSQGREHSHAPTR LPTIPPAAMSAAG\ARGLRAA\YHRL LDKVE\MLPEKLRPLYNQSRQVPR TVFFWAPIMKWGV\VCAGLA\DMA QTLPEKP*AQLQSACFGW\TRGLIW \SRILHL*IIPNTN\SLFGW*FPFVG AAGASQLFRTWRYNPRTKKLKAH K
1144	6641	A	1204	20	400	
1145	6642	A	1205	457	1011	SRRPWGHFTEEDQGLLSQSLWGQ/V *NVEKMLGRKKPLGKAPLVVLP TPRGSEKALGNLVLLPSCPSMGNP QKSRAPWARRVLTFFPWGDAHSTP G*SSKGTFCPA*SEPA/HCDKLH/VL DPENFKLLGNVLVTRFGQSIFGKE FHPLRCKAS\WQKMGELQVGHFPV LQIPLSSL\PMMQSFQG
1146	6643	A	1206	3	452	
1147	6644	A	1207	9	485	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAGHAGEYGAEALERM FLSFPT\TKTYFPHFDLASHGFCPR GPRQRRWPDALTK\A\VA\HVDGHA QTALSGPEATLHGAQSFQVDPVQLS SS*SHLPCWLT\GRPPSPAEPNPCR V ARLPWNKFPWVSC
1148	6645	A	1208	37	298	RQGLPLSPRLECHDRIIAHCNLEVL G SSSPPTPASPIA*\TTGVGHHTQLP FK LPYFFHSGLFFFLKKILYQFCDTY RA RISSDFCR
1149	6646	A	1209	49	564	SQTPMGHFTEED\KATITSLWGK\N VEK\SWKEKTPGKGSLLVLPWP TP RGSF\DSFGQTCPSALCPSMGKPP KS RAPWPRRVLTSLGRCQSTWDDPQ GAPFAQA*SELHC\DKPAMWDPEIN FKAPGEMLLVTRFGQFHFRANKFTP EGCRASWAERWVT\GVASALVPSR YH
1150	6647	A	1210	134	673	QRRTKATITSLWGKGEMWKDAGG E\TPGKGSLLVVP\WTQ\RFDSFG\N LSSAFCPSMGKPPKSRLHGK\KVL TSLGRCP*KHL\DDLNGHLLPKPDV NLHC\DKPAMWDPPGTFKLPGENV AGLTRFWAIPFSGKEF/TPLEVARLP WQKMAEDGDWQWASCPVPPRIPL EAHWPMISELFGK
1151	6648	C	1211	50	373	MGTVGSAWAAAPVQTHMFCSSSSC ISSLSTLPDAAPLSPLASSWPVPPRP LLHWPFQDQSSLLFSLSPSFXXXXXX XXXXXXXXXXXXXXXXXXXXX RALHTSLA*
1152	6649	C	1212	45	424	MNGDXGLCLAAAPDQTHMLGSSSS

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						CISLSTLPDSPAAPLSPLASSWPVPP RPLLHWPFQSSLLFSLSPSFXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXLTHTFSLSLERGGVLSISIRMW VRLS*
1153	6650	A	1213	97	1382	SACAWRLPSPGPSAMWPLWRLVSL LALSQALPFEQRFWDFTLDDGPF MMNDEEASGADTSGVLDPDSVTPT YSAMCPFGC\H\CHLRVVQ/CAPTL GLKSVPEISPDITLLDLQNNISEL RKDDFKGLQHL\YALVLVNNKISKI HEKAFSPLRKLQKLYISQNHLEIPP NLP\SSLV\ELRIHDNRIRKVPKGVFS GLRNMNCIE\MGGNPLENSGF\EPG\ AFDGLKLN/YT*RHLQRSKLTGHSP KYLPEITNELHLDHNKIQGHRTGR DLLRYSKLYRLGLGHN\QIRMIENG\ SLSFLPTLREV\HLADNNKLARVPSG FPDLKLLQVV/YILHSNNIHQSGVF NEFLFPWGFGEAGPYYNHGSASF TTPLPYW/ERLQPATFRVVTDRLAI QFGQLQKVEAAATLVSQWGS LG NRARHPDGEAEPGS
1154	6651	A	1214	938	1501	AGVGPDGFLFQGIVANDSHPTALL KRMFASGGRRSWCQPFQGTAMG GPWAKGCLGPASCAAKVGGPHPKT NPGPKPTGGQGFATGLRGVGISPP K*PCQ*AVQPGSHCPATCAEPSPPW G/PGVPRFEAPPPQTPP*PRLWPETG EPPLGVQKPP/QMPGPGAPLEN*S ASGGPRSPRGWESVWF
1155	6652	A	1215	883	1216	YISNSQLVQHFFFFFFFLFFFETESC PVAQAGTQWCDLGS LQPPP\G*SN SPASASRVAGITGVHHHAGANFLYL *QRWGFTMLAQAGLELLTS*STRLG LPKCWGLQT
1156	6653	A	1216	197	821	RLFHSNQTVDHSQKNVDITLKG\RP SNRVRAPKGTLR\RD FNPHQM*NSA LLGKEQQRGFRVD\KWWGYQKGN WPTRSGLFGSHVQD\MIKGWLPGL PVTMNR\SVYAHFPHPTLLSRENGV SLLKSRNFLG\EKYIPQGFRMKTRVL LCQYLKAQKR*N*SLEGND\IGLVS\ NFSRLIPASPTRLKTKGIRKFLDGI FCLLEKGLFRQA
1157	6654	A	1217	241	514	DGQRLGKPHFVLLVLQ*LQTGLWS WWGKLGVE/MLGVGEILGS AFISP VLERVEGSGSGGNQAGPREEGWLG KPLRPEAPPSTFIQHHTLG
1158	6655	A	1218	3	496	SSGLFTQQSPEAWFCVSKCSYPAW QNVKVIVDSHKLQEIQRSLIPFAQF PAMVTVCAPGRFCHPCWHV*P/HP HSHDTEHGHHHKCLVLCYPFTASA PPSCAPLRICIYGCILSCLVDVPWRT DRLNKQRVCKEAQSRREGSPA WLI GQSHRLALPLLAALS
1159	6656	A	1219	1326	2014	QLMIYTRTELAWPGDQKH YFHT CVMILFFLRQSLALLPRLGVQWHDL

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						GSLQPA\PPPPGFRLFSCLSLPSS*DY RHVPP\QLIFFVLLVETGF/TPMLG RMVSI*/PSDDPPTSASQSARITGVS HSWVNSCDLPLKNFFFFLEESHVS QAGVQWHDLGSLQPPLPGFKLFCL CLLNSWDYRHAPPCANFCIFSRDG VSPCWPAWSPSLHLVIRPPWPPEVL GLQA
1160	6657	A	1222	1	459	IEIHKCGGIPAVLAAPAMGLELFLD LVSQPSRAVYIFAKKNGIPLELRTV DLVKGQHKSEFLQINSLGKLPTLK DGDFILTE/SANRSVYLQGGCWHIT EMRFSKCKAEGPAKSRSAILIYLS KYQTPDHWYPSDLQARARVHEYL GWHAD
1161	6658	A	1223	2	310	
1162	6659	A	1224	205	454	
1163	6660	A	1225	2	384	
1164	6661	A	1226	1	1276	MPGLGFREKKGGSRTPVPASRGCGL PAPILCTKWELPLSGSSRCLAAAL QGTVWTAESSLTPAFQSRGWGLIP YFPARRDPATAAHTALSAFTAIPA VLAAPAMGLELFL\DLVSQPSRAVY IFAKKNGIPLELRTVDLVKGQHKSK EFLQINSLGKLPTLKDGDFILTESLAI LIYLSCKYQTA\DH\WYPSDLQGF ARVHEVPWAWHADLHPVGTFWY YPWGVQGVWGHSLGVQVPPEKVG TQTRTAMDQALQWLEDKFLGDRPF LAGQQVTLADLMALEGS*CKPVAL GYELFEGRPRLAAWRR\RVFAFLG\ AELCQEAH\NILLSILEQAA\KKTLPT PSPAEAYQAMLLRNRPGSPGSGM GAKEISNKDSFCYLLAPFYLSLLPQS LLSKLQCEALHRQRHSSVLWQVLL LLRCKHT
1165	6662	A	1227	151	278	G*KYDSDIYHEAVVPHQNQMSARS DKEKKRFIFYSSYYIPFC
1166	6663	B	1228	1	690	MASWDEKDLTVQPDPTRKGSVLRC GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGVELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
1167	6664	B	1229	1	975	MSPPGREQGLLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWVVD SADRQRMQDCQ RELQSLLEVVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLQL SSLTCIYTAGKMRLQDRIATFFPKG MMLTTAALMLFHLHLGIFIRDVHNF

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						CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH*
1168	6665	A	1230	1	211	
1169	6666	A	1231	950	1326	RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCLA CLPLRTECLGIKPIVHLFSTRPVIV PSLELNVDVDSIAHMFVADLLMIT LPSYDIPFYCLVFQNLVLEFQYL
1170	6667	A	1232	271	927	NQGLRHVRLCRMCLVNQMFASSIL GKSHHSLVLPINQGHNALWKAAG\ PLPLKAGYC\QGFSPCHSLKYGSW DEKDLTVPQRDTHKRSVLKVELVQ RGKNLPVEDGGKAHCLPELPPGELE CPG\ILKHGLYHWSSEMGEKPAPM VGG\RHV\CSNAALVIPLPLRCLGG EKHKSGLAHARPVIVPSLELNHDTD SFAHMFADLLIITLPSYYIPFC
1171	6668	A	1233	62	1158	GHLCARPETSLLQVRPGLPSSFSG MDVGPSSLPHLGLKLLLLLLLLPLR GQANTGCYGIPGMPGLPGAPGKDG YDGLPGPKGEPG\PAISWIRGPKGQ KGEPG\LPGHSWGKMGMGPPGDC QGLPGPLGDFPG\EPG*G\GRYKQKF QFSFSLRQTHQPPRTNSLIRFNAV L\TNPT*ITYNTCTG*FTSKVPGLYYF VYHASH\TANWCVVLYRSGIAKVV TFCGPHVPKPISSNSGGCACLRLQV GRGRCGWLS\MTYYGHGWGIQGL* KSVFSGLPWLLPRTKGGARCGSRPT GPSPSPQLPAWTQPYWPVCILALDH SPHQMDFSPPGSPPLTHPHCTPLPM GSLLPLNFFRSHCLCGSWDT
1172	6669	A	1234	2	907	AVAFGAKGTDPAEARSSRGIEEAGP RAHGRAGREPERRRSRQRRGGLQ ARRSTLLKTCARARATAPGAMKM VAPWTRFYNSCCLCCHVRTGTILL GVWYLIINAVVLVDFIECPG*SGSSI TFQVLELGGDFEFMDAN\NGAFAI AISLLMILICAMATYGAYKQRAAWI IPFFCYQIFDFAL\TC*VAISGLIYANS IQENIRELPPKFPYRDDAMSVNPTC LVFIILLFISISLTFKGYLISCVWNCY RYINGRNSA*CPWFMLPAMTLRCC YPPYDDATVNGAAKEPPPPYRVCLS L
1173	6670	A	1235	966	1564	NDFFKTNKSSIIRNSCLTAILVFLCC YDLTLTGTLF*ILTFRWL*LGLIIRLN MASRSTIYVYGSQPSLFTFENTDF YQLWILFLVICLPFLFKFTIFLWP KLLTLENQILHQIQCFSVVFLMSAPI TTVRGIHVLPVIVILQTDLAWINQLL HLLFSKLGYYDDSVQDWVSLMWN GTHGRKCRSQFYMPIKGHL
1174	6671	A	1236	155	303	AFQEGDPMFKPSRCPYLPKPCPS TCLP/SFAFRAVVTQVP*CCVCKCPG
1175	6672	A	1237	739	1629	GTSQMPTSAVPSLLSPSKFARKGFS

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						KVLQLCLYRRIGLCPAPPPPPVPTQC PRPQELIGP/WRE*CPPGSFRNSPRNL FSFLQELPEESV
1176	6673	A	1238	1	554	NFALEAKNSARAISLVPDA\MGHF TEED\KAT\NTSLWGKGEMWKDAGG ET\LGRL\LVVYP\WT\QRFFD\SFGN LSSASHPWATPKVKAHG\KKVLT\ SLGDA\TKHL\DDLKG\TFCPSLK*TC TC*QACNVGS*GTFKLPGEILLVTRF WQSHFRQKNFTPEGCRLSWAERW VTWSWPVPLFLPDYH
1177	6674	A	1239	29	454	
1178	6675	A	1240	1	1368	
1179	6676	A	1241	1	1266	LSRVAEFEHLGWSPKPTTCTPACQ GLSGAAMKSLVLLLCLAQLWGCHS APHGPGLIYRQPNCDDEPETEEAALV AIDYINQNLPGWYKHTLNQID\EVK VWPQQPSGRAVLRFEIRTPWGTTLP CCWDPTLVGQDASLEGLSKEHAVE GDCDFQLLKLDGKF\SVVYAKCD\S SQDSAEDV\RKVCQH\CPLLAP\ND TRVVHAAKSCPGPPFNAQNNGFQF FSLEEISR\AQLVPLPPS\TY\VEFTVS G\TDLLFA*KKATEAAKCNLSGQKS NMGFCK\ATLSEKLGSGQRLQLTCT VF\QTQPV\TSQPNPEGANEAVPTPV\ VDP\DAPSPPLGAPGLLPSWLT PKT TMVLL\AAPPQHQLHR\AHYDLCHT FMGVVS\LGSPFRKCSHPRKNT/RT VVEA*WLGAAAGATGFLPLFRGGI RHFKV
1180	6677	A	1242	1134	1247	
1181	6678	A	1243	1330	1517	KLNMVFKKISHGMQLRKSYNLFYQ KSGKIMT*IWEIFFPEFFFIPTV\LF LKREFLLNEPS
1182	6679	A	1244	213	287	
1183	6680	C	1245	249	323	MYKLRRKLEDRNKIENENIVKSFR*
1184	6681	A	1246	1021	1985	IAWAFKINWLP\IFLIFS\VFYPIFGFI FFYLLYFSNTCLS\FVFPFSYLKLLTI FSFSILFLSSNLLSLYILPLAFCFLAC LFFFCFLFRFKFIFFLPKSMFLSSNF PIF/CIFFFAFPYSCLPVFHCQTFYLL QIVVIL/IHSQLIFPSSAFSKCG*QGF *MTQFSRLRHGFQGLLITFGLISF*KIA FKLF*SPTTFKLNFKLKF\YLHFNK ALPSLLGLNSGLL*/FLSHQFSFKYIF YSMKKLHLNLRHVLETVLSFPSSCY SSKFVHFALSFLFPSLSFFFCFLFRF KFIFFL/RKSMFLSSNFPIFSILFYLP F
1185	6682	A	1248	147	460	PFYKNCVSIVVVVFETGSCSVTQAG VQWHDFSSLRPPPGASSDPPTSASR VAGTTGMCHHIQLIF*SFFIETGTHY VVQAGLKLLGSSHPPTFSLPKWLGL QA
1186	6683	A	1249	168	407	ISHTREHSLDFFSFLFFETESH/STR RLEYNGGLSAHCNHLHLLGSSDLPTS

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						AC*VAGTTSIWQHVQLTFVFFFLLI IIF
1187	6684	A	1250	163	396	TRFPILGSIA*IFFLFFFFFETESH/STR RLEYNGGFSAHCNLHLLGSSDLPTS AC*VAGTTSIWQHVQLTFVFFFC
1188	6685	A	1251	37	698	RSSSPALEGGRKRVDMCELGSTIGP GPGSGQPACPLIWLHC*NPVEQAGP KP/PARPARSGP/QPPPTAGPA/PVGP KPPPTAGPA/PVGPKPLPTAGPARS WRP*PSGARGIKETHTEI*VP/PQGF ACLIPTAPTGP TD**WLHLDLPTTP\ QPHPEAVQHTGGSC LTPYDGP PPPQ PISSKHPLPSYPTSPKLPLEHPSQIL GETDFSNHQILVSHSLVSV
1189	6686	C	1252	150	308	MALQRTXLLLLLLLLTLLGLGLVQ XPMARMXCTSDSCGNTCTLRQVA SDRY*
1190	6687	A	1253	2	470	
1191	6688	A	1254	92	1047	RAAWQGGAEASGPPSALRGGSALA AAARWGPAEEGARIPGSFFA WAAP AAPGAGAAAAPAPRADPGGRLLG EAGRGP NYAEAGTPTLHTLPRHLR PCTHTHTRTPTPPRCKAGFKRTSLR FLPAPHHRTREEEAGEKQNFPLSC PFLRTCSEAEPEVLEEMVMGLGVLL LVFVLGLGLTPPTLAQDNSRYTHF LTQHHA\KTRGR\DLPSCKTFMRSR GLTSPCKD\NTFIH\GNKRTLKGQS CEN\KNGKPLTEKNLKE*SKSFLSQV TNTCK\ LHGGSP\WPPC\QYRATAGF RNVVVACENGLPVHLDQSIFRRP
1192	6689	A	1255	199	792	PGSTAAADQRSRNWNPNRVRKKPD LEGGCGTVLSGRWRSRRNRRTSGQ SLVPVYIYSPEYVSMCDLAKIPKR ASMVHSLIEAYALHKQMRIVKPKV ASMEE\MATFHTGCFICSISRSAKR AMMIIRTSLEYGVRFINFPATEGIFT LCSS*GGATITAAQCLIAGMCKVAI NWFGGWHHAKKKTCVYVALYKAF
1193	6690	A	1256	1368	2229	WHPRQVLTGNDEVIGQVLSTLKSA DVPYTAALTA VRPSRVARD\VSVEA GGLGRQLLQKQPVSPVIHPPEYND TAPRILFWAQNFSA\YKDQWEDLT PLTFGVQELNLTGSFWNDSFARLS\L TYERIFATTA\TFSFIPAHQRYPPSAR HWFTMERLEVHSNGSVAYFNASQV TGPSIYSFHC\EYVSSLSQEG*SPRW ARTQPSSWQMML\QGFDPGPFSTL MGEQFSYA\SDCGQASSSPGIWMGL LTSLFMLFIFTYGLHMILSLKTMDRF \DEHKGPTISLTQIV
1194	6691	A	1257	2	630	PDSSGPHRLRENPPWCLSPADKTN VK\APAWGKVGGAHAVRSMCAEAL ER\MVLFPPPTPKPYFPH\DLSHGVS AQV*GPRARKVADALD\TNAVHR GTD\DCPNGVVPPLSDLHAHKLARV GPGSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVATSSLGTKFPGFLVEA

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						PLLTQITFKGWKPRVGHAFALW ASPQPLLPAPVPPWSFE
1195	6692	A	1258	207	591	
1196	6693	A	1259	1	541	WNLSASPARQHPLLPHPVSCILLKPS SKKCLPNLTGYRFRVSQKNMEDYL QALSSPH\DISLAVRKIALLLKPDKEI EH\QGNHMTVRTLSTFRNYTVQF*/ HVGVEFEEDLRSV\DGRKCQGPCW HCNFSSQSHLLSSRAMFSTAYKIQL ALHIHGFCIHSFSKLQMEKYLKIKI KNNNTK
1197	6694	A	1260	214	491	ESHGAQIYIPHFCVPWSRWGNVRR CEALAVIYVTNNKIYVLSDPESCLQ PTSIN*QSNLLACK*GKN/RKTGQAR CHACNPSTLEGRSRIN
1198	6695	C	1261	48	173	MVRKRMEMKMRKLSQLRASGQLK MMRMXMSIPSRPRGIX*
1199	6696	A	1262	59	306	FGTDRTA\QTSSSQRLCLPWWAQK TYWLLVPSSLLKDLKEKKEVVEEA* NGRDAPANGNAVSVCFAPWPQLP PHKIFPVLL
1200	6697	A	1263	279	889	TLAVFLIPCIGSPACPTMSDAA\VD SSEITTKD\LKEKKEVVEEA\ENGRD APANGNAVEEEDGDEDEEAESATG KAGQPED\DEDDVDYQGGKQKTDE D*IRQQKRKKLNLKKRPAHRGQC HPADDTRSPPNPNHENLQQGREKR NQNFQGAFFLKSTLKRKFVCIFYL HFIFLYILLRVSHFLMISDDQTSLPER SLSYF
1201	6698	A	1264	358	508	DDDVDTKKQKTDEDD*TAKKRKV KLKKKKAAVTYSPSTSLRYLYVFT FE
1202	6699	B	1265	46	386	XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKAACL KEKYEKDIAAYRAKGKPDAAKKG VVKAEKSKKKKEEEDDEEEDDEE EEEDXEDDDEEEDDDDE*
1203	6700	A	1266	263	484	
1204	6701	A	1267	157	886	TWKGDLKKPRANMSSYAFFVQTC RGG\HKKKHDPASVNFS/ESFSKKCS ERWKTMSA*/R/EKGKFEDMAKA\D KARYER\EMKTYIPPQRGRQKRKFK DSQLHPRGPPSGLLSSSCSEYRPKIK\ GEHP\GL\SIGDVAKKLGRDVGINTA AD\DKQPYERRAAKLKEKYEKDIA AYRAKGKPDAAKKG/VVKAEKSKK KKEEEEGEEDDEEEDDEEIEE EEDEEDDGLMNLGSGAVFFFSCL
1205	6702	A	1270	2	343	
1206	6703	A	1271	3	647	
1207	6704	A	1272	59	1297	NHASVQVKLWILSRSYLQLTMEAN GL*PQGLPDLKNDTFL*AAWGEETD YTPVWCMRQAGRYLPEFRETRAAQ DFFSTCRSPEACCELTLQPLRRFPLD AAIIFSDILVVPQMFSPPPGTGQWKV TMVPGKGPSFPEPLREEQDLERLARD

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						PEVVASE\LG YGFQAIT\LTRQ\RLA GTCAG*LAFAGAPMEP*MTYM\VE G\GGST\MAQA\KR WLYQRPQASH \QLLRILT\AL WLPYL\VGQVVAGA \QALQLFES\HAGHFWPHSSFNFCT ALT SRDVAQAK*RPRLPGSQALATR CPCIIFA\RDGHFAPGRSLAQAG\YE\ VVGLDWTVPK\KARECVGKT\VT\ LQGNL\DP\VALYA\SEEEIGQ\LVKQ MLDDFGPHRY\ITPHLGHGLYPDMD PEHVGA FVDAVHKHSRLLRQN
1208	6705	A	1273	7	1047	
1209	6706	A	1274	7	960	
1210	6707	A	1275	3	53	
1211	6708	A	1276	237	441	AHFLHIVLVLLSCWYSV\RSRCTSQ QGVQSD\LAQLLPLRQRLEGEALV ALGAGVERRHVRPGPRNST
1212	6709	A	1277	94	1003	VRVSLSLRLECNGAILPHCNLHLP SSDSPASASQVAGITGVCHHAPPIFV LLVETGFHHVGQAGLELLTSSDLPA WASQSAGITGGSH/LCLANVKYFKS HFKIFVIDETWFQHT*L LSLSSCD*V *TSI*/PQVLD*NVLCPDV/SQ*LLPW LIKIFLKYTLDCW*KRQAWLYWY* FGTELFGCP*GRQTL CFFLRRL/DS VAQAGVQ*CDLGS LQPLPRFK*FS CLSFNSWDYRCAPPLPANFCIFSRD /MGFAMLVRLVSELLTSGDPPASAS QSAGITGMSYRAWPKPYAFEVECR PCDN
1213	6710	A	1278	4077	5102	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERP KKG GGSRAAQ TASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASCKGRR/HTPSTINLFLNDPPPLP KH\PH*ASPPTLGIEFQHEIWRGQTS KLSQHPSFSLRLLTYSSTQAAFEFL FCRCLPTGHVPSSLLHSAADTAVSG DYATEGWECHCCWGCWEAKVGV LLH
1214	6711	A	1279	316	1180	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERP KKG GGSRAAQ TASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASTQAAFEFLFCRCLPTGHVPSS/TP PFSSRYSSFRRLCLIFRGCWTEVLNE GGANSDSWSLTKLESGSSECCS
1215	6712	A	1280	2	315	

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1216	6713	A	1281	195	739	KFSSRITVCHWKDVLLSGFQEPDRG SAMDYVRKIYAAIFLVTLSVFLHV LHSAPDVQDCP/EFTL/RENPLSPAR VPPILQCMGLPASPRAYPTPTKGPR KDGCWVPKEPSPSESPPCLW*PKIHI NRGPQ*MGGFPKVGEPTACPLGS YLFYYPQIFKMFLPQVLSWMDWLDF LGIGKI
1217	6714	B	1282	29	200	MSRTRLVCPSLIPFCIYVVDVGFSPG PQSCTSHPEPKDIHAKCELAFLHHQR FYKNEGX*
1218	6715	A	1283	138	1908	ASRTAVARWECVLQNVRRPSPSR AWPSQLRPIASTATKCRE/CGPGYST PLEAMKGPREEIVYL/CILPETQGT EGPRLSWATVDVDPKSPQYCVIHI RLPMPNLKDELHSGWNTCGSCF G*LAPSRGTK/LVLP SFHLLFGIYVG GTWGSEPRAPKLAQGSLSPRDIHAK CNWAF LHTSHCLASGEVMISLGD VKGNKGKGGFVLLDGETFEVKGTWE RPGGAAPLG YDFWYQPRHNMIST EWAAPNVLRDGFNPADVEAGLYGS HLYVWDWQRIEIVQTL SLKDGLIPL EIRFLHNPDRCPKAFVGCALQAPNI QRFLQRTRGGTLFSGRR*FQVAPPRK LKGWALLPKMPGLA/ITILASPWNDG FLYFSNWLAWGP*GKYDISDPQRP ALTGQLFLGGSIVKEGPVQVLEDEE L/TSPSPEPLVVKGKRVGEGP/QMI/Q LSLDGKRLNNHHGRCTSA LGQSSF YP*SQSGERLLVNAGRVEW*DNSK KGGA*KLNPQLSWVDFGEGAPLPK PLPH*ARYP/GG\DCSS\DIWILNSPPS HPSLFWALHFPGGPGLSFCISLGTR TLGKHVPTTAKLRLWQCVES
1219	6716	A	1284	155	336	HFKIINRGWAPWFMVPVIALWEAE GG\HLKL**AMIVPLHSSLGDTVRL KYLCIYSLIF
1220	6717	B	1285	251	570	XELLVQLASLQTSFVTLDEAIKITNR RVNAIEHVII PRIERTLAYIITELDER EREFFYRLKKIQEKKKILKEKSEKD LEQRRAAAGEVLEPANLLAEKDED LLFE*
1221	6718	A	1286	83	977	HNQLTPVEEDTVESQFWSYCSLGCP AGDPSRKVIVRMSGKDRIEIPSRM AQTIMKARLKGAQTGRNL/L*RKKS DALTSDFRQILKKVIGDLKCLMGIE VMREAAFFTSWKPSFTAGDFQALT VIPKCSIKGGKLVSE/DEGKVIVRP VFTFASNFEHYH*RN*PVMELTGLA RGGEVQLAKLKRNYAKAVELLVEL ASLQTSFVTLDEAIKITQAC*MPIE HVIIPRIERTLAYYSSQSWVRRE EFYRLKKIQEKKKILKEKSEKDLEQ RRAAG\RCWSLLIFLAEEKDRGSFL F
1222	6719	A	1287	1	3249	
1223	6720	A	1288	504	932	RYRCGVGSVLQAGGLILHLRKEGIL

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						HNKGKIEGMGLLEYVQGSLLQGW VMFVSVTAFFSLLFLGMFLSGMV AQIDANWNFLDFAYHFTVFVYFYG AFF\MEAAATSLHDLH*NTTITGQPL LRDNQYNINVAASIFAFYDDS
1224	6721	A	1289	66	1363	RTAVMPREDRATWKSNYFLKIIQLL DDYPKCFIVGADNVGSKQMQQIRM SLRGKAVVLMGKNTMHAQAPFEG TL*NNPSLWRKLLP\HIRGEFGLLFH PGRTLTE\RD MFAGPIRLPTAARCW CQLPPCEVTVPA\QNTGLG\PEKTSF FPGL*VSPTK\ISQGAPIENPEVNVPA ESRTGDKSGKPSE\ATLL\NML\NISP FSLWG WSSSQVFD\NASIYKP*KCLI SPEETLHSR\FLGGCPQMLPSVCLQI GYPTVASVPHSIINGYKRVLAL\VE TDYTFPLAEKVKAFL\ADPSAFVAA APC/AVVAPPAAPAAAAAPAKVEA KEESESEDEDMGFAAAVLPGGTKP GALPPLAPGLALPRGPCDPEAFRK RFRSQPRQDGGGHAELQKFTLPSLY FFSPKPSGCEPRANAKSSLNFVFSKY SLSTYYEQGL
1225	6722	A	1290	3	231	CSSSTSPSSEYCPSWGTEFRSGEMGS K*SSL*GASSLS PDTGRGTGSSSSSS GGGGP GGVLG PLGCGLGGLPLN
1226	6723	A	1291	221	984	ETGLMCSSPLDQNSV*RLTPWTLA PGTTAEVNQEDQKKSQIL*KKWQA AANSSRLVKNS*MP\T*KIQNGRMD KNSPTKYLLSSRDSS\THKESHKLKD IALILPSSSEGSISELEQLSNSLPNKL MTSICDLLATLANSESSYNCLLTC VRTMMFLAEHDYGLFHLKSSLRKN SSALHSLLRVVSTFSKDTGELASSF LEFMRQILNSDTIAPVCVAALSVSM CSHRSAPTWFPPKGLKGARTTSRNS SEA
1227	6724	A	1292	817	1826	SCYPFCTS*KSFHSCHTNDTVQSFK SI*LKR\SDT*SANRSSNNPLITPACSS PVTP*APHSASEDTNLVPALSCRTFK AIGWRSATCKFKACMVQSTNWP SCFVFFNCK*LNPFIKLGISSKAVTH FAPLSSLYKSSSVNFTEASIAPEFSL SGP*SFILLISISKVVLYGQLKYKSGT SSLSYGSYVIGGTEAKSSAVYSTSKF GYLNVSRKSAIPSSSLEICS*PSSPSP SSSSSPSSSSSSSSSGILSTVRRSSSS SSSSSTSTSSSSSPSSCCSSSTSPSS EYCPSWGTEFRSGEMGSK*SSL*GA SSSLSPDTGRGTGSSSSSSGGGGPGR SSWSPWLWSWRASIKLIFFLPISMF WDSFNLGCGLGEGGWREGGGG GRVSVMTLSLYPLDPYIASVRQLYQ PLSTRPSVFTFELGLKMMEVFSSYS RLPNLSKTGALGLPYIVEE
1228	6725	A	1293	25	771	LDGPQGTSRPWGLPSLPPPRAGAGL SQGFGSSLRPARTPPSSGSKMSTEA QRVDDSPSTRA\QSSDGDQRESVQQ

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						EPEREQVQPKKKEGKISSKTAAKLS TSAKRIQKELAEITLDPNNL*VAGP KGDNIYEWRSITLPPGVSVEGGVF FLDITFSPDYPFKPPK\VTFRTRYHC NINIQGVICLDILKDNWSPALTISKV LLSICSLTDCNPADPLVGSATQYM TNRAEHDRMARQWTKRYAT
1229	6726	A	1294	449	826	QKSRLIDDLFFFFFFCETGSCSVTQA GVQWHNHGSLQPPPPG\NDPPTSA SQVAGVSVACHHSRFVCARVCVCV CVCVCVCVESGLKLLGSSNSPLAS QNARIIGMS*IVPKKLYFKSKVKGRI
1230	6727	A	1295	1	727	NTEDQRNEEKAQREANKKIEKQLQ KDKQVYRATHRLLLLGAGESGKSTI VKQMRILHVNGFNGDEKATKVQDI KNNLKEAETIVAAMSNLVPPVELA NPENQFRVDHILSVMNVPDFDFPPE FYEHAKALWEDEGVRACYERSNEY QLIDCAQYFLDKIDVIKQADYVPSD QDLLR\CRVLTSGIFETKFQV\DK\I NFHIV*RGVGQDERRKWIQCFND VTAIIFVVAASSYNMVIREDN
1231	6728	A	1296	2	1271	PVRSSAPRRGHSVASAPRSGLRQVA GRRGAALPCSLAPGCGAAAGASPC PGAGRRAAGGRCLACECTSLTCA GESGKSTIVKQMRILHVNGFNGEGG EEDPQAARSNSDGEKATKVQDIKN NLKEAETIVAAMSNLVPPVELANP ENQFRVDYILSVMNVPDFDFPPEFY EHAKALWEDEGVRACYERSNEYQL IDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLTSGIFETKFQVDKVNFM FDVGGQDERRKWIQCFNDVTAIIF VVAASSYNMVIREDNQTNRLQEAL NLFKSIWNNRWLR\TISVILFNKQ\ DLLAEKVLGKSKIE\DYFPE\FAR\Y TTPE\DATPE\GEDP*TRAK\YFIR\ DEFLRISTASGDGGHYCYPHFTCAV DTENIRRVFNDCRDIIQRMHLRQYE LL
1232	6729	A	1297	235	1571	GRPRPPPPQGRAPPPPPRMGCLG NSKTEDQRNEEKAQREANKKIEKQ LQKDKQVYRATHRLLLLGAGESGK STIVKQMRILHVNGFNGEGGEEDPQ AARSNSDGEKATKVQDIKNNLKE AETIVAAMSNLVPPVELANPENQF RVDYILSVMNVPDFDFPPEFYEHAK VLWEDEGVRACY\ERSNEYQLIDC AQYFL\DKIDVIKQAD\YVPSDQDL LR\CARVLTSGIFETKFQVDKVNFM HMF\DVGGQ\RDERRKWIQCFNDV TAIIFVVGSSSYNMVIREDTGHNG AGRL*TSKGIWDNRWAAAPSLVIL FLTKQ\EILLA*ESPLAGNSK\KDYF PE\FAR\YTTPEGCYSRPGEHPGV YRGQVTPFEDEFLLRSSNCPVEDGRH YCYPHFTCAVDTENIRRVFNGLAV DIHFSGMHLSFSYGAGFKEGEPKPF

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						NLKA
1233	6730	A	1298	176	505	ILKFPWIDIFLYSFNLVFLIFETRPFI LSPRLECSGMTSAHCNLCPCSSDP PTSAS*VAGTTGTQHHAWLI*LFGE RELHHVTQAGLKLLS*VILSPQPPK VLGLQA
1234	6731	A	1299	310	326	SQHFGKLRRVHSLNSGVQDQPGQH EETSSLLKIQQLARHGCVCVLAQL LRRLGWEDHLNLGGRGCNEPRWC HCTPA*VTE*DSISKNNNNN*QAGV QWHHLGSLQPLPPRFK
1235	6732	B	1300	99	430	XVITQRELVSQRQVSNDLTEQAATFG LILDDVSLTYLTFGKEFTEAVEAKQ VAQQEAERARFVKEKAEQKKKAE QKKKVEQKKKAAVISAEGDSKATE LIANSLAHRGGPP*
1236	6733	A	1301	64	967	NFRVEAGVRGVQKQKTCFAFKVLESI GKLG/LALS/VAGGAENSALYNVDA GHRAVIFDPIPGQK*QDIVVGEGETHF /LIP/WVQKPQLSNDCSRPRNCCQS ITGSK/DLQNVNITLRHPSSGPVRQP SFPRIFTSIGED/YDERVLA/VPSQLEN LKSV/VAPFDAG/ELITQR/ELVSRQV/ SDDL/TERA/ATFGLILDDVSLTHLTF GKL/LTEA/VEAKQVA/QQGKQRRAR FV/VLEKAEQKKKAA/ISAEGDSKA AELIANSLATAGDGLIELRKLEAAE DIAYQLSRSRNITYLPAGQSVLLQLP Q
1237	6734	A	1302	424	598	
1238	6735	A	1303	3	371	
1239	6736	A	1304	1	1596	
1240	6737	A	1305	2	556	WDMMYVTRFASFLRNVLPSFISDW LYVQKMNTWFKHENYGLMPLNGY LKMEIFFIQKRGALI**IYLSIKPSVK EFTETSAVFEDGTMFEAIDSVIFATG YDYSYPFLDETIMKSRNNEVTLFKG IFPPLMEKPTLAVIGLVQSLGAAIPT ADLQAWWAQVFASRWAILSFHFI NEHLLNTCY
1241	6738	A	1306	955	1187	IFFFFFFFKMESCFAQAGVQWCDLG SLQALPPGFTPFSCLSLLSSWDYRRP PPHLANFLYF**TWVFTVLARMVSI S
1242	6739	A	1307	6345	9041	
1243	6740	A	1308	236	437	LLTLRWSHSSHVLLKTRGQPRRSG WCL*SH/HFGRPRRADHLRSGVQDQ PGQHSEIVSTKNTKIGWAWWQVPV IPAT*E
1244	6741	C	1309	182	433	MHLDFLNLKTLPIRGVESEQSSRL HPLPDRGDRHRMADNLPMEIHGS SATSSGKPSDFNQAAVDGAGERGG KEVLGGTLDVL*
1245	6742	C	1310	72	254	MVSTQLRQASDPRTTIGRERFELL RRVDKLMSPRLPTGTLPNPHFWTL SIPQVGRCNAP*
1246	6743	A	1311	225	735	GELRVNSLHVSTHFQIPEETDIGWL

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						VSPGQGPAPFEDIQLWPPGSLMAA EPTDQSLEESH*DRWITFTFFAR\Q EGRK\ID*PQRSNEFKE\VTQQLPHL\A LKDVGSLDRKN*GAWDVNQDFGG SRFN\EY\WRLIGGAWPKEIRKEEKT LKIQUERSKAAWLEDGVGQGR
1247	6744	A	1312	165	629	TGEMLIRKHCLYIVCKLSLLFIFRDM SCSVAQ\AGMQWHATNAVDGD*LT ASLKLLGSSNPPCNPKRAGIIGMH QHIQLIFCWSFF*KQAFRLITKALRN FKKI*FQNTLVTKY*HCSLTFFFCH FNENRILHLLAQMAKQDSGLLRV AWEA
1248	6745	A	1313	76	523	ELGRNLWNASQGRGLEWVSNRKF WAVYAYITFLSHPERVVNKHNCPL FE*KGECWEW*EARAQTDRVQKQ MWLLRIQTSFSSRKETQSLRVTFWR YPVSPSPISMR*MSPGNSYRTLYKR NVPLKAHFPTAVLAVVPPAVTNQG KEQG
1249	6746	A	1314	55	391	
1250	6747	A	1315	996	1334	WASVGLSGPRSPSSRPQ*ARPRPG APASLRQADLGRGWRDRLGAPRPR PPRTGGWRSCCRGRGPGSRPRGAR AGLGPGAPGGWRRSRRSWTRARA ATRPRAAARGSRTPRG
1251	6748	A	1316	1	993	
1252	6749	A	1317	72	496	PPWARGSARRPPAWRTVRMPSCHP RMFGAPQKTFLRVSVWSRCRPWGI VMRMM*PMRGQVRRHNSCMAPKT EE*NPTVSATFCCCSFVSCSWPPVTR YSSILFTAAM
1253	6750	C	1318	202	378	MTPYLTLFLSPLPPKGEIWGLLLFLT PLGFLLPSLPLLLPCPAPAGVRRQW DGPTEGA*
1254	6751	A	1319	1	1541	
1255	6752	A	1320	9	345	YLSEVGVS\GVIRPRQWIRPEGDP FHGGRLKMDPLRAQQLAAELEVEM MA\DMYNRMTSACHRKCVPPPFKE AELSKGESVCLD\RCVSKYL\DIHGA *WGKKFDRVLLQG
1256	6753	A	1321	199	985	VRGSGADPGGRLCSASVRRGGPLE GAFNSRTRQATMTENSTSAPAAK\P KRAK\ASK\KSTDHPQVFQT*IVACN SSPRRTGAGS\SRQSIQ\KYIKSHYKV G*ERLTSQ\KLSIKRL\VTGVPSTRQ TK\GVGASGSFRL\AKSDEPKKSVA FKTKKEIKKVATPKKASK\KKAAS KAPNPRNPKSSPVKKA\KKKLAAPG PKKA\NPKPTVKAKPGKAFKAHWR PYLV*PKCKCPVAKEGRARRKLTMI VFFLRDTPSWSPIFK
1257	6754	A	1322	3	129	
1258	6755	A	1323	376	545	NILHRLFTFREKTSYAPFVVRRFH GRHTFPALKWEVWRKKGPGE DSDMALSYSPPPPPPPPMVMG*/SP PSH*PLLLCRRVKKEGF

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1259	6756	A	1324	14	262	FQTQTKYQAPLHPAPGHRPTPLPPP PPASHCHLFLWSVCKRSNKPQAPFI SPPPSNPLPEPGPCSSLCQPWGRGTG EGLAPPD
1260	6757	A	1325	234	275	
1261	6758	A	1326	52	454	SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGK\KVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDDK FLASVSTVLTSKYR
1262	6759	A	1327	3	616	PTLLVPTDSERTHPWLLSPADKDQR QGPAWG*G*GSHPPSNVAKTLER/M VLFPPPTPKPYFP\HFDL\SHG\SAQV\ KGHGK\KVADALTNAVAHVDDMP NALSALSDLHAHKLRVDPFNFKL L\SHCLLG*PWAHLPRSPFTPCGCK ASL\DKFPGFLVEAPLLEPSKLPKL GSLRLAMLLCPFGFPQPLLPFPAPV PPWSLK
1263	6760	A	1333	732	1634	RRFWQVENHEILTEQAFVGQKPIFR/ MKSLEKELKTLATKRKPKNIGDILT KRKNNRTGSEAGEPQRWKPRRCPI RRAQEKNSQRPRKRREGKVPIWRK KPLKTGRDRSW*P*KLLALCPSTVG IRSRAG
1264	6761	A	1334	1	531	FFFLHVVAHLIFTATQMGSNILITVL QMRSPRRRVEYLAQDHTPFATPHS KSHRQLRLSTSMVYHLPLQTISS LVPYSQWGHLLQSPGPKLGNRKPL TPPSPPTPSKWN\SPGTMYFFRVLI QSPLSSPRPRC*PIVRCPAAAPGSSLP STLFAGPSPFPASYTLRLRCFA
1265	6762	A	1335	130	361	GACCPLSPGGESGT*C/SPRGPRKPS GPSPKAKCS*QSTGCGQCASSPPSPS PGRAPCDSPILACDLGQGGFLQLHT H
1266	6763	A	1336	144	224	
1267	6764	A	1337	1111	1200	PGVVTLGGGACSEPRCATALQPGR ESETLP*TLHSHNQSKPLPPICYPIS VNGNFILLVAQVKKPKCKAGCGGPR L*SQHFGRPRQADHLRPEVQDQTG QHGKTASL/LKNTKISQVS/WTLGG GACSEPRCATALQPGRESETLP
1268	6765	A	1338	344	512	ETLYTME*YTAIEKNEIMSFAGTWL ELEA\VLASNLV*EQKTKMLPCSP MGWELK
1269	6766	A	1339	274	393	
1270	6767	A	1340	1	561	VRSAVGGTGMSSGASRKSWDPGKP WPPDWITGRK\MK\VLWAALLVHI SCQNPMPKW*QAV*NKSRPELR\Q QTEWQ\SGQ\RWEL\ALGRF\WDYL RWVQTLSEQVQEELLASSQVTQ\ELR ALM\DETMKE\LKAYKSELEEQLTP VAEETRAR\LVK\EPQAAQARLGAD MEDVRDRLVHYMFV*AI
1271	6768	A	1341	1	746	MAAAGAFRLRRAASALLLRSPRLP

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						ARSCRPRPDSITRSPDVRLEPLEKQL KNAINQRGTGKPYIRYYPEVVDHY ENPRNVGSLDKTSKNVGTGLVGAP ACGDVMKLQ\QVQ*KRGRFVGC*G FKTFSAVGSA\ASSSLSHLNGVKGK TVVEALTIKNTD\A\KELCLSPFWK LALAPMLGLKVAFAALADYKIET RTQKKGEAEKKWSPPLGEASSRPT AVPQPAVPVTLDVSGSRLPSPTEGA L
1272	6769	A	1342	160	381	SWGLDSALGVSDTTHHPKVVGRAK HRGFLKWLPPPGPPLGKRNCQPYP NP\QLPESGPPQQYFYLKCCPFYEL
1273	6770	A	1343	653	814	WDSTPLSSFTDWMLWPEKRQVGA CSHPTPNFL/C*GKLNISPNPCQPKV LDLT
1274	6771	A	1344	954	1245	DLSLTTSRQRKHEFKEVILPNYTHD KLYLINSNHPTKMCP*NQVLKKLIHK ITQQW\TGAMIHAYNPSTLGGRWG WIT*SQELETTLPHIRGTLHKI
1275	6772	C	1345	155	431	MRERGLGPLGVFRSDAGLKSLEP RRESGALEECVIHTQRCWDWKVPE HPLAPLLLVSAVLRILAKPLPTQR DLFLLLSRSSLFNQHFPLC*
1276	6773	A	1346	2	70	
1277	6774	A	1347	1	271	LFF*TESCSVTRLQCSGMISAHCNLH LPGSSNSPASASRVAGTTGARHHAQ LIF/VVFLVETGFHHVQDGLDLL/N LVICPPRPPKVL*LQA
1278	6775	A	1348	117	229	KKTMFRQKLFYKRKQLQKGRP*G SAKKKLCFGKSYFIRGSSFRKGQGH EERGLKYKKKTGEGV
1279	6776	A	1349	255	381	IHFSINSQLFSPSSPPNKKG*FPKVT* KR/P*NGPRYIPQRFP
1280	6777	A	1350	72	577	TTGVRGALQREGGSLPTQPQGERA LGRRRNQAPGDPGFA\G*RG*WP TGCKQGRGSPSPQPLGSGGR\QNL ARLKPPRPPP/PQGEQDKGRPRQGG PSWRSSPPILPTSYPGDGKGVVP KHKLEAVNSVRARSSVRNKCWSN RMDIALRCPVTVAHELTYS DAL
1281	6778	A	1351	160	336	
1282	6779	A	1352	1625	1920	LSFPAKKGNDCLPHVPGLSFKGRVP ESRQEFCEQESSLENPRLCIPV/CHP WAPWRWEPGETAEPVLRKEAF* PGPPCPPPNRVSETREAVLLQPRI
1283	6780	A	1353	9	249	KVHTKPRTSICRSHIGFCLFF*ETES CSVTPPGVQWCNLG\SLQTPPPG\SS DSPASAS*VAGTTGMHHAQLII*F YVFTGFFWQ*QLSDGILTH
1284	6781	A	1354	426	744	DNLLKSFHLLISINCLFFCFFFL*TESC SV\SR\KCSGAILAHCNLCLLGSSDS HISASLVAYRCLPPCQANCFFSFLAE TGFHHVVGQAGLELKIQLAEC SG MRQ
1285	6782	A	1355	184	422	GYIQGSPALVSTHGGHAV*PPTQSK PTEHAHPLQPRRWARTRVGE GIPC

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						AHPSPSCSPRPLATQKRFQANRRGR LEGLC
1286	6783	A	1356	3	1221	HFIYLFIFIFLRQSLALPLRPECSGAIS AHY/RHLCLPGSSDPPN\SASRVPGT TGMPRCTWLIFVFLVEMGFHHVQG AGLKLITSGDPPALASQNGGITSVS HRVQPKNFFE*SRYYLNFKGN*DS KRLKK*KIRQLEN/RRNMIQILLFF* L*NSCSRMKDNS*AREKYLQHILRG LRFLTCKDSTKLDLKA TNRNTTLE* MENMMKQFTEEKIQMPNKLKRC* TSLGVREMQIEVIRYYFSRSS*QKFK RVV/IIPGQLQRKCQF/PCTW*KSKPL KRFSEEI*YNINQIHLFEAGSCCVVQ DRVQ*YHHSSL*PQPPRIKQSFHLSL PTSWDYWHMPP/HPS*FCVCLFCFF SRDEVSPGCSSWS*TPELKLSSHLNL PKCRDARPEPPCVAQYDINQNCKK HVLS
1287	6784	A	1357	703	918	TREVEVAVSRDHATALQPGQQRQD SVSKKKKKGRVQWLAPVIPSTLGD QGGWIT*GQEFETSLTNKVKPHLY
1288	6785	A	1358	273	561	DRQAEKKRNIL**NEIVLDLPR*PHT AS*ISSTT**FENTALRPGVVAHACN PSTLGGGA/GQIT*GQEFETSLANV VKPISTKNIKINWEWWCRL
1289	6786	A	1359	375	663	LITKQLGLGVVAHVCIQHFGRPRW ADHLSVAGVQDQPGQ\QGETQSPQK NTKISQVWWHVPEVLAP*KAEAKG LLEPGRQRLPPTLHSLRGSETL
1290	6787	C	1363	79	153	MPDMIRQHSSCLIKRVYLTRWFR*
1291	6788	A	1364	4776	9134	WLHDSVNILKNIEHFFFFFFWRQSL APSSRLECSGAISAHCNLHLPSSDS PASASQVAGITGAHHHAQLIFVLV ETSSHVVGASLKLLTSSDPLALAS QNAGITGMSHHTWPNH*IEHF*WV NCMVWEHYLNKAILKFYKEIKSRR DPTPKAYLIWGR*C*/TVL*NKEQVT DTKFLT*LFKGVGRM*KFTVPAPEV VRVS*LYLA*DKCLVIIVAMLMDRN VIFLKGPLMGFVG*LCSGFQGKEWF LFESYPSLPTSPTTLSPALPKYFL*VN VTKANFLQ*SIPFYIMVLTFPST*S QYTNNFFFSF/HFFFFFF/CFFETESH VTQAGVQW*DLGSL*PLPPRFQ*FS CLSLSSWDYRHAPLRPANFCIF**R /SGVSPCWPGWS*TPDLK
1292	6789	A	1365	3	287	
1293	6790	A	1366	75	301	AHKKLRAAPLAPMTGTH*KVVFVK AGDKVKAGN\PSWVMFPMKMEHTI KSPKDGTVKKVFYREGAQANRHHS FSRV
1294	6791	C	1367	155	377	MKASSFKKLQKFYIDPYKLLPLQRF LPRPPGEKGPPRGGRGGRGGGRG GGGRGGGRGGGFXXXXXXXXXXGF RG*
1295	6792	A	1368	363	423	SIKGTENGFLIVL*PKSQV

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1296	6793	A	1369	157	723	KTLWRYGNRG/GFQRGGST/RAGGC /GAQGGQPEGHVAPY*GEFLHPCE DDIVCKCTTDENKVPYFNAPVY*E TKEQMGKVDAIFGQLRDFYFSVKW SENMRLSSFKKLQKFYIDPYKLLPL QRFLPRSPGEKGPPK\SGGRGGRGG GRGGGGRRGGGGRRGGGRGREG GGFRGGRRGGGGFRGRRTLSETC
1297	6794	A	1370	1	810	ASPPLVCTHARSFVLAFLHFLPDL PDRRSRSFRAVHFWGPRSSPPHAAV RLREARRGRDRREKAESPTGEKSTS PSSRRRQRGPPTKVRRPPAPFTMQP ASAKWY\DRRDYVLKWEFVFLNTL RDV\NVNFAEKSPTYNFSCLGGS\DN F*GILNEIDLH\CID\PNSDKHKRTD RSIL\CCLRKRRIWASSWPGLTK\IE RGKGLIWV\SVDFN\NW\KD\WEDDS DEDMSNFDRFSE\MMNMGGDEV VDYPEVDG\ADDDSQSDDEKMPD LE
1298	6795	A	1371	1	588	
1299	6796	A	1372	179	989	KWRNQSWRWPKPGTNWMLSCSVC WRRVTWTGSVWMRKLGKHPQTPT /IKDCSIAATGKRPSARFPHQRRKKR REMDDGLAEGGPQRSNTYVIKLF DRSVDLAQFSENTPLYPICRAWMRNS PSVRDAECSPSS\PLPPEDEEG\SE VTNSKSR*CVQACPPHTPGGQPKN ACRA\SRIPASPLAALRMQGT*RWSPF EPEPSPSTLIYRNMQRWKRIRQ\W RPPACLPLVGPFATAESPLCLSRWK EASHRNQLRYSESMKILREMYERQ
1300	6797	A	1373	245	336	HIPSQGDGK*VKNRARKIVSYSRG GWHSG
1301	6798	A	1374	127	872	EATGQTVGTVPSLSRPRPLHSSG GVRJQTLFATSRPLDKTASIFLVLSN ACIF*KILIA*KEIQDS*SHH*K*LLLI RLDFLSSFFPP*LIN*FFFFPGNSLVH RLFFFNLGMVAHTYNPSTLGGQSG RIA*A*EFKASLGNLVGPHFFFLGGG VGYKSPFIKILNKKKTKSLQKKR YRKRIPLLHMVPKREKNKGDNRQH AQQIKASFSYFFNVQNTSKGYTYLK QELSDAGHAGPGKPFQ
1302	6799	A	1375	37	80	
1303	6800	A	1376	1452	1700	
1304	6801	A	1377	316	373	
1305	6802	A	1378	144	356	FQFRLTSLRNSTDVHRCPLPPPPPS PPPYPGPWGMGCGRFPKGGQGGPRP PRLSGLG*FLSFFALGFSDG
1306	6803	A	1379	860	924	
1307	6804	A	1380	263	616	TTCFSFESRASCHFHVASAVSPPTPL CSPATLMAQDKAGKPSPRK/PSLAP EKPLSPLSPQ*RHSPKPKAPHVESP SGPSPTRAKKRV*FSSPPSLWGQEP RGHAECLPYLGEGAPA
1308	6805	A	1381	152	272	YSVLKFNYEILKNCFSFFV*VSEPPF

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						KTIIIVYFTLTEKL
1309	6806	C	1382	71	316	MCHHSQTLFLYFVKTKSHCVAQAG LELLASSDPLDSTSQSVGITGMSHH TQPLILFFNFSVSVKYTKIMVLKNGF RNSYKK*
1310	6807	B	1383	165	520	XNLKLLDNWDSVTSTFSKLREQLG PVTQEFWDNLEKETEGLRQEMSKD LEEVKAKVQPYLDDFQKKWQEEM ELYRQKVEPLRAELQEGARQKLLP VLESFKVSFLSALEEYTKKLNTQ*
1311	6808	A	1384	3	558	
1312	6809	A	1385	3	118	
1313	6810	B	1386	28	384	MKAAVLTALVFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK *
1314	6811	A	1387	2	1093	GGASCCLPRSLWLPSSRFRPCPRPG LWVPEVFSRSVPFSSPGCNEWGSTG LLHAEGTPLSQALLLQVPHGPFRRM KAAVLTALVLFSDG*ARRRHFWQG G*SPPRAAWDRVKDLATRVPTV LKEQRTETYVSQFEG\SALGK\QLNL KAPLTTGDSVDLPPFS\KLREQ\GP C*PRDFLGINLGKRETEGP*GKGR*G KDLWKEVKAKVAALTDDFQERS WQEEIGAFTQKV\EPLARKNFQEG\ ARPESLHELARRSLPLGEEMRDRA RA\HVDALRT\HLAPYSDELRLQRLG AR\LALRENGGARMGQYHA\QAT EHLSTLSEKAKPALEDLRQGLLPVL ESFKVSFLSALEEYTKKLNTQ
1315	6812	A	1388	1	2076	
1316	6813	B	1389	560	752	XSVAAVTALNSESNFARAYAQGISR TKYWELIYEDSMDLIAKLPCVAAKI YRNLYREGSVTRGH*
1317	6814	A	1391	1031	1407	CVGGRAQVEKEGAALRLRPATVPR ALMSLSSLVKPETA\ALCGTEMQDF FTPLLCDFKS\PGISFCKGT*MCLRSC *HNVRWR/DQPTPVSTVTPVPTLT CVPSPHFPVPER\GAGCLHLCLKFM VH
1318	6815	B	1392	97	880	MAPRTVLLLLSAALALTETWAGSH SMRYFYTSVSRPGRGEPRFISVGYV DDTQFVRFDSDAASPREPRAPWIE QEGPEYWRNTQICKTNTQTDRES LRTAARLLQPERGRMTYGCVDGPD GRLLRGHNQFAYDGKDIALNEDL SSWTAADTAAQITQRKWEARVAE QLRTYLEGTCVEWLRRLYLENGKET LQRADPPKTHVTHHPISDHEATLRC WALGFYPAGDHTDLAAGMPRTKL RNTELVETRPAGR*
1319	6816	A	1401	1380	2180	EIQSEWNLDLAELEERLAGAWE E/LSFRAVRMPSP\FRSSALMG\MCG SRSADNLSWPFFH*NVMPEVTELM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QEQSYLKSELGLGLGEMGFIPPGE SS\ESV\FSRAQQDSFCECSGSPSNATR KMGVPS\TASVGKSKTPLVARKKVF RASVALTPTAPSR\TGSVQTP\PDLE SSE\VDAA\EGSPRKL*GPKSESEV/ EKEGHGKLP\MPAAEEMHKN\VEA RLSLQQVIR\EIKESIVGEIR\REIGKL DFWAAVSS\SKASNSR\QDYH
1320	6817	A	1402	119	301	INDKRKKRPARPGAGGLHLQLCL SQPPQPRGHPAPIPTGQAGPRDSGP GASP*/GRDPPSD*WTPADLGSDPW AGPLPTPQEP*GSRWPSSATVLSAS TATGTPCTYSHGTGWTQRLWTRGL PLSRDPPSD
1321	6818	A	1403	1451	2495	RGLAGNFEDRKS AHYVFQTFRGGE RRSLELEAHLEGWSLGLRFLGLPLK GPPA\QGHFHP\SLPISSWRGAGVPHS R/SPFPTLGIPG*IFPPKPGRRPRGPPR KEDLPGMVG/RPSGPLQLPSAVL SADPAGPRPHVPFCEP/SPSHGVRAS PGSKWVEEIGGEEGRQ/PKCRQAF QEA WLMQG/GARGQGLPGS/GCWR INKPSKPSKRGGKGLTCQTFSTNIC* SPPLMPRSL\GPSFILHLISSQQP*SG LLFIDIPPEKGRGGLSERWGRAFG DSVACSFQKPTPGPWEVFEQDAWP NPWP/QGPPPENFPKGNPSHSRNIHK GDEQSPVVRTKTEPTPWGGKHSQFA SR
1322	6819	A	1404	3222	5798	PLLTPLVSKVTAAGVPLFFFFFFF* DIVSLCHPGWSAVV*P*LTAASNS*\ VKQSSHLSPSSWDNRYAPPRPANY FYYFYFL*RLDLALFPKLLNCWAQ VILPSQPPKVLGL*AQSSEGGIHSGL SLPSPCFLLCNPI
1323	6820	A	1405	38	402	
1324	6821	A	1406	2	380	
1325	6822	A	1407	1	477	
1326	6823	A	1408	1	1104	
1327	6824	A	1409	524	1584	IVKMEKYSIMKSMNMHLTERKKDH FRNDTNTQSFYREKWIYVHKESTKE RHGYCTLGEAFNR\DFSSAIQDIRTF \NYVVKLLQLIAKSQLTSLSGVA\QK NYFNILDKIVQKVLDLHISLLFKDL PQVLSSNLCTLIRGVGKSVLVGNIN IWICRLETILAWQQQLQGLQMD*G K*TMGLT\SDLPLAHGWNNILLPV FQDGWGHSTFRPR*PPRLYMAVG EDRQLWKKL\CQYHFAEKQFCRH LILSEKHS/VEWEVGCNFATFRKH YPAKEQYGRQHCIFCRHCSILFWKD SGHP\CTAADPDSCFTPVSSQQFIAL FQVLRACPLPIPYWRFVNPCCPVQG LIVSVL
1328	6825	A	1411	588	855	VLLSSYL\TQYSLVFICWLFICLFICIFI FMYVTM*IWFVAVFVWNLVFPYKV VK/TPWRSRIHVHCLYF**NYSPIAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LYSA*CYSLCVH
1329	6826	A	1415	277	509	YMLSCHHTFVQTHRMYNTKHEP*C KLWTLC*DNLSM*VHQL*KFPTLVG DVD/ERRLCMYGDRGYMGNLYIL LSILL
1330	6827	A	1417	15717	16041	
1331	6828	A	1418	41	544	TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTKPRHQWVRCNPDS SSAHCLEEKGHMFELLPGESNKIPR LARTDLFPKTRIQ\DLNRIFPLSEDYS GSGFGSGSGSG\SGS\GSWFLTGNNGN RNYQL\VDE\SDAFQ*QPLGSLDRNL PSDSQDLGQHGLEEDSMV
1332	6829	A	1419	168	467	
1333	6830	A	1420	2	196	ASTRSRRSGSRGLTRRAAFGVRA GWVCGGPAGSRRRRKLPLTGP SFQCRSRGGRGSVNMKGDPNPKPR GKMSSYAFFVQTCREEHKKK\HPD FSVNFAEF\SKKCSER\WKTMSCKG RSSKF*RIWAKS*QSFAIDR\EMENL RFLPKGDKKGGKKDPNAP\KRPPS AFFLFCSEHRPKIK\IEHPGLSIGDTA KKLGEMWSEQSAKDKQPYEQKAA KLK\EKYEKDIAAYRAKGSEAGK KGP\SRPTG\SKKKNPPRSWRGWEG *EA**DPASGIWGAGRRGLGLWRA GGQSEEAETAPDRARFWEFSMSVT RWTRICQHG
1334	6831	A	1421	3	107	
1335	6832	A	1422	450	851	KTEFTQNYFWKSCTGVDGFFFSILF CLFV*DGVL LCHPGWECGCDLHS LATSASQVQAILVPHQPSK*AWDYR RAPPQLG*LYC\CRDRVFTMFVPG LSNFW\PHV\HLPQ\PPKVLRIIGREP TCAPASMAF
1336	6833	A	1423	6	461	AEMTPLHSSVSGSRVRLHLKKKNYI KKPRKALFISIFGIIFHLIYVSTYIYL STFSFTSLILMEFILCVV*VLHLQLK NAILMAYWY/TFILITWLPSEEDLK VL*LFMPKNELIFSKCFHFLFIVPKFT LLDHLAFLRLKLAFWRLGWHST
1337	6834	A	1424	222	350	GAHTWTGISQAALQPTAPGRLSRTL LFLC*KCGEICNLLSGC
1338	6835	A	1425	198	385	
1339	6836	C	1426	207	385	MFFYKLAQMXQISVSTLKFKLVLFV PTGXQVNGGEPSTLYGRWGRXGSA PSWRYQPFCP*
1340	6837	A	1427	327	516	
1341	6838	A	1428	58	255	FSPDFYRGYIYFYHYFGFEKFFFTPS NFFISQSR*FFCVKMFSFFNLRFKIPL PNHVDFAFCFFVV
1342	6839	B	1429	242	509	MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DXGENDLEVKEENGVLVLNDANFD NFVADKMDTARDLPPX*
1343	6840	A	1430	338	511	NSFSKSKTPCVAHGRGVHAEAGNK RQYLGFLFFFF*FFILWCFTSCSEY

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1344	6841	A	1431	2	454	
1345	6842	A	1432	671	955	FFFF*IFTLGCFSTSCSEY*ITMNDVK* FSPEFLPEGYLLFLSLFGV*KIFFYTL LISLFLKAD/RFFCVKMFSSFFNLRFKI PLPNHADFALCFFVV
1346	6843	B	1433	46	3152	MRPRKAFLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLIFYAPWCGHCKQF APEYEKIANILKDKDPPIPAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEVFDEVNDADIL VEFYAPWCGHCKKLAPYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVHIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQQLVVMQPEKFSKYEPESH MMDVQGSTQDSAIDFVLKYALPL VGHKVSNDAKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFKKGKLPVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLEIFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIAKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEELMDVQGSTQDSAIDFVLKY ALPLVGHKVSNDAKRYTRRPLVV VYYSVDFSFDYRAATQFWRSKVLE VAKDFPEYTFIAIDEEDYAGEVKD LGLSESGEDVNAAILDESGKKFAME PEEFDSDTLREFVTAFKKGKLPVI KSQVPKNNKGPVKVVVGKTFDSI VMDPKKDVLEIFYAPWCGHCKQLE PVYNSLAKKYKGQKGLVIAKMDAT ANDVPSDRYKVEGFPTIYFAPSGDK KNPVKFEGGDRDLEHLSKFIEEHAT KLSRTKEEL*
1347	6844	A	1434	785	1271	LCTDQLHNFNNYFQDKDKCFYFPM FWSFLGLETEAACFKPDSKGKALQ NRKYFN\VYLPSATSRDLWISPGWS QPFFFFFFFFFFFFFF*RA
1348	6845	A	1446	549	791	GLLSN*NFFFSILIFFQTESRSVA ECNGAISAHCKLRLPGSRHSPASAS RVAGTTGAHHHAWLIFFVFLVETG FHHVSQDGLDLL\NLVIHLPRPPKVL G*QAGVQWCDLRLSLQAPPPGFTPFS CLSLPSSWDYRCPPCLANFFCIFS DRVSPC
1349	6846	A	1447	59	485	NSPCSGSSIATASPERRKGINPAPPST PAAPCRS*ACTAAAAAAVR\DDRLN VTEELTSNDKTRILNVQSRLTDAKR INWRTVLSGGSLYIEIPGGALPEGSK

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						DSFAVLLEFAEEQLRADHVFICFHK NREDRAALLRTFSFL
1350	6847	A	1448	125	927	NPPCSGSSIGPCSPKRRKGKPGPIH RKPAPSGS* \ACTAAAAA \VRVPGS PSTAV \VTRVRG \LGGAPDAPHPPLK DPRVGEQNSQRNPNL \SANLFYS \DD RLNEQKEL \TSHDKDEHSRRPSSRLT DGKTPLNWRNNC*SGGSLFNKPAG GRRWPEGSKGQLLQFLLEFA*GATC GADPKVFICFQTRTREKAEPPLLR \T FSFFGLCRLVRPGGIPLVPKETPDAC FMALQRSRESLPGEEEVGARLRG WAIPPPWGHPLVCTGG
1351	6848	A	1449	1	866	ESVDLAAEAVRIRRSPLIFSKAVHIM AAAFRKAASRQREHRERSQPGFR KHLGLEKKKDYKL RADDYRKKT RITSKALRK \KALEK \NPDEFYKMT RVKLQGSYILLRETGRK*PQEQ KADEELQDVKYIEMKRVAEAKKIE RLKSELHL \VWDFQKQNKHVFF FDT \KKEVEQFDV \ATHLQTAPELV DRVFNRPRIETLQKEKVKGVTNQT GLKRIAKERQKQYNCPAHQRIERE KKLIPLLPQKIQTRKDLMDKTQKVK \VKKETVNSP \AIYKFQKSVENR
1352	6849	A	1450	3	896	LRAVRVGLLLGGGGVYGS \RFR \FTF PGCRA \LSPWRVRVQR \RRCEMSTM FA \DTLLIVFISVCTALLAEGN \TWVL \VYRTDK \YTRL *AEVEKQSKKLK GRKETNTEFSWFGQKKKKIERQEEE T*RN \NNRDL \MVR \MKS \MFA \IGFC FTAL \MGMFNSIFDGRV \VAKASF*P LFSYIQ \GLSH \RNLLG \DDTHRLVPF IFLYILCTMSIR \QNIQK \NLGLAPSR A \ATKQGRVDFLGPPPPSGEVLLEL KELFIFYSFGLGHTHIRMGQLFCSQE PIGSLYYLGLFLVLNYFLSLLGYD
1353	6850	A	1451	2	125	
1354	6851	A	1452	18	1374	LAEQIVPRGVGIRPPDKADQAPCRS PIRTPAPESWHCDSRQFRQDSSRM KMRVLGLVVCLVLWTLHSESGG KLTA \VDPETNMNVSEIISYWGFPSE EYL \VETEDGYILCLNRIPHGRKNHS \ DKGPKPV \VFLQHGLLADSSN \WVT NLGNSRLGFILADA \AIDV \WMGNTR GNTWSPKHKTLSVSQDEFWAFSYD EMAKYDLPASINFL \LNKTGQEQV YYVGH \SQGTTIGFIAFSQMLELAK GLKMFFAWGPV \ASVAFCTSPMAKL GRLPDHLIKDLF \GDEEFLPQSAFWK VAGVPHLATHVIL \KELCGNLCFLL CGFNERN \LNMSRV \DVYTTHSPAGT FVQNM*HWSQAVKFQKFQAFDWG SSAKNYFHYNQSYPTYNVKDMLV PTAV* \TGGH \DWLEDVYGVNI*LTQ IT \NLVFHESIPEWEHLDFIWGLDAP WRLYNKI \NLMRKYQ
1355	6852	A	1453	165	1353	LPKPRLGPGQPEKDRTESSVRMAIT

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						LEEAPWLGWLLVKALMRFAFMVV NNLVAIPSYICYVILQPLRVLDSKR FWYIEGIMYKWLLGMVASWGWYA GYTEM EWGEDIRAVSKDEAVTLV NHQATGDVCTLMMCLQDKGLVVA HMMWLM DHIFKYTNFGIVSLVHGD FFIRQGRSYRDQQLLLKKHLENNY RSRDRKWIVLFPEGGFLRKRRE\TSQ AFAKKNKLPFLTNTVTLPRSGPTKIH NALV\AQQ\KNGSPAGEDAKELASK SKGLQWIIDTR*PYPKAEPI/DNIQT WVFGYRKPTVTHVHYGIFPAIKDV PLETEDL\TTWLNQRFVEKEDLLSH FYETGAFPPASKGHKEAVSREMTLS NLWIFLIQSLAFLSGYMWYNIQYF YHCLF
1356	6853	A	1454	313	650	FVICV*TYTGMNTHSPHTKTLSFSL DSG*FFYCRSL/CNIG*QKTYPPQNR LHTHTHTHTHTHRGYFSHTSSTVEK ALLTRIPEGSEEDNGFYGWALRTI LVAFKSQCQMH
1357	6854	A	1455	2	401	VSVGGLVGEVACACRDCIPETMAE GDNRSTNLLAETASLEEQLQGWG EVMLMADKVLRWERA WFPPI/MG IIYYLDPSVLSGVSCFVMFLCLADY LVPILAPRIFGSNKWTTTEQQRFHEI CSNLVKTRRRRA
1358	6855	A	1456	18	741	AACGAFSRVVVGVRVSVGGLVGEV ACACRDCIPETMAEGDNRSTNLLA AETASLEEQLQGWGEEMLMADKV LPWERA WVPPIMGVVS LVFLIIYY LDPSVLSGVSCFVMFLCLADYLVPI LAPRIFGSNKWTTTEQQRFHEICS NLVKTRRRRAVGWAWKRLFTLKEEK PKMYFMTMIVSLAA/VLLAWGQQV HNLLTYLIVTSLLLLPWT*TQHGHI FERTLGMANMEINKLLKHK**TN
1359	6856	A	1457	2	529	GRVDPKAKKEAPAPPKAEAKAKA LKA/RRKAVLKGVHSHKKKKIPHV HPPFARRPGRHLR\LRQPK\YPPEEP RPRRNKLDHYANIKFP\LTESAMK KIE\DNNTLVFIVGCLKPTKHQI*Q GC*RKLFWTLDVGAKVNTPGFGPD GRRRKAYVPTWLPDLPIAFGMFAN KIWGFI
1360	6857	A	1459	323	624	IVVHLVPTTQRSGKGKIMELVERSV VARVEVGHRGFLERGLPIAINDM KKSPEIISGRMTF\VQPRNWLLFACH ATNEVAQLIQGGRLIKHEMTKTASA
1361	6858	A	1460	438	549	
1362	6859	A	1461	210	556	QFWGPVATWGLPIDAINDMKKSPEI IQWGG*HFALC\CYS\LT FMEILPYK V\QPSGTWASCFA CHGTNEVRPSFI QGEGLIPNTRMDLKRASGINQWG KGKNKVFE GDSLCPGCC
1363	6860	C	1462	110	509	MLLICSFAPATLXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXVSA*
1364	6861	A	1463	93	180	
1365	6862	C	1464	128	382	MYLGISRRLSSMLTFLAYLHPRERP PHRAPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXQQWAQG TGISIPRTCTSTGL*
1366	6863	A	1465	3	140	
1367	6864	A	1466	1	609	
1368	6865	B	1467	1	690	MASWDEKDLTVPQPDTRKGSVLR GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAAELGAR GEEAAGDRLIHEQDLEWLQQADV VVAEVTQPSLG VGYELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPPTT*
1369	6866	B	1468	1	975	MSPPGREQGLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWWVDSADRQRMQDCQ RELQSL VEEVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLLQL SSLTCIYTAGKMRLQDRIATFFPKG MMLTTAALMLFFLHLGIFIRDVHNF CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH*
1370	6867	A	1469	25	353	EVCYYRSSEAFFSELIKVILRHLCSV AGKGLCSIPQLNREGSVLRRISK GSPLAVEIEEGHCL\CLPLGTECLGI KPIVHLLNSEIGKPPFSPLSPCSSA AFLLLR
1371	6868	A	1470	79	467	RPESQRANGVDSPGNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCL\ CLPLRTECLGIKPIVHLFSCTRPVIV PSLELHYDIDSIAHMFVADLLLIITLL SYYIPFYLGFQNA GITGINHRAWFY
1372	6869	A	1471	368	611	LCPSHFAPTTLTQSGSSLKTCVVVLS RFKACRAVPGCLVNQMFASSILG\ KSHHSLVPINQGHNA LWKAAGPL PLKAGY
1373	6870	A	1472	441	1178	FVALPQPLCPSHFDPTTLIQSGAHKN MCCIKSRFKRDLGLCRTCLVNKMF TSSILGKSHCHSLVSINQGHNA PWK AAG\PLPFRAGYC\QGFSPCDSLKYG \SWDEKDLTVPQPDTRKGSVLRWIS QRGKPLAVEMEEGHCL\CLPLGTEC LGIK\PIVHLFNSEIGENRPMVGG\ RHVLQ*CCLG*FL*LPLRCLG\GEKH KSGL/HVHIPVIVLS\LELNYDIDSFA

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						HMFF/SVDLLLIITLLSYIPFC
1374	6871	A	1473	1540	1812	GKFQLIKTLQNPVVCSLPVIPALWVGQRWVDHLRLGVRD*PGQHGETPSLLKNNNNNTKISWAWWHEPVIPA\MGEAEAGESLEP\GRRRLQ
1375	6872	A	1477	1	354	
1376	6873	A	1478	1	411	
1377	6874	A	1479	2	265	RMYGKIIFVLLSGIRNVHPK*IVSISASSTTGAMHTSTSSSVTKSYISSQTNGITLINWWAM\ARVIFEVMLVVVGMIILISYCIR
1378	6875	A	1480	111	520	
1379	6876	A	1481	106	395	EEALPPPLHCTWVPFSPFECLQEMSKEIVSISALSTTEVAMHTSTSSSVTKSYIS\SQTNGRKRDNLSDRFHCTSSCSDNTSLFLCVMGWYYWERSS
1380	6877	A	1483	3	1078	TRAAGLRAGVRVPRSPGPSRRMPARSGAQFCRRMGQKKQRPARAGQPHSSSDAAQ\APAEQPHSSSNPAQAPCPRERCL\GPPTTPGPYR\SIYFSSPKGHLTRLGV\EFFDQPAVPLARAFLGQVLVRRLPN\GTELRGPHRWETEA/YTLGPED\EAAPLQGGWPGKTPRN\RGMFH*KPGD/LWVVYIYGYMYFCMNISSQGDGA\CVFL\RALEAPGKSWRPMPRLRS\TLR\KGTRQARVLKGPPKLCSGP\SKL\CQA\LPINKSF*PEGTLAQDEAVWLERGPLEPSEPAVVG/S\APRVGVGHAGEWARK\PLRFYV\RGSPWASVVD RVAEQDTQACAKGLPRQDFLHCLKTRINVLFLEKKKKK
1381	6878	A	1484	3	452	
1382	6879	A	1485	26	493	NSTDSETHPWLLSPARQRPTSRPAWGKVGAAHVSRMCAEALERMFLSFPTVTKTYFPHFDL\SHGF\CPG* RATGKKVDDSDAQTPWPTWDDMPKRRCP*SDLHAHKLS/RLDPV\NFKAPKATCLAG*PLAAHL\PAEFQPLAVARLPWGQISWGFC
1383	6880	C	1486	30	200	MCISYTKGHFVVVWVWFPGFSKILF RYISCPAPCRSSRMQSQCAHSSQSE VPGHRA*
1384	6881	A	1487	31	664	APALPGCEHMMMAIRELKVCLLGDTGVGKSSIVWRFVQDHFHDNISPTIG\ASFMTKTVPCGNE\HKFLIWDTAGQERFHSLAPMYRGSAAVIVYDFTEAGFHFHPLKKWVKRLKELGPE\NIVMAIAGNKC\DLSD\IREVPPEGMLKEY\AESIGAIVVETS\AKNAY*YRKS SFKEISRPDPHPWTPHENGNGTIKS*EANPCKPVRRC
1385	6882	A	1488	124	1180	DLGKPLFKVQEEGGRPPTLNQSEVVALCPQGGGANHDARSLIMDSPRAGTHQGPLDAKTEVGADRCTSTAYQE QRPQVEQDGKQAPLSPGLPAMGGPGPGCKDPAGCGGAGA\GGSEPLVT VTVQCAFTVALRARRGADLSSLRA

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						LLGQAFPHQ\AQLGQLSYLAPGEDG HWVPIPEEESLQRAWQDAAACPRG LQLQCRGAGGRPVLYQVVAPPPK RGTPKPKRALDPFPPSPPPPKGPE DLGFRQGD\TVDLCE\VGWAWPFP GSTVVPGVWGA*SSACAVSRRGTQ KATPG*RPAPDPVPLAVDQAWLEG HCDGRIGIFPKCFVVPAGPRMSGAP GRLPRSQQGDQP
1386	6883	A	1489	1	229	
1387	6884	A	1490	3	461	AASTRFRASGQFVMAGAGSAAVSG AGTPV\AGPTGRDLFAEGLLEFLRP AVQQLDSHGHA VRESQVELRDQID NLATELCRIN*GQKVAL\DLDPYVK KA\ILNARRRV\VLVNNILQNAQE\RR LRRVNHR\VAREQPARRAMLDSGIY PPGSPGK
1388	6885	A	1491	1274	1416	FGIFSQFSVLH*SGK*A*NYYYYYY YYYCYFYKMEYGSFFNLQVTF
1389	6886	A	1492	243	1125	FQRLYRAARRFTMVKIAFNTPTA VQKEEARQDV\EALLSRTVRTQILT G\KELRVCHPGKKEGSSGEMLWFTL FRAFQFILG\GLYLFGGACIYK/YTF MPKRHHFTVGEMCFDSEDPA NFPP GGGEP*LSCLVT*/EEADIREDDNIAI IDVPVPSFSDSDPAANYFMTFEKG MTA\YL\DLLLG\NCIYLMPLQYFYL LWPPKKIWVELFGQTGRVGRY\LP QTYVVR\IEDLVA VSRKIRDVSNL GIF IYQLCN\NRKSFRLRRRDLLGFNK RAIDKCWKIRHFPN\EFIVETKICQE
1390	6887	B	1493	28	282	MYHDWRLVPKH EEEAFT AFTPAPE DSLASVPYPPLLRAMIIAERQKNGD TSTEEM\LN\VQIRMEP\WDYPAKQ EDKGRAKGTPV*
1391	6888	A	1494	2	187	QNDRKMETQA/PEEPMLNVQIRRM EPWDYPAKQEDKGRAKGTPHPTPR AHAGESGKRS\LPFH
1392	6889	A	1495	302	771	RKRGVCTHLLCRRRSASNCRAPALP SLTFEGQDAPGLPVVQVLRVVG HPREAPVARLVVLPQPLARDQAA QAEEREAAEQLO/AGGSRGARRPRP GPAAGVQRTAASRSRSPRRAGSRA ACSVAPAGRARGGPAPRSAADAPS SAPWRVRVLSG
1393	6890	A	1496	497	1212	SWPGGEAGTARRPGCLPAPA*TR*R PPRAWAPAASHGT*RVRSAPRSQ SSLMKKKRR\FEGQDAPGLPVVQV VQSHKQAGSARKALGPRGQEVGAS /DHANLQGGGEAGRPAGCRVGVRT GCTHLLRVVGHPREAPVARLVV PQPLARDQAAQAEEREASEQLQ SGSRGARRPRPGPAAGVQRTAASRS RSPRRSGSRAACSVAPAGRARGGP APRSAADAPSSAPWRVRVLS
1394	6891	A	1497	852	1562	FGKAGWELNRRERGSWRVEEKDL QRWGVCGGGLCLPKPVRRSGVCLS

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						LKHISGGLRTLSQAPNWRNNSNGR VRGKHSNLNAQPFHPSLSYELKPCC VSQGLQRGILPPPQVSGPTFCSPKAL TPPSVRVLPPPPPP*CAVCMVSNSP PALPTPLAKVSPADLAPRD*AHISG* RG*PLGHPHLSPLMLFTSPEPSE/PPP YPPSAP\PSSFSARPAPPTVWPPPM QHRLWLPFPSS
1395	6892	C	1498	127	355	MKNRILQRNGXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX*
1396	6893	A	1499	529	2082	FLDLLHFTTSLIIPHYKRIRDLTYTIR HFPFVHLSPKCLDRPLSLFLIHLGVL VIL*ALEPIH*SSSFLFH*LKIFSSPLW NI*VSPTFDSHF/CFLILNLFLLSFPL SALI/NFQLQF*IKNETFHTLLIG*SEH *I/HT*MISTLFWLWK/LLLTGSLV*A RIFSCVHTQYHHACAIEKEMYLSSL FLFFMNSKSLILFCSIIGPEFFDILL IC/LFFFLD*IIFSSIPALQ*YYLWALN AHSSQKARDSMLS/F*/ILVCWIAVT LG*DTLLAVTLE*DILSKVHCFMDPI SSSFLVFNPHFGWENFPQRYFPQVR VQRRLS*KFA*QEKCPPLWMFLPEQ SALTMKFLGYQKISLKALKDVPID FWAFSVG**QIC*QSISHPFLC*ANR DDLICFLPGHFNIFLLSLIFQNFILC LDVRLYWALSIWRLSL/RLFFN/IFF LFLHLTSLASLPGTPNITY*MTMSL FFLYFYYSLSLALYLGEIPSTLFFQT VYQILLAVLFYFQRDLPSQSLSFP
1397	6894	A	1500	3	930	SSRGRAGGVWRFERDEDGTGAGCG QWTRFCREPKMAVNVYSTSVTSDN LSRHDMLA\WINESLQLNLTKIEQL CSGAAYCQFMDMLFPGSIALKKVK FQAKLEHEYIQNFILQAGFK\RMG VDKIIPVDKLLKGK\FQDNFEFVQW VKKFFDANYDGKDYDPVA\ARIQG QETA VAPSLVAPALNPK\KPLTSSS AAPQR\PI\STQRTAAAPKAG/PLGV VRKNPGVG\NGDDEAAELMQGQR I*NLLFEDLGGERDFYFGKLRNIEL ICQENEGENDPVLQRIVDILYATDE GFVILDEGGPQEEQEEY
1398	6895	A	1501	3	87	
1399	6896	A	1502	1	667	RRSSARRGGRSEPGRAAGGGAED TRRRAGDMRGEQGLLRDPVPPEE GEDVAATISATETLSEEEQEELRREL \AKVEVEEIQTLSASVKQQRKHLA EIQAGNLGINSLQELKQNIAGGW*D VTVT\SAYKKT\SETLSQAGQKASA AFSSVGSVITKKLEDVKNFPNLFNH FEEKVENLKS\VRGH/TKPAGGDF GEVLNSAANASATTTEPLPEKTQES L
1400	6897	A	1503	1	395	AKAKMADVLDLHEAGGEDFAMDE DGDESIHKLKEKAKKRKGRGFG/SR

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						*VWGKWGRVA**GRSYGFWSPPH HRNNGRKEEFSVISCMSLIEEGSRA RMREDYDSVEHDGDEPGPQRSVEG WILFVTGVHEEA
1401	6898	A	1504	146	833	CLSGTDEISIEGEMADVLDLHEAGG EDFAMDEDGDESIHKLKEKAKKRK GRGFGSEEGSRARMREDYDSVEQD GDEPGPQRSVEGWILFVTGSP*RKP PEEDIHDKFARIMGEIKNISSSTFDR RTG/YILKGYTSLNIETYKE\AQAA MEGLNG\QDLMGQLGGV\DWCFVR GPPK\GKRRGGRRRSR\SPDRRPSLT GPLLSRCSLQDSIWTMAALGQIGLG WELCCVYI
1402	6899	A	1505	717	1563	APLPAVLTQTIHLVTGTAFHSGKVD IVTIGYPFIDLNDMVCMSQYDSTHG *FHSTVKTENGKLVINGNCITHHPR RDPTKIK*DDAGTEYVVESTGVFMT MEKAEAHSAPSADG\LNDEKYENSL KIIGNASCATKGFAP/LPAKVIHDF GIVEGLMAMVHAITATQKTVDGPS KK\WHD SHGALQNIIPASTGATK/A GMAFLVSTTNVLVMDLTLEGILGY TEHQVVASDFNSITHSSTFKAGVGI ALNNHFVKLISWYENEFGYSNRVV DLMVHMASKGSS
1403	6900	A	1506	625	2919	
1404	6901	A	1507	2	76	HHYAKLGTRAVRRARRCAGWQSY VDNLMCDGCCQEAIAIGYCDAY VWAATAGGV\FQSITPIEIDMIVGKD \RKGFF\TSGTLGA\KKCSVIRDSLY \DGDCTMDIRDKQS/QGGEPTYNV A\VGRSG\RALV\VMGKGKVFHRR HTLTRKAYETPLYT*RQAWHEGSA KGSKMCRLAELRG
1405	6902	A	1509	63	290	GGILLSISRPYKTKPTHGIGKYKHLI KAEEP\KKKKGKVAVRAINLGTDY NYGVLNIHLTA YDMTLAESYAQY VHN
1406	6903	A	1510	315	1092	RPRSSKRMSGTSEKVLCLRNNTIFK QAFSLLRFRTSGEKPIYSVGGILLSIS RPYKSK\PTHGIGKYKHLIKAEPPK KKGKVE\VRRAINLGTDYEYGVNL\ HLTA YDMTLAESYAPLFSTTFCNSL SH*KSEESYAMPTQNHKKWLPVCR DQGQPKCLLGLKCLPTHE\RVVQIS GLSATFARKFSWKIIPKVPVLP*RESG LFS*REHTERKTSRGRFQRFDPCLGR TFWAKFEVATVDPFHCQQWSYLSA KEKSLLGS
1407	6904	A	1511	284	758	KQNPSSPLQRLIAGSNLDSEPRIQTD ILKQATKDRVSDFHKLKQSRFFDEN ESPVD PQHGSKLADYNGDDGNVGE YEADKQAELAYNEEEDGDGGEEDV PPDEEREL/PNGKKQAMESNISMMS FKS*RNAENLKCKMKSFYFVLS D FCKDELYQL
1408	6905	A	1512	148	476	

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1409	6906	A	1513	204	620	GDAMAAVTPRPPLPEGCRAPSSAPT VSLPELRSLASGRARLFDVRSREE AAAGTIPGALNIPVSELESALQMDQ LAFQGFIFLLEKPKLGR*ASSFSFLFR WGKRGLQATQLARSLGYTGGFATY AGAY*EWLEKES
1410	6907	A	1514	1386	1711	FPKSIMGLVTIQDMNLCIKFIGLSHL PALVLLYC/DVRACVMSGC/LRKTS EKNLKSRSFFACSLSRNVQCQNT KIGMFKDI*GFFCFPYFYLFVSCIFA YLCRFSGF
1411	6908	A	1515	481	1380	TSKQNAAPLVKYFQEKGLIMTFDA DRDEDEVFYDISMAVDNKLFPNKE AAAGSSDLDPMSMLDTGEIDTGSDY EDQGDDQLNVFGEDTMGGFMEDL RKCKIIFIIGGPGSGKGTQCEKLVEK YGFTHLSTGELLREELAS*SERSKLI KDIMERGDLVPSGIVLELLKEAMVG \SLGDTRGFLID\GYPREVKQGEEF GRIWRPHSWVICME\CSADT\MTN RL\LQRSRSLPVDDTTKITMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTS*LTLFSEGKNA CLG
1412	6909	A	1516	47	416	NSYIYMCISYINTIYIHIYLESNISLP LNIYISTPT/HIY*RHTV*VHTKAYV HML*HVIHFCLCVHKSFKGTIYRD ASFLESCSKVNTECHKLRKVCRKYS RIHHTGIHQSSLIITSPFTF
1413	6910	A	1520	1386	1666	SLMAPQKMGRGTSCSPSERLGN*GPE TGSDSHKTPQOGCKGGRTRGSIVSL GDRRPLAP/GACFAGDKDFLGLRSP GVGTALLGCTSINQRLWA
1414	6911	A	1521	304	1253	VTNEMSQGVGKYDFYIGLGLAMSS SIFIGGSFILKKKGLRLARKGSMRA GQGGHAYLKEWLWWAGLLSMGA GEVANFAAAYAFAPANSSGLHLGAL \SVLVKCPFFLSYFLNERLNLHGKIG CLLSILGSIVMVIHAPKEEEIETNE MSHKLGDPGFVVVATLVVIVALILIF VVGPRHGQTNILVYITICSVIGAFSV SCVKGLGIAIKELFEGSLCCGIPWA WILLLSLIVCVSTQINYLNRA\DIFN TSIVTPIYYVFFTTSVLTCSAILFKGV GKDMPVGRCPVL*SGFFTIVGGY SCCMPLKTSALA
1415	6912	A	1522	20	131	KEILPKQAFVAPTYITEPVEIKFFFF SRIRL*VPPG
1416	6913	C	1523	7	348	MSKLYIMQFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX TV*
1417	6914	A	1524	1103	1388	VLLIFNLFPMALYFVCFSF/CFFETEA HSVT*ARVQWHDGLSLQPLPP*FK* FSCFSLPCS*YYRHLPPYPANFCIFSR DGVSPCCPGWS*TPNLR

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1418	6915	A	1525	149	421	
1419	6916	A	1526	1	1107	
1420	6917	A	1527	25	1486	GPQQPHSRSTHASGRPQSLSPVLSLS PDSMSFTTRSTFSTNYRSLGVSQAPS YGARPVSSAASVYAGAGGSGSRISA SRSTSFRGGMGSGGLATGVVAGGL AGMGGIQNEKETMQSLNDRLASYL DRVRSLETENRR\ESKIRE\HLEKK GPQ\VRDWSHYFKNIEDLARAQIFA NTCGTMPRIRSARIDNA\RLA\ADDF RVKYEDRSWPMCPVLWRTDIHGLP KVH\IDDTNYHTDLQLETE\EALKVE ELLFQ*RRNHEEGS*KALRRQ\SSS GMNAWRLD\APKSQDLAK\IMADIR \AQYDELGSKKNPRGSLDKYWSQ Q\NEESTTGGSPQKSAEVG\AVETHA HRSLKRTVPVLGRSTLDSMRNLKG QLWRTSLREG*RPAYALTRLEPAPT GSL\HLESEL\AQTRARGTAARPRE YEALLN\IK\VKLEAEIATYRR\LED GEDFNLGDALDSSNSMQTIQKTTTR RIVDGKVVSETNDTKVLRH
1421	6918	A	1530	277	693	PWHCPDSHYSQQPGSTASSVPART GGPCWSSSCSPN*CCTSCCSTTPTPT LDPR\GSRHCQLPW\KQLPKGM\CT STCLHGSCGCICGSCGPCGIDGPTL GRNHNEPHHHSHGDLPYRFPEHAH HG\HATLMGLMDTPLY
1422	6919	A	1531	1	364	PFVSLGLMCFGALIGLCACICRSLYP TIATGILHLLADTML*SPGHMEVSC VDAPAEIPS*APN*QPTSFPAMCGSH PGCPALTS\QRTSATAI\LLHPCETLI KNQLAEPNQPMELIEIK
1423	6920	A	1532	1	898	RGESRVLWSELEGEAGGAGGWASS LNARMDNRFATAFVIACVLSLISTIY MEG\SIGTDFWYEURSPGQENSSDL NKS\WDEFISDEADATYN\DALFR YNGTVGFLRRVYSPYKTLHWVLA HHERTESFDV\VTK\CVSFTL\TEQFM EKF\VDPGK\HTNSRGLDLLRTYL\W RCQFLLPFVSLGFDVLWGALIGLC A\CICRSLYPTIATGILHLLAGLCTLG SVSCYVAGIELLHQKLELPDNVSGE FG\WSFCLACVSAP*QF\LWASALFI WAAHTNRKE\YTLMK\AYRVGMSK KPACF
1424	6921	A	1533	939	1591	LQSLCRVLLQMESGRDTPGVCKR ERENREDTEVLQPRFPYQGGQLVG KAATPQFP*STVGWTLQPQ*P*YP AGQGCPP\RCPPAPSS*GSKRPPEPQ QGRLGPKPGSPA*GNASPPKCPA PVPTPC\PTLCTGEKTGGARAGPW VGAGSPW*DPR*DGPIPCPVGDPLSP HPCCVIVALLPFNVSPGGRGGAPP QPP*T*PKAMAVAPPFV
1425	6922	A	1534	34	912	GRIRMQRQSTTGGRGIMEGPRGWL VLSVLAISLASMVTEDLCRAPDGKK GEAGRPGRRGRPGLKGEQGEPEGAP

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						GIRTGIQGLKGDQGEPPSGNPGK VGYPGPSGLGARGIPGIKGTGSP GNIK\DQPRPAFSAIR\RNPPMGG\NV V\FDVT\TNQEEP\QDPSG\RLVCP EPGYYYFT\FQGAGPQWEICLSIVSL LQGARVRRSPGAF*HPPTRGLFQV VSGGMGL\QLQQGDQ\WVVEKKPP QKGS\HFYQGS\EADS\VFTGFL\IFPIC LSQGRTPSPPTSLASMLRL
1426	6923	A	1535	919	1260	YSVSEFRGQTLTAKFCFFERESH\SV PRLECRGTILAH\CNLC\PGSSDSPAS ASRVAG\TTGACHNARLIFVFLVET GFHHVVQAGLNS*PQVIHPPCPPKV LGLQACTWHLAH
1427	6924	C	1536	130	441	MVQNKGQLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1428	6925	C	1537	5	316	MVQNKGQLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1429	6926	C	1538	74	91	MTLAM*
1430	6927	A	1539	368	430	
1431	6928	C	1540	191	592	MGQQPGQARAPSYCRCPLSPGSGR ALRWERPGGGQGPKEIVLSGCVPE KGPQTPAQPHSLRHLQNPEATARTG EEATSAAGGPWASPSFGGTQLCSDT MPALLGARSTCWIATHVCTLPLS ECGPINILLE*
1432	6929	A	1541	58	1531	VIAVTSALPGRTQAAWTRVVKMDL LAAKMAVGGGSLMTDLTSSISKPL VPVGNKPLIWYPLNLLERVGFEEVI VVTTRDVQKALCAEFKMKMKPDIV CISDDADMG\TADSLRYIYPK\KTD VLVLSCDLITDVALHEVVDLFRAYD ASLAMLMRKGQDSIEPVPGQKGGK KAVEQRDFIGVDSTGKRLLFMANE ADLDEELVIKGSILQKHPRIRFHTGL VDAHLYCLKKYIVDFLMENG\SITSI RSEL\IPYLVRGKQFSSASSQQGTRK EKEGGSKGKRGLKSFRISYSFY*KE ANYTGTGAPYD\AC*NACRGDRWE DLSRSQVRCYVHIMKEGLCSR\STL GLYMEANRQ\VPKFLSALCPGRTHQ SISSPDCQHYTWVGVD\SLIGPRDH RLGEKVIPLSASVIGSSL\CLIKDRVT ITNCL\LMNSVTFWRKEANIQGSVI L\NNAVIEKGADIK\DC\IGKWARRI EA\KAKRSVCR*S*GNDQLMEI
1433	6930	A	1542	315	644	EEETPKDQCLGAHFSSDTFPRQSRL LGVHGRGAGSLCTGLLSEHCPSTPP SGSPRVTYYLPH\PLPPSP\SWAPTP PAHR*KPSTEPFPGSTQVV*PLPMF TTKGAPP

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1434	6931	A	1545	1	364	FFFF*DGVSLLWPRLERNGVISAHC NLCLPASNDSPASASLVAGITSAC/R PLPPKQK*LFFFLRWSLALSPGWSA VARSWLNATSPGYF**KQGFHHAG QDGLGLLIHPPWPPEVLGLQA
1435	6932	A	1546	1	391	
1436	6933	A	1547	2	2371	GPPGRARARGLRRAPAAFLRRSLSL PAAFSSAAGPSSPQRSQEGRRERTP RSSRGSRSRPRRRLRLRRGRSAIH GEGRTAKGSAAWSARTFRSPPGVG RDPMRRAHEGREIPSLGGARRREVL QAGRSQRAAGRRRRRQLELGVG GRPGGPPPGPGRRGTCAAALPPEWP RRRTGLPRRGPRPLAMAKWLNKY FSLGNSKTKSPQPAPRPDYREQRRR GERPSQPPQAVP\QASSA\ASASCGP ATASCFSASSGSLPDDSGSTSDLIRA YRAQKERHFQDPYNGPGSSLRKL AMCRLDYCGGSGEPGGVQRAFSAS SASGAAGCCCASSGAGAAASSSSSS GSPHLYRSSERRPATPAEVRYISPK HRLIKVESAAGGGAGDPLGGACAG GRTWSPTACGG*KLLNKCSSSAEE SGAGMKDKVTIADDYLDPFDAKND LKSISGKGESAGYMEPYEEQRIMTE Y*RQECVRSQH*GIQLYETP*EPEGQ NFESESESTVNPRMRENKLPQDYEQ /RPAD*YDQPLELNPV/TQFPALAA QFNGNEKQSSPSR\DRRRQL\RA PGGGFKPIKHGSPEFCGILGERVDP AVPL\EKQIWYHGAI SRGDAEN/LCL RLCKECSYLVRNSQTSKHDYPLSLR SNQGFMMHKLAKTKEKYVLGQKS PPFDSVPEVIHYTTTRKLP\IKGAE HLSLLYPVAVRTLLSGPDSALLCDR AWRLARCQRPTNQPATVAGCVV CVVCMVLAHHCMSLECCCHLRGLE KAWIKTEGRQHTTSPNPNEALEFL
1437	6934	A	1548	304	678	PQVILPPLVSQGCWELPDVSPLRPSL VW*FL/RK*KLDLPCDPAIPLLGVPY RKIKACFHTKTCIQIFIATLFGIAKKK GKQPKQPSAGEWINTWW/HIHTMK HCSAVKKEQTITISLFRSRIWRI
1438	6935	A	1549	80	623	LGGVTRGFNMRIEKC YFCSGPIYPG HGMMFVRNDCKVFRFCKSKCHKN FKKKRNPRKVRWTKAFRKAAGKE LTVDNSFEFEKRRK*YTSNYQRDLL GIKT\IDAMKRVEEIKQKPPS*YINEQ IE/GKIKSYRKFDIKRSPSQNIPSL RAPPCQAKGKQLGEEMGTARLQGG CGHGKMPP
1439	6936	A	1550	1021	1544	EPTKKCCVYYAQFLSLPSLFFPTGSE EQDSIYFILFFEMEFRSVTQAGVQW CDLGS LQPPPGFKRFSCLSLPSSWD NRLLPQGPANFCIFSR/GWGFHVRG QAGLFSRDGVSPS*SGWSRTPDLVI RPPWPVRVLECSGQYIIFPWLFSRFS LSIFSKFDCNLSQFGFIWICLFYSS

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1440	6937	A	1551	2	210	
1441	6938	A	1552	2	310	IGVKMEEYAREPCPWRIVDDCGGA FTMGTTGGGIFQAIKGFNRSPVGVN HRLRGSLLTAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWNSI TSGCLNGEPYWQARNGTQWPMVG VSPQWVGIFPSF*FEGSWYLCLTRF ASGTVFPMGP\QFA\EDPSPVCLSTQ LPSLAPFGGIFQAIKGFNRSPVGVN HRLRGSLLTAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWELH HKWVP
1442	6939	A	1553	1	4629	
1443	6940	A	1554	96	721	PGQLSSLTPPRPASLLPWRAAYLFL\ LFLPAGLLAQGGYDLDPPLPPFDHG QYTHYMDQIDNPDDYDYQEGTPR\ PSEGQFQ\F\QSQQEVQQGVIPSPNPR AQGNAELAEPTPEGPLDCREEQYPC\ TRL\YSIHRPCK\QCLNEVCIFYSLRR VYVINKEICV\RTVCA\HEVELLRAD LCSGTSFSKCGR*WASSGL\CQSV\A ASCA\RSCGSF
1444	6941	A	1555	262	732	FQNKGNFFSTKRTEVSPSTQFNFYFA RKNTTLIRISHSSLGQVRIRLVWFG LVWFWFLETGV/CTLVIRGWFEQW\ CDQNSLQP*TPGLQRIPTSASQSTG ITGVSHSLVRYVVFTEIQLKFWILI TKITVLLVYN*L*NKGY*YIFITFFL NLQN
1445	6942	A	1556	162	496	HSYIHIVHVCNFFMYSFAVVFVKKH LLLCLYNRTVIIYYNLGKL*INS*FK QPVYMH*VLYC/INLCFTYMKVAAA RILLICNYTHKIYICMIHEIYLEMFII LMDILWCE
1446	6943	A	1557	2	247	GEIVVFKVEGRDIPVHRVIKVHEKD NGDIKFLTKGDNNEVDDRGLYKEG QNWLEKKDVVGRAR/GYALLAVM GAYVLLKRES
1447	6944	A	1558	1	503	VRAGAVGAHLPASGLDIFGDLKKM NKRQLYYQVLTAMIVSSALMIWK GLIVLTGSESPIVVVLSGSMEPAFHR GDLLFLT NFREDPIRA/GDNGDIKFL TKGDNNEVDDRGLSKEGQNWLEK KD/VVGRARGFLPYVGMVTIIMND YPKFYALLAVMGAYVLLKRES
1448	6945	A	1559	180	257	
1449	6946	A	1560	2	676	FVRCSAAVCATQSRRAARSPENPA MVRAGPPWGLNLPASRLGISSADL KKMNKRQLYYQSFKPSPWIVSSAL MIWKGLIVLTGSESPIVVVLSGSME PAFHRGDL\FLT NFREDPIRAGEIV VFKV*RPRTFPISSQR*SKVHEKD\N GDIKFLDLKGDNN*SLMD*EALYK KARNWLEKKDVVGRARGFLPYVG MVTIKMNDYPKFYALLAVMGA\ YVFLKR
1450	6947	C	1561	449	820	MVIXGQISPMTATSGQKAFLAGPLG

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						SLGTLPRSQAVKRRLLLKLT KDRI RDVLLLMFLKGHRETHGQCLQRQQ TKESTSIVVLALCGLYGKQVVTLLN VGIPFSINVFYFTTPKSPLIMKLII*
1451	6948	A	1562	251	473	
1452	6949	A	1563	22	212	
1453	6950	A	1564	160	397	
1454	6951	A	1565	17	262	LFKWAKALNRHFSKKHIQMANQH MKRCSTSSAIREIQVKIAMVYN*YTI *HSQ\YSLQLPFPLWKTWVKFLT VVKLLNCSVK
1455	6952	A	1566	2	294	GNKMAAPKGSWVVRTQLGLPPLLL LTMALAGGSG\TASAEAFDSVLGDT ASCHRAQLTYPLHTYPKVGPVRS GLRPFPCSPFLGSPHVCRLWQPGC
1456	6953	A	1567	366	1412	QRGTRWRRERGSWVVRTQLGLPPL LLLTMALAGGSGTASAEAFDSVLG DTASCHRAQLTYPLHTYKKEEL YACQRCRLFSICQFVDD\GIDLTRT KLECESACTEAYSQSDEQYALPFL GCQNSACHFAELRQEQLYVPRWP KMAPTFFL*LLGEGSFWELT*WDSA Q\SFITSSWTFYLQA\DDGKIVFPV* SQKSQYAPHFGAREPTNFEENHLLS KMSSDLQMGKFHQAHQGIFLKNEE RDGLFKKPSILNSGWILTT\TLVLSV MVLLWICCATVATAVEQYVPSGE AGVTMGDLEFMNEQKLNRYPASF SCGLVRSKTE\DHEEAGPSYLPKVN LAPFLEI
1457	6954	B	1568	76	384	MSGWGVLSGRLNPAAREKDVERFF KGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELCSERVITIEHAR ARSRGGRGRGRYSDRFSSRRPRND RRNAPP*
1458	6955	A	1569	3	229	
1459	6956	A	1570	152	536	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDP K\ADDAVYELDGKELCSERVITIEH ARARSRGGRGRGRYSDRFSSRRPR NDRRNAPPVRTENRLIVENLSSRVS WQVC
1460	6957	A	1571	771	1383	ILIEYKCGKCHVCTLSNIFSSSLVFF ISCDCLCVFPLCLTQLSCVKDLK DFMRPAGE\VTFA\DAHRPKLNEGV VEFASYGDLKNAIEKL\SEKEINGRK IKLIEGSKRHSRHSRHSRHSRHSR RSRHSRHSRHSRHSRHSRHSRHSR DVPVLLSRSPRA*EEPRNRGSSRSK SPASVDRQRSRHSRHSRHSRHSR SDSGN
1461	6958	A	1572	236	1377	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCSERVITIEHA RARSRGGRGRGRYSDRFSSRRPRN DR/RVCEGWMAALNNYW*G*PFKI QESLAVMILGPAV*SVLLFPR*PIVL DESI*VIEHKSIDGSH*NGL*YLMA*

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						TCPQLNTSAVIAFLPL*IRIFFLRNAP PVRTENRLIVENLSSRVSWQDLKDF MRQAGEVTFADAHRLPKLNEGVEF ASYGDLKNAIEKLSGKEINGRKIKLI EGSKRHSRHSRHSRHSRTRSSSRHSRHS RSRHSRHSRHSRHSRHSRHSRHSRHS SRSSPCPEKS\QKRGSS\SR\SKSPSHL WNRPEVPGPRSRHSQIQLDQWPIKPV K
1462	6959	A	1573	568	770	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCS\ERVITIEHA RARFTRLGRGRGRYSDRFNNSAEL RNDRRNAPPVRP\ENRLIVENLSSRV SWQDLKDFMRQAGEVTLPTDTRL NL\NEGVVEFASMGDLRNAIEKLSG RELNGRKIKLIERPAKRPQ*VQQSRS SDPGTQKSPLGPRSRSPSPVANLN SRSKK/RRGSREPGSPEPSRSC*VGS SPVP*ERFFKGYGRIRDIDLKRGFGF VEFEDPRDADDAVYELDGKELCS
1463	6960	A	1574	22	202	TKSSS*CDSVATCGIHKFSCPHNLSKI HDSISPRVC\SICKPHGSIHKLCIKIKF HIFAR
1464	6961	A	1575	1	1878	MQYSHHCEHLLERLNKQREAGFLC DCTIVIGEFQFKAHRNVLASFSEYFG AIYRSTSENNVFLDQSQVKADGFQK LLEFIYTGTNLDSWNVKEIHQAAD YLKVEEVVTKCKIKMEDFAIANPS STEISSITGNIELNQQTCLLTLDYN NREKSEVSTDLIQANPKQGALAKKS SQTKKKKKAFNSPKTGQNKTVQYP SDILENASVELFLDANKLPTPVVEQ VAQINDNSELELTAVVENTFPAQDI VHTVTVKRKRKGSQPNCALKEHSM SNIASVKSPYEAENSGEELDQRYSK AKPMCNTCGKVFSEASSLRHMRI HKGVPYVCHLCGKAFITQCNQLE NACKELHTGEKPYKCGICVIKGAQ KC\QLVFHSRMHHGEEKPYKCDVC NLQFATSSNLKIHKHSGEKPYPVC DRCG\QRFAQASTLTYHVRR\HYW EEKPYV\CDTCGKAFVLLVLFHIS FLRK\HTGEKPYICGICGKSFSSGEL NKHFRSHTGERPFICELCGNSYADI KNLKKHKTKVHS\GADKTPRTPSA\ EDPNLGVKQDP\IQKSPFNPETYGCE SPS*YELYPLALPLGTED\HHMLLPV TDTQSPTSDTLLRSTVNGYSEPLIF LQQLY
1465	6962	A	1576	42	134	
1466	6963	A	1577	154	768	HVACGLLWIYVSPSAHLNLDGTITT K\ENLGTVNEILLGSNPTEAELQDMI NEVMSDGNGTIDFP\EFLTMMARK MK\DTDSE/EKEIRRKHSRVFGLRVG NGLYL\ACRNFRHVM\TNLGRRK NQIEEV*WN*SRGSQILDG*WSKLT YEFEVQMMTAKVRPLSRNVNLFLV

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						QNCFICLFLWFV/TLSCKKVFSPTCQ KKNMHVIGN
1467	6964	A	1578	3	202	RRMVSAFSCRCMPSEPCIAVTAPCM MAGQAPAERTAQ*PLYF/CTLFQGS LSPT*REVGWPLGPAGM
1468	6965	A	1579	133	378	
1469	6966	A	1580	891	1744	DMFPITPSRSVLPSFLLTYLPRQSL/N SVAQAGVHWCDLSSLQPPPGFKQ FSCLSLPSTW*LGLQACTTVPS*FFV VVVICIFFFLVETGF/TLGWARLVLN L*LQ/CDPPTWASQSAG/ITDVSHHA QPILRFKCLS*CIRSFNEGRIKGTRO NKVELSL/CFLRQESHVSTQAGVQW CNLSSLQPLPPGFKQFSLTGLPKC WDYRSKRPRPANQTSILGC*RKDPY *LHWAKKATEDIKLESCRLTPGKAR PTANFLRQQQFFWGPILGGLLPQE GFPFLFFKGF
1470	6967	A	1581	2119	2436	TTRYLKKTSTTGQRKKRGRNGSF PTENLVPSGTVTGSQQLGPPFR*N/H TEECWGPPTADGRAGKGPRQQPGR AQRIYRWDPDGTTHHHRPGSR GTDQPETK
1471	6968	A	1582	208	296	
1472	6969	A	1583	185	947	SHCSSGMEIPVDQLPSLPRAALVAQ NYINYQQGTPHRVFEVQKVQKQSA WKD\PGKEGHKYS/HLKFAV*KKL YKKQVKG*TCTA\EVLLPFQRGQET LHQEVNFHILKEKLGKNPD\EEDNT FYQRLKSMKEPLQAQNI\PD\NFGN VSQEMTLVLNLAWVACGLI**WQK FLLKTTWYK\MVKI\QTCQARQRI DDF\ELDYPFFYFINIASQEII\WQM QVLWHPQYGTKVKHNSRLPKEVHL GYTPKPLTEV
1473	6970	A	1584	5060	5662	ESQAAPPPRSTLHRPARATAITAC WSSQASGPQAVRRRLTPLSSPAAR DLVSKEGFRRARHVVEIRRTAQA AAALRRGDYRAFGRMLVESHRSLR *GPLGAPLLPGTGRPRPTPSISSLQD DYEVSCELDQLVEAALAVPGVYG SRMTGGGFGGCTVTLEASAAPHA MRHIQEHYGGTATFYLSQAADGAK VLCL
1474	6971	A	1585	2	987	LREGCPQR*RQPTQLDWPYF/CPFSP VC*KTKTKKPYPCAPKLGHVRCPT ASTLQAHTGPCPPSPQTGPQTRAGL LHICVGVGARFLFLLSLSPFGDIPL
1475	6972	A	1586	318	382	
1476	6973	B	1587	106	293	MAGRVCQCQSAGSGAIGPVEAAI RTKLEEALSPEVLELSFRGTEPPTT PAGPRSAGRAGS*
1477	6974	A	1588	442	905	PMLSGRLVLGLVSMAGRVCQCQS AGSGAIGPVEAAIRTKLEEALSPEV LELRNESGGHAVPAWAVRLHFRVG CW*ALVFEGLSPLTTDTGLFHAALA EELGRFRSHALA\IPGTDPPPQWREN

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						\SQLEQLAPPCLG\GKQENFLGTPLE PPKRG
1478	6975	A	1589	1206	1335	KTQERYFNLKQN*TGQAWWLMH/I WEA EAKGSLEPRSLRP AWAT
1479	6976	A	1590	136	837	PSEKTSPDRDKKKRAVRSILFLELQ NIIQDHDQGEKENESQIMKEENT GAGAEAKREEDMNPVKSSKKHKS EEHNDKEHSSDKGRERLNSSENGE/ AQAQTPRKEGH/RKGRGHSRSRSRE RRHRIRGRERKKSRSRSRERKKSR SRERKKSRSRSRERKRRIRSRSRSR IQRHRA*D*KAGVGPRSRSRDRKKR IEKPRRFSRKFKPDSQVHLPLEGRTO PWDAQEAFS
1480	6977	A	1591	209	1545	PYYFLQANSPPGPLLTPALLPHRILS DVTQGLPHAHSACLEKLKRSYEFY RYFETQHQSVP\QCLSKTQQKSREL NNVHTAVR/SLWQLHLKALLNEVII LEDELEKLGCTKETQELVSEAYPILE QKLKLIQPHVQASNNCWEEAISQV DKLLRR\NTDKG\KPEIAC*KPTCY SSTF*RQPTLHIADQDPIEEQVLEA YVDDIDIDSAFQNRHDFYLSQEDK ERQKREHEESKRVLQELKSVLGFK ASEAEQKW\KQLLFSG\H\VLK\SL FPVGPQWEPISNSEPSMNSDMGKVS KNDTEESNKSATTDNEISRTYLC ENSLEGKNKDNSSNEVFPQGAER MCYQCESEDEPQSKIGSLT\TAPPT P\RDLSQPSIKQRL\ARLQLSPDFTFT AGPCWQEVGCLDLLLPFTTMAGNR LFGDEEEQIIEEN\KN\IEEEK
1481	6978	A	1592	1	296	DFPLPTLLKTGPGPGF/YNGPP*GER FYVASPG*IWAPQGF*KGPPSSSSS SSSQSRKPLFPCFANKTG*VGCFLVI SQRDQIPYRPTPTLPWLQP
1482	6979	C	1593	15	350	MLISLNINQTLTYCNKTENCXXXXX XXXXXXXXGGPFKRTPGPKFNRG WQGKIFPLKGGLLKPWWGIFXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXEKGEKQPEKPGG*
1483	6980	A	1594	11	129	APWLSVLY*SESPEAQPPYMMGPLE SP*AQRCPGLERGR
1484	6981	A	1595	2	660	NFPTARLFRLFYPLFPLKIFFPKAFN FCREVGPFCPPPK*GFFPKIPK*VFN RPP/SKGKSFTLPAPVKFGPPRGPFK RAPSSSSSSSPVV*APWPTVLY*SE SPEAQPPYMMGPLES*APHEGVTA WVES*GPCPA*PWGRQAAPQPPPP QERAG*EPESKFGPGSK/PPERPVYA GNSPVLRSGLTSPSPSPAPPGGFKY MEERSKADLGPGMEKG
1485	6982	A	1597	1	680	ESRIRRRSSRRPREPPGSRRRRRR PDPRTMPSEKTFKQRTFEQVEDV RL\REQHPTQIPR**LERSKGNQPP \VLDK\TKFLVPDHVNMSEL\IR\IR RRLQ\LNANQA\FLLVNGHS\MVVS VSPHP\SEVYE\SEKDE\DGFLYMV

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						LCPPPE/YGLR*TLNV*N*KKKNAAS S*NCLNPLPKEKIKECYPTIDQFPI TDHETSSVPTLGLVGLSCVCSRRKT
1486	6983	A	1598	2	508	PDSSGPHRLRENPPMVAVSCPTKTN VKGPPGGKVGAGAHAG\EYGA\SEALE MFLSFPTTKTYFP\HFDLASHGLCPR LKGHG\KKVADALTNAVAHVDD MPNGVVRP*SDLH\AHKLARVDPVN FKLLSH\CLLVTLA\AHLPAEF\TPA VPRPPWDKFPWLSVKHRLCTFKYR
1487	6984	A	1599	295	758	VLSRKQCRSLTAFSSKCPNSWFSITQ TECKTMTTCGMPQHVTQQ*RPINTS HQYSVKLGHP\DTLANQGEFKELVR KDLQNFLLKENKNEKVIEHIMRGP GTQNAQAELREFIMLMGEA*PG AFPRRKIARGLTEGPGHPNK*PGPG GGAPP
1488	6985	A	1600	411	1259	SQGTTSRGSWEFPHSPEIETSCLAE LFEKAAHLQGLIQVAKQGATLCT LYAKYKQVKVGNCTPKPSFFDFE GKQKWEAWKALGDSSPHQAMQE YIAVVIKLDPGW/ISSDIQRRNGKEA NTGFGGPVISSLYHEETIREEDKNIF DYCRGKQH*PYNQKPSNPKNVDVN VKDEEGRAPLHWGL*SEDIKELVH SVAANIELTLNCQD\NERPKQALHY ASACGVSGIL*ELAAPSLGADPDSPR PGWLPARGGDRQLQNSFFGAAAAHN WQGLIKRENCSL
1489	6986	A	1601	177	409	FLQASGILKGFEPNLL\NLVLTVTI*Y MRDPDDQYKLTGGHPGKLGVLVFR G\TSLVL\ICPDGMEAI\NPFIIQQ DA
1490	6987	A	1602	1	165	PLKRS DGCNDGRPTRPPTPTTVF TSNLKQTRMVHLTPVEKSAVTAL WGKVNVD\VGKALGRLLVVL WDPKRSFQSPLGESVPTP*MVHLTP VERVCRYCPVGQGERG
1491	6988	A	1603	240	461	
1492	6989	A	1604	2	206	
1493	6990	A	1605	2940	3296	
1494	6991	A	1606	189	736	ENKISSVFKADFLPPAPCSLPGLEVS VSPKGKNTSGRESFGWAIWMEGL VFSRLSPEYYELA\RPHLRDEEKS\CP CLAQE\GPQG\DLLTKTPELGP*ITR TC\TIVQKT*RKMMVDKPTQRSVS NAATRVCRTRGRSRWRDVCRNFM RYQSRVTQGLV\AG\ELAQQNLVST SRLCIPSTGPL
1495	6992	A	1607	3	452	
1496	6993	A	1608	3	485	PTLLVPTDSERTHPWLLSPADKVTN VKGPPGGKVGAGAVRSMCAEAL RMFLSFPTTKTYFP\HFDLASHGSAQ V*GPRARKVADALTNAVA\HVGRT LPNALVPPLSDLHAHKLARVGPSTF KLLKATCLAGLTLAAHLPARVQPL AVASLPWDKVSWSAC

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1497	6994	A	1612	77	636	QPQTD TM VH L TPVE\KSAVTALWG\ KVN L DE\VG G KALGRLL\VVYPWD PQKVL*NPLGESVPTP*MLVKWGKP PKGEKAQWQKKKCSGAL*VNGPGL T/HGQPSKGTFGPH*SE\LC\DKLH\ VDP\ENFRLPGQQLVCVAGPITLG KEFTP\QLQACLFRKLVA\GVANAL GPTSNHLSLAFLAGPISN
1498	6995	C	1613	167	391	MNVFMCRLGTTFHLVLLPSVLPSL RKT V FLNPFSIKQRFQRWKHWVFQ VASELTDAILSSCGHLFLPGSHNLS*
1499	6996	A	1614	1402	1871	GLQGSQSLHPSLTGLRHACITLGKT AHSSRLHPSAPPPYL*STDTRDNN APEPTPPRSWTWRA*/PMGRGSSQE GQASQQPWPGEKSGCEMPPLVY KVKPEP*P/SPDPWGL*QSMPLDYL HLSVILRWRRGGGQWQGATKISRR DRRGGALLHL
1500	6997	A	1615	8	551	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVH L TPVE\KSAVTALWG KVN V DE\VG G EDLSRLLPVYPWTQ TFFD\SFADQSTPDAAMGNPKVKAH S\KKVLG\AFSGGPGCTWDNLKGT AHEVSLHC*QACTWD P ENFRLLG\ NVLVCCCWAHSLLGKEFQPHQLQA CLIKKIGWLGVG
1501	6998	A	1616	3	389	
1502	6999	A	1617	1	672	
1503	7000	A	1618	18	621	RSLRCSRHSCLATSSPLPCARRAWH PARGKADQPFCSRAGPSVPAQPR GENREKEETTRIGPGVMESKEKRAV NSLSMENANQENEEKEQVANKGEP LALPLDAGEYCVPRGNRR\RFVRVQ PILQYRWDMHR\LGPTGQGMKR RE*WKRIGEEVRQLMEKSWRGKSQ LASH\SLRGESGTDPPSPMTHHD*VF ALMPLNP
1504	7001	A	1621	3	700	HASDRRHGSHACSRVSSGHQAGL LGGGWEEDRECGQRAEGMMFWA ALALAATSPSRLLLSPGKGPVPSRLL PLSDAASPTWLKLT*RR*RSQIYQT G\QEGPLLPSQIGVILRDSHGVA\QV RFVVTGNKIL\RILKS*GTC*IFLIDL YHLN*ESQFAVRKGILRREQERDKG G*NFPSPDF*IGEAGFHPFWLRYKD QAESSLPNWEIWNHLTASALGRINL VWCTPSN
1505	7002	A	1622	1	340	GEHSMAPPAHFRALLYHPGTATLV PHPASISQHSPPWGNA/RG*PV*RQ RHLTAPRSPPHPRFRHKPGKDPREN PSRWPEVPSLPQTHVVPQAAWDT VNTTVCKNRSTKPQD
1506	7003	A	1623	3	1076	HPVPSSYSVHTLSPAAMTEQMTLR GTLKGHNG\WVTQ\IATTPQFPENNL PASR\EKAILRKPARGWSQPMNFQ RRSRRIHSHLLRMVVIS*DGQFC/AF QGFWDWKPCALGDLTNG/TPTRGR

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						FCGPIPKDVLVSFAFSSDNRQRLSLGSLG RE*THQSLWN\TLG\VCKFNLSRNE H/SESWVLCV\RLAPTTSKPLSIGLP VAWDK\LVQV\WKPGLNCKADAPN PHLATTGFL\NTGDLSSSRWDPLCA SGG\KDQQA\MLWDL\NEGQPPLQR *NGGD\NNA\LCFSPNRY\WLC\AAT GPS\KIWDLEGGKI\NDELKQEVIST SKAEPQCTSLAWSADGQTLFAGY TDNLVRVWQVTIGTR
1507	7004	A	1624	1	1189	LQGGGRRGCGASFSKPSSAILVAAA THALAAAMTEQM\TLRGTLKGHNG\ WVTQIATTPQFPENNLPASRIEKAII LRKPARGWSQPMNFQRRSRRIHSHF V\SDVVIS*DGQFC/AFQGFWDWKP CALGDLTNGHPHEGDFVGPYPRNV LSVA\LSSDNRQRLSLGSLG*THQSL WNTPGWCANTTVPG*EPTQEWVVS CVPLPRPNNQQTPIIVLLWPGNNLV QVMETWANCKLKDPT\NHWPTPGY SETPVTVLSRMDPFCA\SGGQGMAQ AHVYGD\NEG\KHLHARMVGTISI NALCFSP*PATWLCAATGPSIKIW GFRGERSIVDELKQEVISTSSKAEP QCTSLAWSADGQTLFAGYTDNLVR VWQVTIGTRLEVYGRALPIKKKTGF SEKKKK
1508	7005	A	1625	3	445	GEFADSF/SSMGSPVNAQDFCTDLA VSSANFIPTVTAISTSPDLQWLQPA LVSSVAPSQTRAPHFPGVPAPSSGA YSRAGVVKTMTGGRAQSIGRRGKV EQETDQLEDEKSALQTEIANLLKEK EKLEFILAAHRPACKNPDDLGFPE
1509	7006	A	1626	7	514	
1510	7007	A	1627	3	462	RRSERAVTVLLPSSASQRPPVSAPRP LARLCLTATMMFSGFNADYEASSS RCSSA\SPAGNSLSY\YHSRRPPFSA WGSPVNAQ\DFCTGPGPFSSANFIP TGHLPSWTSPD\LQWLQ\PALVSS V\APSQTRAPSTFSESPPPTAGAIYSR AGVVKTMTGGRAKSIGRRGKVEQ LSPEEEEEKRRIRRERN\KMAAAKCR NR\RELTDTLQ\AETEQL*DETAFA WTRMSHPVEEEGKLEFILAAHR\PA \CKIPDDLGLPRKRMSVASLDLTGG LPRGLPPRRSEEAFTL\PLLNDP*/DP KPSVEPVK\SISSMELKTEPFDDFLFP ASSRPSGSETARSPDMDLSGSFYA ADWEPLHSGSLGMGAHGHRGWEP LCTPVVCTPSCNCLHVFLRLHLPR G*LLPQLCSCPPQGGQQQ*AF*LA QLTHAAGPVRGQGRGSRHPQV\PL PELVHYREEKHIFP*RVPRPGIASLT TTHPADLLFQHGARLSTRRDFCTGP GPFSSANFHSGLAILDQSGPCSG WCKPALVSSVGPIADQSPFNLFQVP TPYRWGLAPGLAL
1511	7008	B	1628	43	674	MDWTWSILFLVAATTGVHSQVHLV

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						QSGAEVKKPGASVKVSCASFNSF DTYGFNWVRQAPGGGLEWMGWV SAFNGDTNYIRKLQGRVTMTTDSST STAYLELRSLKSDDSAIYYCAATNS DKYFWGQGTLVTVSAASPTSPKVF PLSLCSTQPDGNVVIACLVQGFFPQ EPLSVTWSESGQGV TARNFPPSQDA FGDLYTTSSQLTLPATH*
1512	7009	A	1629	3	1639	SPGIFRGFQSVIRTEQRELTMESGLN WLLVAVLKGVCQCEVQILESGGGQ VQPGGSR TLSCAASGFIFSNYVMTW VRQAPGKGLEWVSSTAASGANTFY AESVKGRFTVSRESENMMYLQMS SLRDEDTGIYYCAKGDGVPNLGVA WIVAGPGNVRPRKWFDAWGQGT VTVSSASPTSPKVFPLSLCSTQPDGN VVIA\SCLVQGGFFPQEP LSVTWSESG QGV TARNFPPSQ\MASGDLYTTSSQ LTLPATQCLA\PKSVTCHVKHYTNP HPDVDG\PCVPSTPPTP\CSLNSTYP ISLMLPPPTVTAPTGPSKDLFLGSEA NLTCTLTGLE\NASGCHFQSEGLQV GKSAVQGP\PEA*PSVAAYSVVQLS CRGWREAMEPLVRPFTCTAA\HPV VQGPALTAHPLQNPNTFPGRVHP FAPAVGRVCPFNDLLTLHCLAR\AF SPQGPCWVRWLQSGPKLPPRKST*L G/PFPAGA QARAPTTFAVTSILGR/V QPEDWEE/EGTPFSCMAGH\EALAL AFTQKTIDRLARKPTHVNV\SAVMP EVDGTCY
1513	7010	A	1630	3	497	SSGPTRLRENHPWLLSPADKTTVK PL/WGKVGAAHAAEYG\SEALGEGFS LSFPQPPKTYFPATSDLE/HNGFAPG LKGHGQRKFGRTR*PKSRGGNV D MPQTALSAPERPCTAHKL\RVDPV NFQASLSHC/LCLVTLAAHLPAEFT PAVRRLWSKFLAS\VSTVL
1514	7011	A	1631	9	489	NSARATDSERTHHGARLLPDKTKA QRPPRLKLGANA\GEYG\SEAL\ERM FLSFPNPPKTYFRQFRP*ANGFAQG* RGHGQRRWPDALTQ\AVA\HVDEH APNGAVRP*SDLH\AHKLARVDPVN FQASLSHCLAW*PWPAHLRPSSTP GGATPSLEQSSWASC
1515	7012	A	1632	2291	2960	INCPAQAKVADILQFNFKKFVCLF/D FLRQSLALSPRLQVQWYDLSSLQSP SPRFKQFSCRLRPSS*NYRCASPRPT NFLIF/M*RWGFTMLARLVFVLLTSS DPPTSA/SHSAGITSVSHCTRPLQSIFI *PLEQVS*VKDKNNNNKTHFFVLFC FLRQSHSVTQAGMQWHDQSSLLL QPPRLKQFSHFRLLSWYYRCLANF *IFCKDGVLLCCPW*SQTPGLK
1516	7013	A	1633	1	1233	
1517	7014	A	1634	233	884	ESPGVGCSARRGPRPRSPGPPPAAP GTPRPHGIPLYTRAGHQ**GEIRRRP CTFISKFLRPQGGASERQLPDLQAR

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						AWQELLGRPFNKH\HWFPR*SPCKG IGVTRC\NRINP*KWIPLIGPGQHS LSSQELFRLP\SEL\TLWG*PPIEVS YRIGEDGSHLCACMKPSA\GGSTQ NQTNVQMVD\SRISCKEELLGRTE PFKTTNMMTVSG
1518	7015	A	1635	2	402	SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASL DKFLASVSTVLTSKYR
1519	7016	A	1636	2	522	GLEFGTSHRLRENPPWCLSPADK TNVKA\AWGKVGGAHAGEYGAEAL ERMFLSFPTTKTYFPHFDLSHGSAQ G*RAHGK\KVA\DALTK\VA\HVDD MP/HNGAVPPLSDLHGAQAFGWDP VQLQSS*SHLPCW*PLARPPSPA EFQPLAVATSSLGQSFLGFLK HRCLNLPNYR
1520	7017	A	1637	344	742	GFLIGVNEKTCFFTSPMLHDSYFF FLVNVIRCHFICGTLYWAKHIFS FVFPFLSFLFTSFISLFLPFPFFL FFFFFW*LLLPTPFYVSF\MKG* SFNF*FFIFKCRLLTLLQNIK* TREMTTFDYFLSVFL
1521	7018	A	1638	1	519	PLKRS DGCNDGRPTRPPTRADTT AYTSNLKQTLVHLTVTEEKSAV TALW GKVNV\VEKVGKALGRLL VVYPW TQRFFESFGDLSTPD AVMGNPKVKAHSQESSPRGL* WWAWLTWDNLKGTFAHTEVSL HCDK\LRGSLKNFRL LGQRA WSVVAGPIHFWQKNFNPTS CRLA
1522	7019	A	1639	3	452	
1523	7020	A	1640	3	484	PTLLVPTDSERTHPWLLSPADK DQRQGPWVGKVGAAVRSMAEAL ERMFLSFPTTKTYFPHFDLSHGSAQ V*GPRARKVADALD/TNAVAVGRT LPNALVRPL\SDLHAHKLRVDPVQ FSSFL\SHCLLG*PWAVHLPRPS FNPWRLQGFLGDKVSWAFC
1524	7021	A	1641	180	613	SFAGISNGLAGRSVKDSGKAQ\AKA VSR\SQRAGLQSQWGR\INRH* KSRDASHHERGGATA\AVYSA\A ILEYLPQKVLELAGKASKDFKGA YYPLRHLQ\LAIRG\DEE\LD SLIK\AT\IAGGGVPTTSHQIS DRGGKKKDNQKTV
1525	7022	A	1642	107	368	IYIILRD*VLSTFVCFILCKAIY KNIWTAFWKCS*ILICSI/LCNY VCTCTSVYALCYIYIIDL*QQT YLCESKCTCICYVCIFLC
1526	7023	A	1643	790	1252	CAKPETQNNGNLRVRLRPLHFGHT LN*VRT*LKRRIFFFLRQSLALSP RVECSGMISAHCKFCFLGSGHSP ASAS*VAGTTARRQHAWLFLCVF SRDEFHRISKDGLNLL/NLVICPP RPPKVLGLQHEPPCPAKRRNFLS KIMGGHCFEL

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						SSCN
1527	7024	C	1645	171	329	MGARASGRSPLCQVGRQEQGLRGR NGPLPASRLPQQPQVVPATPQSPRD DLA*
1528	7025	B	1646	196	514	MGRDTGPELCLHDSSLPAADDGPSL PTKQNEEFRRPFIRRLPEFKFWHAAT KGILVAMVCTFFDAFNVPVFWPILV MYFIMLFCITMKRQIKHMIKYRYIPF THGKRX*
1529	7026	A	1647	43	321	
1530	7027	A	1648	35	821	GRPRLGRSGAASYRMSEGDSVGES VHGKPSVVYRFFTRLGQIYQSWLD KSTPYTAVRWVVTGLGSFVYMIRV YLLQGWYIVTYALGIYHLNLFIAFL SPKVDPSLMEDSDDGPSLPTKQNEE FRPFIRRLPEFKFWDASVCGDGRC CKAGGGRQCPVLAADAALTFSPHL K\HAATKGILVAMVCTFFDAFNVPV FWPILVMYFIMLFCITMKRQIKHMI KYRYIPFTHGKRRYRGKEDAGKAF GQLEAGLRLPHVLQEQF
1531	7028	A	1649	156	818	HSYRMSEGDSVGESVHGKPSVVYR FFTRLGQIYQSWLDKSTPYTAVRW VVTGLGSFVYIDSEFTCLQGWYIC* PMPLGIYHLNLFHKLSPKWDPSL MEGLQDDGSFGYPTKQERREF/RA PFIRKGSFVNLFWHAGYPRASLVA LWSCTFFDAFQTSPVFWPILVMYF HHASSCITDGRANSRHMDSLRYR MPVSHMGK/RGRYRGKED\AGKAF AS
1532	7029	A	1650	154	685	PPLHLRDCFSPPGRALSPVGFYPPYR RSVP\TWLKLTSDDVKEQIYKLGQ EGPLLLSQIGVILRDSHGVAQVRL G\TGHD\TFKILKSKGLAPDLPEDLY HLIK\KA\AVRKH\LERNR\KD*GC* NSRLILIESRISPFWLRYYK\TKR\VL PPNWEIWNH\LTASAPGRINLVWCT QAIK
1533	7030	C	1651	127	435	MAASXNPEVLDITEETLHSRFLEGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALS\VETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCS S*
1534	7031	A	1652	1	689	KCFI/VGADNVASKQMQQIRMSFRG KAVC*WGKNTMMRKPIRGHLENNP ALEKLLPHIRGNVGFVFTKEDLTEIR DMLLANKVPAAARAGAIAPCEVTV PAQNTGLGPEKTSFFQALGITTISR GTIEILGVRNVASVCLQIGYPTVASV PHSIINGYKRVLALS\VETDYTFPLAE KVKAFLADPSAF/VAAAP/VAAATT AAPRAAAAPAKVEAKEESESEDED MGFGLFD
1535	7032	A	1653	68	1110	RTAVMPREDRATWKSNYFLKIIQLL DDYPKCFIVGADNVGSKQMQQIRI VPWGEACVLMGQKTM\MGQAHPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GTL*NNPSLWRKLLP\HIRG\NLGFC FTQGGPSLEIKGHVCLANKGLPSWL PVVGANC PHGEVTGGQPQNTG/LSG PEKTSFFPGL*AITTK\ISQGAPIENPE VNVPAESRTGDQSGKPSEANAA*TC SNISPF\SFGAGSSQPGVSTNGSHLPP LKGLDIHRRNLCIFWLSWRGVRNV AKCLSARLAYPTVA\SVPHSIINGY KRVLA\LSV\EPDYTFPLAEKVKAFL \ADPSAFVVAAPVG\VAPPAAPGG\ VAAPAKVEAKEESESESDMDMGFGL FD
1536	7033	A	1654	1	364	
1537	7034	A	1655	70	253	
1538	7035	A	1656	151	657	APTPTGPGDPLDLVALAEQVQKA DEFIRANATNKLTVIA\DLQQLHPE QARKVLEEHRDANLHHVACNIVK KPGDIYYLL*TRGVGQQYFSIISPKE LGDKFVHIDFLGAYKLQHDLSWTP V*GH*EGKMLKISMMGHVAKPVSG PASVHWNPTFQGTDSLEEWGF
1539	7036	A	1657	345	547	GFKPPDFFLCNENKWRKINTSSFS EY*CLMHIHLLIFNITIFSS/LHTYIHKH THTHTPFSVFIMEGC
1540	7037	A	1658	228	900	PSQAGNTSPSGARSSFPKDMKLEN SSFEAINSQT TVETGDAHIIGRIESYS CKMAGDDKHMFKQFCQEGQPHVL EALSPPQTSGLSPSRLSKSQGEEEG PLSDKCSRKTLFYLIATLNEFQA*L *LQHSPQLSSAGSPALSWLG*MQS TAVCSQLCGEDFKDLKPQLWNAVG RGDLPLGLKCDIYS\YNPYLSDPFG EDGSLWSFNFFYNKRLKRNRLL
1541	7038	A	1659	35	1288	
1542	7039	A	1660	1	1641	
1543	7040	A	1661	212	369	HPVTVYLLLG YLLFQLPCGSEFSTSE THGHSADRLGAAFAVSRLEQDEYA PG
1544	7041	A	1662	63	255	VLMFSSSHG*GYQSS\RLQCKLQIVQ LIQDILLFFSF*IPE*LLS*LTPLKIFPL HQNGPSDFVS
1545	7042	A	1663	169	391	
1546	7043	A	1664	85	1534	KSSHCIKMGPQIFHKTSELVLPATSC PSCPDQNEEDVSQTQYKECCG\GG WCSHSIFAVWHFI*RPDAT*FGLEQ RLTGLLASGPVSLREVV*LYSSLGT VISGK*KTSNVG*RLALGSWAFSD KYSWFTMTWACISGPTKAL\TTGV \GLIAF\GQCDVIVAGGVELMSDVPI RHSRKMILMLDLNKA KSMGQRLS LISKFRFNFLAPELLAVSEFSTSETM GHSADRLAAAFVSL\ADQDEYALR SHSLSKKAQDEGLLSDVVPFKVPGK DTVTKDNGIRPSSLEQMAKLPAFI KPYGTVTAANSSF/LLTDGASAMLI MAEEKALAMGYKPKAYL/RRDFM YVSQDPKDQLLLGPTYATPKVLEK

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						AGL\TMNDIDAFEFHEAFSG\QILAN FKPMDSDWFAE\NYMG*KKPRFGL PPLWRRFNNWG\GSL\SLGHPFGT GCR\LV\MTAANRLRKKGGQYGLV AACAPG\GQGSATDYVEAYPK
1547	7044	A	1665	294	823	
1548	7045	A	1666	3	1171	
1549	7046	A	1667	1419	1801	TMEIHPIEQLDPSDHLESTAAGQEA LFTYHSF*STFISFFETGPHFVTRLK CSSAIITHYSVELLGSSHPPTSASWV AGNTGVCPHVQLIFLFFVEMGSHY VARLVFNS\GLVIFLPWLPKVLGLQ V
1550	7047	B	1668	68	471	MVRKLI\VPRAEAAEAGGLPELGGH RPQPARAARAAALTGCSGGEDYTR YNQLSRAVPVCSRLGAHARVRWEL CDFVTASSFCRRRLPTVLLKLRLMAQ HLQGSIAL*
1551	7048	A	1669	2	359	
1552	7049	A	1670	1	585	PRGVIGHGPLGTSFIGKYGCGDYW VKAFLDRPSQPM\QGPKKNFE\WWD LVDVNT\DLMA\PVSAKKERKVSC MFIPDGRVSVSARIDRKGFCEGDEIS IHADFENTCSRIVVPKAAIVARHTY LANGQTKVLTQKLSSVRGNHIISGT CASWRGKSLRVQKIRPSILGCNLR VEYSLLIYVSVPGSKQVFIKAL
1553	7050	B	1672	21	410	MPSKVRCXSVQVFDAMKTATAVA HCKRGNGLIKLEPVLLGKERFAG VDTRVRVKGGGHVAQIYAIRQSISK ALVAYYQKYVDEASKKEIKDILIQY DRTLLVADPRRCESKKFGGPGARA RYQKSYR*
1554	7051	A	1673	1	456	MPS/KGPLQSVQVFGRRKKTATAVA H/CCKRGNGLIKVNRPLEM/IEPRTL QYKVLGSGTGVS\GWR\TGDRDVV ALESWGAGISNGMFRSCVGCQWA AGASSASRQERFAGVDIRVRVKGG GPWPRFMSKKFGGPGARARYQKST DKPIVTQNSLV
1555	7052	A	1674	172	661	LLEPVLLLGKERFAGVDIRVRVKGG GHVAQIYGESQELGAWRRWLWEG GLHSAPVPFNCVSFSQLSVSPISKAL VAYYQK\WSEHGSFP*GRWVCGDQ VKDSV*LSKSSSLLFLPDVDEASKK EIKDIL\QYDRTLLVADPRRCESKK FGGPGARARYQKSYR
1556	7053	A	1675	27	554	STLGAMPSK/GVPLQSVQVFG\RK DSGQLLAH\CKRA\NGLIQG*TGGL EMIEARARLQYK\LLEPVLLLGK\IE RFAG\VDIPCPV*KGWSTWPQIYAI RQS\ISQKPLVAYYPEM*VSMGPSH E/YVDEAFQRREIKDILHPSYDRNP AGLAGPFVRCE\SKKFGGPGAR\AR YQKSYR
1557	7054	A	1676	192	836	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKLVFL\GLDNAGKTTLLHMLK

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						DD\RLGQHVPTLHLTSEELTIAGM TFTTFDLVGHE\QARRVWKN\YLP QLMGFVFLVDCADHFSPSWNPKE LNALMTE*NNIPMCPILILG\NKID TDAISEEKLREIFGLYGTGPQER GEL*PLKEL\NARPM\EVFHVAVLL KEGKVVYGRGFSAGLLPVLF
1558	7055	A	1677	196	520	DTVSRKNKSGKIFQLSSRV* IYERSQSGVKVYKCKTFGKAFTQ/HF* AHMRMYTGEKPYKY*ECGKFFILV LLLLLMIQKYFHLIKIVRLYLIRK KVSCQPSNKILQS
1559	7056	B	1678	1	1521	MGIRVTSVIVSRPVPHSEAVFCC WLLGATDVWIPEHPANPRLTFPL FPESGRHLEIKLQSARDASVKS AKNTRVIPKPQRVIHPGGQPTDK MDLDDLLDNPRJIAAIKKAKLKS VKEVLHFSGPDLKRLTNLSSPEV WHLRLTASLHLRGSSILTALQLH QKERFPTQHQRLLGCPVLDALLR GGPLDGITELAGRSSAGKTQALQ LCLAVQFPRQHGLEAGAVYICTE DAFPHKRLQQLMAQQPRLRTDVP GELLQKLRFQSQIFIEHVADVDTL LECVNKKVPVLLSRGMARLVVID SVAAPFRCEFDSSQASAPRARHL QSLGAMLRELSSAFQSPVLCINQ VTEAMEEQGAAGPLGFWDERVSP ALGITWANQLLVRLADRLREEEA ALGCPARTLRVLSAPHLPPSSCS YTISAEGSWGNTCKQNTLHISPET AGPAHAACWPQQDTRVAGHSES WHASCCNPDTDMQQTISTSVNQ QEAQAKPPPTPL*
1560	7057	A	1679	991	1367	AVLVFNNGEANEGSGPRGP* GERSRARRPP/SGPGPWNCAPRP WCPLRGWSSVSWD*TAQAKPVCK SP/AGGSSPGTGSPSAPSPGAGT EPAWAGPAELPGVFSLNVPLSL SCLIF*SLACLA
1561	7058	A	1680	313	429	CIESMVHGGENIFPAGHGGSHL* SQHFGRPRQVDHLRSG
1562	7059	A	1681	552	792	GSASDYQSGIRTVGPRDWLCRR RALDLDAARTQSVRAAEGKCAFL MQMGPRVYTGPRPRRADHLRSGV* DQPGQHGETP
1563	7060	A	1682	508	1085	CQHFRPRRADHLRSGVRAQPGQ HGETPSLLKILKLA/GHGGAPL* SQLLGRLRQENHLNPGGRGCGEP RSHHCTPAWETERDSISKKKTKTQ VVICI*SLNLVREIKNKIGLTAE* ILQKNSLEVDVSIIEI*NEGQRD GKKMDRAFLRSMQQYQAVQYMCN QSPRRVGDRMGRINSQKKCKTYT MTIKHC
1564	7061	C	1683	46	516	MLSDPPARIRTRKGPTETVSRIP RPNSPNGQGPVDSSPSGXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX*
1565	7062	A	1684	2	100	
1566	7063	A	1685	2	814	PGYKKGPQETGSRI PRNPSPNPLRVL WTAHLVAMAPGSRTSLLLAFALLC LALGFKEAGCPSQTVPLSRLFDHG MVQGPSRVTS CAID\TYQGFEETYIP KDQKYSFLHDSQTSFCFS\DSIPTPS NMEGSATRNPILELLRLSLLIE\SW LEPV\RLRSIVPPTTWVYEH LGTAI DYHLL\KDLEGGHPTV*WGRLEDG KPPDLGKILKQTYSKFD TNSHNHDA LLK\NYGLLYCFRKDM\DKVETFLR MVQCR\SVEGSCWLLGCPSSIL
1567	7064	A	1686	3	452	
1568	7065	A	1687	3	516	PTLLVPTDSERTHHGACLLPDKTNV \KAAWGKVGAHAG\EYGAEALER MFLSFPT\TKTYFPHFDL\SHGFCPL RATGKKVADALTKRRG\HTWDDM PKRRCPP*SDLHAHKL\RVDPVQLS SS*SHLPCWVTPGPAHLRPSSTPGG CKASLGQSFLGFLLLKHRCLNLPNNV
1569	7066	A	1688	3	409	SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC\SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIYIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEA EKYAKE SLKEEDESDDDNM
1570	7067	A	1689	2	437	
1571	7068	A	1690	126	409	ILLWMDILICTDFGSVNYFNVWRL PKSYLSLFYSRIYIVHDEVKDKAFEL ELSWVGELTNGRHEIVPKDIREEA E KYAKESLKEEDESDDDNM
1572	7069	A	1691	516	564	
1573	7070	A	1692	224	344	ILLGFLVLASDHLQSKYAL*CPLR HLPENPSLREGSVL
1574	7071	A	1693	1	1237	MGCRPVGQAGLELLTSARTCFVSD LKRGLKIQAAKFNIDGNNECPIDTR KQLAENLVVIGGTSMLPGFLHRLLA EIRYLVEKPKYKKALGKTFRHTPP AKANCVAWLGARSLGYNRFLMF QPFRGEETVWSLLPKIQAYCCPFL KYDLSASTFSPDGRVFQVEYAMKA VENSSTAIGIRCKDGVVLGV\EK*VL SKLYERRVPNKKTFLMFDR\HVGM A\VAG\LLADA\RLADIAREEASNF RSNFG\YTIPLKHLADRV\AHVWCHA \YTLPVAVRPF\GCQFPC*GPYSVN DGA\QLYHD*PHPGVSIPVNWGCAI GQRPQAWQRRKLEK\QMKEMT CARDIVKEVAKIIYIVHDEVKDKAF E LEPSWVGELTK\GRHEIVPK\DIREE AEKYAKESLKEEDESDDDNV
1575	7072	A	1694	1	1083	
1576	7073	A	1695	138	545	RPGMWSTRSPNSTAWPLSLEPDGP MASASTTMHTTTIAEPDPGVS\GLP\ DGRMETPTPHP*LTMVVMAGCDV\

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						AAVPIVLVSLLFVMLRYMYRHKGT YHTNEAKGTEFAESADAALQGDP ALQDAGDSSRK\EYFI
1577	7074	A	1696	2	498	
1578	7075	A	1697	41	510	APSPRRPWGHFTEEDQGLLSTSLWG KGEMWKKCWEGRNPOWERLPGCPT PWTPRGSEQLWQPCPSA/ILAHFW ANPQSPRHHGK\KVLTSLGRCP*STL DDLKGTFAQL\SELHCDKLHVDPEN FKLLG\NVLVTV\LAHF\GKDFTPGG CRASWAEDG
1579	7076	A	1701	153	744	AVNLVPSKDRHLTQSRSQGGGVAN PNSGVYSARPSSPPQIALPAWGTG QPQTLQTSPEGGFSVQTGAEVGVG RG*PRRRPPRARQGGKVHSTLKKL KHYRFHIADGLDRGQAPPLGRPLFL GPGWLRTH*GRAGK/QNPQTVGDH PGAGAPPSPALAVSL*/H/CTGLC*I PSPACSPGSPSPRRRGSHSPDAWV DP
1580	7077	A	1702	35	569	
1581	7078	A	1703	509	2455	LPAATVLTSSPNFQIQPNRTNGD VTKKIHDSLESSKISTLKGNLERYF QPSWMTLRGVRLQLEEVPA DIVEIA RELELEVEPEDVTEFLQSHDQTLAD QKLLLMAEQRKWFLEMETTPGGD AMNIVEITINNLEYNINFVDKGAAG FERIDSNFERSSTA EWVTVKQTQAH PSGGIQEGIVIIRDGSRPYTPEHLPV RPNVEEEDSDIDESSPFLRNYYKA AHSFIGRIRFKHSTSLREAFYIITSK EFFSAIRKLASSPEKKGKGGIHTAINP FTRSINEIYKIQRRRGKERQLNDCV HRSDDANKGPESLGSAGSGQSHDV AQGHLQGLVLGQLFILAPLGKFHPE EDVKQATSNFENLQKQLARKMKLP IFIADAFTARA FRGNPAAVCLLENE LDEDMHQKIAREMNLSETAFIRKLH PTDNFAQKNMNSTLTFVTL SGELRA RRAEDGIVLDLPLYPHPQDFHEVE DLIKTAIGNTLVQDICYSPDTQKLLV RLSDVYNRSFLGEPGKLNTENLLQV ENTGKVKGLILTLKGEPGGQTQAFD FYSRYFAPWVGVAEDPVTGSAHAV LSSYWSQHLGKKEMHAFQ/SFPPE ESWEFPFVQT*RVDIRGCAPVVLEG TLTAYRWLCCDAAVSNHQVFSA
1582	7079	A	1704	1	1503	
1583	7080	A	1705	1	635	
1584	7081	A	1706	1	804	LQFSSALGGGRCRASASSPRRARRR GQRPRHPAPRRPQAARPSAAPRARR FLSQRPA AAAAAA QRAALMQAIKC\ VVVGKPKL*GKT\CLL\SYTTQCHF LGEYIPTVFDN\YSA\NVMVDGKTG EIWGLWDTAVQEDYDRVTPPYYP A/QADVFLFCFPFVSPASFENVRAK WYLNVRHHCPN\PIILVGTKLDLR DDKDTIEKLKEKKLTPIYPQGLA\

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						MAKEIGAVKYL\EC SALTQRGLKTV FDEAIRAVLCPPPVKRKRKCLLL
1585	7082	A	1707	1	848	RPRVRAGAENMMFSAARLSPWE GSPSFAENMNDWMPKAEYDPLKA GSIDGTDEDPHDRAVWRA\MLARY VPNKGVIGDPL\LTFLVARLNLQTK EG\K*KEV\FPRYGDIRRLRLVRDLV TGFSKG\YAFIEYKEERAVIKAYRD ADGLVIDQ\HEIFVDYELERTLKGW IPRRL\GGGL\GGKKESG\QLEFGGR DR\PRKP\INLPVVKNDLYREGNRE\ RRERSRSRERHWDSDRDRDHDGRG REKRWQEREPIRVWPDND\WRRER DFRDDRIGREKKERK
1586	7083	A	1708	3	3067	
1587	7084	A	1709	148	4435	GIQRKYLKGSIMVSSGCRMRLWFI IVISFLPNTGFSRAALPFLVRRELS CEGYSIDLRCPSDVIMIESANYGRT DDKICDADPFQMENTDCYLPDAFKI MTQRCNNRTQCIVVTGSDVFPDPCP GTYKYLEVQYECVPYIFVCPGTLKA IVDSPCIYEAQKAGAWCKDPLQA ADKIYFMPWTPYRTDTLIEYASLED FQNSRQTTTYKLPNRVDGTGFVVY DGAVFFNKERTRNIVKFDLRTRIKS GEAIIANYANYHDTSPYRWGGKTDID LAVDENGLWVIYATEQNNGMIVIS QLNPYTLRFEATWETVYDKRAASN AFMICGVLYVVRVYQDNESETGK NSIDYIYNTRLNRGEYVDVFPNQY QYIAAVDYNPRDNQLYVWNNFIL RYSLEFGPPDPAQVPTTAVTITSSAE LFKTIISTTSTTSQKGMSTTVAGSQ EGSKGTPPPAVSTTKIPPITNIFPLP ERFCEALDSKGIKWPQTQRGMMVE RPCPKGTRGTASYLCMISTGTWNP GPDLSNCTSHWVNQLAQKIRSGEN AASLANELAKHTKGPVFAGDVSS VRLMEQLVDILDAQLQELKPSEKDS AGRSYNKAIVDTVDNLLRPEALES WKHMNSSEQAHTATMLDLEEG AFVLADNLEPTRVSMPTENIVLEV AVLSTEGQIQDFKFLGIKAGSSIQ LSANTVKQNSRNLAKLVFIYRSL GQFLSTENATIKLGADFIGRNSTIAV NSHVISVSINKESSRVYLTDPVLFTL PHIDPDNYFNANCSFWNYSERTMM GYWSTQGCKLVDNKTTRTTCACSH LTNFAILMAHREIAYKDGVHELLLT VITWVGIVISLVCLAICIFTFCFRGL QSDRNTIHKNLINLFIAEFIFLIGID KTKYAIACPIFAGLLHFFLAFAW MCLEGVQLYMLVEVFESEYSRKK YYYVAGYLPATVVGVSAAIDYKS YGTEKACWLHVDNYFIWSFIGPVTF IILLNIIFLVITLCKMVKHSNTLKPDS SRLENIKSWVLGAFALLCLLGLTW SFGLLFINEVETIVDGHISFTVFNCFP

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						GGVFHFPSPFHCALPKGKVRKRIMA KCL/RRHLHTACGGP/LPT*ESPHSS VKASTHPEPSARYSISGTQS/RIRRM WNDTVRKQSESSFISGDINSTSTLNQ GHSLNNA\RDTSAMDTLPLNGNFN NSYSLHKGDYNDVQVVDGSLN DTAFEK\MISELVHNNLRGSSKTHN LELTLPVKPVIIGSSSEDDAIVADAS SLMHSDNPG/VWELHHK\ELEAPLAI PQRTSHLLYQPQKKVKSEGTDYSVS QLTAEAEDHLQSPNRDSLYTSPMNL R\DSPYPESSPDMEEDLSPSRSENE DIYYKSMPNLGAGHQLQMCYQISR GNSDGYIIPINKEGCIPEGDVREGQM QLVTSL
1588	7085	B	1710	98	264	XQVVCCKYRGFTIPEAFRGVHRYLS NAYAREEFASCPDDEEIELAYEQV AKALK*
1589	7086	A	1711	155	1217	DPPSPVPAPPSSPRDGHFLVPDATM AEEQPQV\ELFVKAGSDGAKIGNCP FSQRLFMVLWLKGVTFNVTTVDTK RRTETVQKLCPPGGQLPFLLYGTEVH PD\TTKIEEFLEAVL\CPPR\YPK\LA LNPEVQHSWGWDIFAKFFLPNIQEF QTPALN*QSGRRGFLESP*KVLDNY LT\SPSPPEEVDETSC*KIEGV\Q\RK FLDGGQRRPHPWLDLQ\CCPKVTH* VQVV\CKRK*PGNSPHPPKAFPGKC HRVP*SKMPYAPGKNSPSHPVPDDE EIELRPM\SKVAKALQISPSLGLPSTP SIFSTKAPGGFHIATPMGHTPKLASG QGILGDIEPAKGVVEEGMRERNGGP GSDF
1590	7087	A	1712	39	256	LSVKMEEGILPCSLYETTITDSKT*Q G*YI/EDFRLVFLINLNA\YILKKMLV NHLR*NMRDNSETYRRIRVIV
1591	7088	A	1713	1193	1436	PQSDFLDTLPQTSPIIP/*EVPTGLVC YSSRVN\KRAAPPASIPVPACSPSPV SNPPHPVSNPPHVSAPLPCSSHQTQ QAP
1592	7089	A	1715	2	533	ARDSFLAAMASHR\LLLLCLAGL\VF VSEAGPTGTG\ESKCP\LMVKV\LDVA VRGSPA\HQMWP*HVFRKPR**PPW EAILPSGTRKTQLSLGEL\HGAHKLR EGICTNGIYKSGK*DTKFFT\GKGT GIFPHFPLRH\COEVGISTGQRTSGPR RLTPLAALLEPLTPISTTGCSFTNSQ GN
1593	7090	A	1716	38	661	APSPRRPWVISQRRTKATITSLWGK\ VNVE\DA\GETL\GRL\LVVYPMDP RGFFDSFGNLSSASA\MGNP\KVKA HG\KKVLTSLGDAIK\HL\DDLKG/T PFAQA*SELHC*QACNVGS*GTFKL PGEILLVT/LFWAIPFSGKEFHPLRCQ VFLGQEQKMAEDGD\WSIGQCPCSF QITTELTGP*MQSFSRIWLYSCKQLQ IINLFLLRDHQ
1594	7091	A	1717	32	487	SRRHGSSLWGKVNVEDAGGETLGR

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						LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1595	7092	A	1718	41	597	APSPRRPWVISQRRTKATITSLWGK \VNVE\DAGGETLGRLLVVYPWT\ QRFFD\SFGNLSSASAIHGQPPKVQ GTWSKKVLTFLGEMP*KHL\DDLK GHLLPKPEVNLHC\DKPAMWDP\EN FKAPGEMLLVTRFWAIPFAKEFHP WRLAGLPGQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG
1596	7093	A	1719	3	573	HSLFGTSEVINKLLVPDAHGSFHRG GPRLLSTSLWGKGECGKMLEEKPL GRLLVVYPWTQRFF\ESFGNLVLLP SCPSMGQPPKVKAHGKRRRC*LSLG RCQ*STLDDLAKGTFCPSLKRNLHC* QACNVGS*RTSKLLGENVAG*PVFG QHFHRAKNFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH
1597	7094	A	1720	676	1283	QRKILYTHNTTENKWEIINF*SFR IFLFLRRSFTLVAQAGVQ\WDLGGS LQPLPPRFKQFSCGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFFLSLTVSGVQWRDLGSLQ PLPSGFKGFSCSLPSSWDYGCPPPS PANFCIFSRHGFSPCWGWSQTPDL K
1598	7095	A	1721	41	669	APSSRRPWVISQRRTKATITSLWGK \VNVE\DAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSSASA/LSMGKPPKS KAHGK\KVL\TSLGDA\TKHL\DDLK G\TFAQA*SATCTVDKLAHVDPGGT FKLLGENVAG*PVFGQHFHRAKNFT PGGCRASWQKQKMAEDGDWS\GQ CP\VLQIPLKLNCP*MQSFSRIRLLFL QAITNNKSISAKRSP
1599	7096	A	1722	2	307	TPYLVGQVVAGAQAQLFESHAGH LGPQLFNKFALPYIRDVAQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM
1600	7097	A	1723	20	473	AVEFEANGLGPQGFPKNDIFL*A AWGEETDYTPVWCMRQAGRYLPE FRETRA AQDFFSTCRSPEACCELTL QPLRRFPLDAAIIFSDILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGQVVA GAQAL
1601	7098	A	1724	3	1170	CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPKNDITFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFFSTCRSPEACCELTLQALGME VTMVPGKGPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPQASHQLLRIL TDALVPYLVGQVVAGAQAQLFES HAGHLGPQLFNKFALPYIRDVAKQ VKARLREAGLAPVPSIIFAKDGHF ALEELAQAGYEVVGLD\WTVAPKK AREC\LGKTVTLQGNLDPCALYASE EEIGQLVKQNL\DTFGPHRYIANLG HGLYPDMDPEHVGA FVDAGHKHS RLV*QNMWGPLWMLGINTHVWFD KTECIPLSRTPNPDDWLFSGP
1602	7099	B	1725	92	846	IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHLYPDMDPQHVGAFVD AVHKHLRLV*
1603	7100	A	1726	1	804	
1604	7101	A	1727	178	1093	TFLLPACLLAALLPLRHHVRGRAW VQGSILNEGVG*ALKD\LINE\ACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NLT SMSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSDYEMK LMDLDVEQLGIPEQEYSCVVKMPS GEYA\RJCRESQPILGDV\VISCA\K DGENFSASGELGNET\IKLSQTSNV DKEEEA\VPIKMNEP\VQPNFCH*GY LNFFTK\ATPLSSTVDTPVCSADGTP LVGRSIIAGYGDHLKYLGLPKDP RIEESLGHS
1605	7102	A	1728	58	483	AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQCQLYPRRSQQQVVP VVDFQAE LRQAFLAETPRGTVA AIAATASIAGAPTQYPPGRGTPPPP RRQTTPPPGIMAPPPGMRPPIG/PPPI GFPLARGTPISMPPSGN
1606	7103	A	1729	292	531	FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLPHFALIIANNKCIEQ KKKKK
1607	7104	B	1730	326	419	XRLTCKRSLARSIASLNAPQTDASGI SGGPDA*
1608	7105	A	1731	774	1763	GNPRSYLLSIAFPLGLQKAFKVFNC GTLDGFWNSNHDLFGKSASKLLQ\HI DYRMRCILQDGR\FIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPR VEE/ESRVLGLVLLRG\ENLVSM TVE G\PPPKDTGIARVPLAGAAEGPGV GRAAGRGVPAG\VPISGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVA\ATASIAGAPNTVPTQGT GTPAPTSGRATQPPGIMAPPPGIM RPPMGPMGLRPARGTP\IGMPAPG \MRPPPPG\IRGPPPP\GMRPHKTL SILFDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC
1609	7106	A	1732	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM

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						GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1610	7107	A	1733	1	591	NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGK\VNVEDAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQSFQ G
1611	7108	A	1734	1	477	RRPSWLVAAVLRNANMQIFVKTLT GQNHHPRLRYETQ*HPLKNVQKPKIS KNKGGYPHPD\QQRLDNLPGKQLE GWPALLSDYKHPRKESHAPWCLR LR\GGIIEPFPPLPQKYLRQR*SC RQVLCFAFNPPCLSTGRKK\KCGSH QTTLRPQEGRFK
1612	7109	C	1735	9	254	MEFHSCCPGWSAMARSQTLAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV*
1613	7110	A	1736	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIILRHLDIGATVHEL SDKKKDTVPWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG
1614	7111	A	1737	68	312	
1615	7112	A	1738	317	916	TSSPPSSLCFLSFSHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGEQYCLSEKPKLLPLELEK TGIQNYTVTEFQPLYYVAESINDAK EKVGNSAATIPRPFVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE
1616	7113	A	1739	389	1881	NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQVE TSY\EDNCNQKWVPISLDPPHLKER KLGALGPKYCALF\ENDVNLTTHIE S\RPSRLK\KDEYGFFPPFGIKRSLPA LTNIILRHLDIGATVHELSDKKKD TVPWFPRTIQELDRFANQISYSGS NWD\ADHPGFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEKKTW GTVFKTLKSLYKTHACYEYNHIFPL LEKYCASHEDNIPQL\EDVSQFLAQT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEK KLLPL/ESLEKTAIQNYTVTEFQPL YLAESFNDAQGEI*GTFAATIPRPF SV\RHDPHTPQRIGGSWDNTQQLKI LA\DSI*Q*IGIPFAVALQNIK

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1617	7114	A	1740	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
1618	7115	A	1741	1	360	SGACPAFLVDRNLRRHHETTFNLIMK CDVDIRKDLANTVLSGGVTTMYPG IADRMQKEITAL/APPSTLRFRFIAPP/ ERRKYSVWIGG\SILASLSTFQQ\MC LGKQEYDESGPSIVQRKCF
1619	7116	A	1742	13	1277	INPPPLSRRCQLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPISVGRPRHQGV MV GHGPRTDSYVGDEA/QRSKRGILT KYPIEHGIVTNWDDMEKIWHHTFY NELRV\APEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSGDGVTH TV\PILRGATTLLHAINRLGPGLARD LTDYLMKILT\ERGYSFTTHGPSGKT FRNIKGEACATSPLDFEQEMGTAA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIM KCDVDIRKDLANTVLSGGTTMDP G\IADKIAEGRSTALAAPAP*KIRNIA PP\ERK\YSVWIGGSILASLSTFPARF WISKQEYDESGPSIVHRKCF
1620	7117	A	1745	644	844	ELSPTTFMPFSEGAEHL\LPQGPG* GSESPGGCPA/PPYSPYSAPPATPEP IEKSQPNPIRHRFP
1621	7118	A	1746	2	271	
1622	7119	A	1747	83	420	DSSNPSCQSPTQLSKANTLGWHV CELALPDQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGL\GPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGSPDGPLP
1623	7120	A	1748	154	1030	SDISQAQLSCTGPPAIPGIPGIPGTPG PDGQPG\TPGIKGEKGLPG\LAGDHG EF\GEKGDPGIPG\NPGKKFGPKGP MGPKGGPGAPGTPG\KGDSDYK ATQKIAFSATRTINVP/LLRRSQVIRF RPRCITNMNTN\YE\PRSGKFTLQGC PGLY*FNLSTPVSRGNLCVNLMRG RERAQKV\VTFCGLMAY\NTFQVTT GGHGSSAEE/GPQKEGGGKRPFF LQATDKN\SLTGAWEGANS\IFSGFL AFFQIWEGLTCGLASHPTPAPPARN AHYTPNNNHMTKPNHNRDW
1624	7121	A	1749	3	607	FCPRGQEFEGENKLLSPRRPWVISQ RRTKAT\ITSLWGK\VKCGKNAGKE ETPGKGSLLV\HPWTPRGSFEQLW QTCPSALCPSMGNPQSQTMAKKV LTS\GRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVGS*RTFKLPGEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQ\S FQG
1625	7122	A	1750	2	585	AAAAPAGGNPEQR\LDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPAGSPAPSPAGCGGKGGG

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						LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEPAAAPG PSIR/PVLPQTGS/PWRRPKSLRPVL GTRVGRTPPLPPP/PDPAGPPPLPLPG PHPSRPPPTGPWRPARADGRV
1626	7123	A	1751	25	1295	KLCATKDLSYLAASPTAFAYLG GLFSPKLPVTMAHRFPALTPAEQKK ELSEIAQSIVANGKILAADES VGT MGNRLQRIKVENTEENRRQFR/EIL FLLWDSSIQPGGIGGC*FLFPRR/YPL TQKG TARGKLPFGNIPSREKGD SW VGNQV*DQGRFLFCREPNKGNHH FKGLDGLFERFVQYKKDGVDFGK WRAVLRIADS/CPSSLAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLAAVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVGYGSP*QALHRTGPAAV PGV/CFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYGRGLQAQCTG LPWGGKAANKGGNPRTA FMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRLHKPCLYPT
1627	7124	A	1752	1	186	IFSRDGA\HRVTQDGLDLLTS* SARL SLPKCSDYSREPPRPAQTPILRHFIH NSKHEKTME
1628	7125	A	1754	74	595	RGGQGLLSTSLWGK\VNVE/DAGGE TPGKGSLLVYPMPGQRFDFSG\NL SSASAIHGQTPKVK\AHGKKGADFP WDDAIKHL/DDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFPQKDG* LGVGQCPCSFQ\PLKPLGP*IQ\SFQ G
1629	7126	A	1755	21	457	NPRVRGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLDDAQ ADEAVL\DNKNSLEILLGSIGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTL SVQNTDSPSYPEISSSCSMEQL QDLGGKLDASKSLGKSTQL
1630	7127	A	1756	1	455	
1631	7128	A	1757	3	468	
1632	7129	A	1758	50	895	THASDGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLDDAQ AD\EA VLDHPADLKHIDP\VLKHC\ HAAA\ATYILEAGKHRA\DKSTL\ST YL\EDCKILTEKRIELFFAREYQ\NNK VNSLEILLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRM/YRPA YLG DLKV VQNTGIPPSYPREL VFSCQPW NQL\QDLVGETLKDASKKPWK RAT SVVTLGKVNRSPSSRRKTQKPPLP FSWNHRLCRAGCPFSVEKNFSLNL YPFIHFGHFKNV
1633	7130	A	1759	470	737	RKSFFLAQTVLKWCCCEKMSSPGKK LFPGEIWGVKGNKNKLWLPDP SIRS HRFERVPSHKRPLPGWVRWLTP IIPS TLGGQSAVDHLRSGVDRDQPGQHGE

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						TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGGARGCSEPRSHHCTPA WATE*NSWDYSCLPPRPANFYIFST DGVSPCWPGWSRTPDLK
1634	7131	A	1760	1	297	
1635	7132	A	1761	1	162	
1636	7133	A	1762	54	504	YTAIMSIMS YNGGAVMAMK GKNC VAIAADRRFGIQAQMVTTDFQKIFP MGDRLYIGLAGLATDVQTV AQRLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLNAV DRDAVSGMGVIVHIEKDKITRTL KARMD
1637	7134	A	1763	51	748	YTAIMSIMS YNGGAVMAMK GKNC VAIAADRRFGIQAARLLTTFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGNLNLY*V*REG/RQIQTFITLM EAWLANLFVMRKRFGLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLREC ESLWGGPTWVPDSTVLKTIFPRPW NAVGPGWQCSGMGSSLFHIIEKDKI TTRTLKARMD
1638	7135	A	1764	433	851	KPOPFLCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN FFETESHVST*L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV
1639	7136	A	1765	213	617	KRFLV*KVASVLKGLHA\VVSDRD GSTLLLKWANDNAPEHAF/RGPGFL \STFALATDQKQTWDFSKNKSINIC LLLPYQGGFNFSFYLVWGEFS*A QAGSAQLQGLICSA*EKGTWFPLF* RN*GQVVEVSLI
1640	7137	A	1766	2	140	
1641	7138	A	1767	157	371	
1642	7139	A	1768	3	135	
1643	7140	A	1769	1	1431	MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALV TASTDGIGFAI ARRLAQDGAHV VVSSRKQQNV DQ AVATLQGEGLSVTGT VCHVGKAED RERLVATAVKLHGGIDILVSNAAVN PFFGSIMDVTEE VWDKTL DINKAP ALMTKAVVPEMEKRG GGSVIVSSI AAFSPSPGFSPY NVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCSEDASYITG ETVVNLSVMFTGGGVCRAASWKE GGTGTPRTPRESRQREPGETSSTD QENKVWNGLPANPQRPAAEGPVRR KTNKQKGIASTSAKDSINIRTGKDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNW MENKFDDLTDV SFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV

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						QELHEGYTSFNS
1644	7141	A	1770	53	582	RKETVSVSPQQSRHLIGVRS PKGLS EVALAGLIHAQGAATSVH CARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SAALAQIAGATSQGPT/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARDLTL DIIG
1645	7142	A	1771	44	1059	AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHV VVSSRKQQNVD Q\AVATLAQGEGLSVTGTVCHVGKA EDRGAAWPPAVKLHGGIDILVSN AAVNPFFGSIMDVTEEV\WDKTLDI\ NVKGPKP*MTKAVVPEMEKRGGGS VVIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRV\NCLAPG\ LIKTSF\SRML\WMDKEKEESMKEIT LRIKKV*ASPEDCAGIVSFLCSEDAS LHSLGKT VVVGGGTPVPASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPHSNQFLPL
1646	7143	C	1772	1	174	MWIFIFNKYYQHVKSPMTSRTGKS ATCDGCGMAAHCSRCWGLSWG LG EALSYSKNVS*
1647	7144	A	1773	154	765	RAGLEELTA AVMVRL LNCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMG\KKTWFSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGA\HFLFQKF*D\AMPLKLTEQPE LANKVDMVWIVGGSSVYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD
1648	7145	A	1774	1	676	DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLQDFSRN LSAKSSALFFGN\AFIVFAIPWLYW RIWHMDLFKSAVLYSVMT*LSTYL VAFAYKNVKFVLKHKV\AQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\KNEV\ADYEATNIF PIFYNNTLFLVLVIVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALLTG SK
1649	7146	A	1775	99	362	
1650	7147	A	1776	3	403	
1651	7148	A	1777	184	360	
1652	7149	A	1778	1	885	EFGTRWDFSMAVFADLDRAGSDL KALRGLV\ETA AHLGYSVVAINHIV DFKEKKQEIEKPVAVSELF TTLPIVQ GKSRPIKILTRLTIIVSDP\SHCNGFER QLLRGARLYDVVAVF PKGQEKSLF HIA\CTHLGCGDLV\CITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLSR TPTMRKVYNFSPAPPILMPNLAKGK NVNYYLGGWQERAFREIR\GP\YDV

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						GKS*ACLFGPFF*K*TPRVRVST\NCR AALLHGETRKTAFGIISTVKKPRP\S EGDEDCLPASKKAKCEG
1653	7150	A	1779	175	534	DCSLPSVCHFPPLSPHPTHTPPWG /CPSGGPEGLPIT*RHQVGSCPTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHIMCNVVALTFYATYIED LCCTCNKYIEKAHTSVW
1654	7151	A	1780	190	390	TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSC GV*CSWGQKSIRVSLLWGF
1655	7152	A	1781	805	1325	ASKLEGSPCGKGGVGLGGCFPKRPE PRNHHPFVLWYLPQTRLEPKPLP PQLPSVG*\KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGFPACA TSSGKPKLKRPLCAKSTMP*THPPT VPKPPGQEA VENQAPMASEFPSPSP SVSGDLKPWGFRSFLCQGGAWS
1656	7153	A	1782	1016	1560	KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYRP FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGPSLFPHTPFL TTP/LPHG*LFPSAPPALHHATHFRT
1657	7154	C	1783	68	223	MSPSSVFFVXXXXXXXXXXXXXXXXX XRASFIPFLDLXXXXFFLSFQMKSI DF*
1658	7155	A	1784	1373	1651	LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLISSNHI*I NVKAYIVLYVN*ILKITKYMILLSTT
1659	7156	A	1785	6	140	
1660	7157	A	1786	223	397	QTPP*KSKQPFRTSS*DQVPSQP*VPI PPINPPIPPPFGEVYYFEPILRKWV KGR
1661	7158	A	1787	2287	2854	
1662	7159	A	1788	1	610	SGRPFFFFLSGGARATAQLAESWRG GQHLQSSSPPPPPASPGGPSSSDQRS PCSNARW\NTSIYSLVADGTC*D TALVGNKDP\PSIWAAIPGKTFLNIT PAEVGVL\VGKDWVKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSP\TFNVIVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY
1663	7160	A	1789	157	610	GYRKKQLRGDRRWAIHRIRITLTSR NVKSLEK\VCA*L**RRRKKEKNLK S*KGP\VRMPTKT\LRITTKT\PCG*/ EGSKDRWDRFPD*GFHK\RLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQISIHTIDDQLKKKKKKK KI
1664	7161	A	1790	1367	1582	METRWESPPPDNFIAPVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFRCALQEKWFF
1665	7162	A	1791	122	344	ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFPAP

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						FRKSPSQVQAH*PGSDEDPRPL*EDPRPL
1666	7163	A	1792	656	1068	NQINFCLNGKYTYVCIDTLPLYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNRQRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK
1667	7164	A	1793	138	396	
1668	7165	A	1794	143	327	CGVQLLPDRRRESRDIIIVEL*AAVA AAGGNPDGKKGGGGWEAGQRKER KESEDPDAEPDCV
1669	7166	A	1795	23	483	KAIVLLHIICTEVISIILFNDFIQDKRP CRLFTCCSLLRSASPSSAANMP FSSSTSSSTVSWLSLSSSLSSCFLSFR FGNSSCMSFSIIIPFVRPEDWKRMLL AK*GPLMALMLCALFFSSSRLKPL FMSTTILSLKYG GGVQDVG GWQ
1670	7167	A	1796	429	1394	TISFEADHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFNHW LKVPEAKLTDYLFVDRKLFGLMP LLDDIEDNSKLPTWAFPVASHIYGI PSVINSANYVYFLGLEKVLTDHPD AAKLFTRQLELHHGQGLDIYWRD NYTCPT*EYKAMELQKTGGLFGLS KCLKHIVSDYQEYLKPLNLTLGLFF QIRDDYANLHSEYSENKSFCELT EGKFSFPTIHAIWSRPESTQVQNILR QRTENIDIKKYCVHYLED\EGSFEYT RNTLKE\EA KAYKQIDARGGEPLS LVA\LVKHLK*RCSKEGKWNV
1671	7168	A	1797	145	172	GGCLLESVDTS HGQSLISASLNTK HPTGMHSTCWFHVELCGKGLGRH TLKQHQSFA*SMPPA/PPAPCHIVP\QE PTS*VHPCWVFCVETG
1672	7169	A	1798	197	378	VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET
1673	7170	A	1799	32	377	SSMPPTPGPSILSSLVPIVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKGS GFCF
1674	7171	A	1800	168	224	
1675	7172	A	1801	224	527	CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRPDKYEYDNK*FIEIKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW
1676	7173	A	1802	22	430	SPGCRRAESEKSQGSERGVGPSYRI WVGSKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDYRSHVCSGDGCTKVSEITTKN LFM*PKTTCTPKTTE
1677	7174	A	1803	386	511	
1678	7175	A	1804	362	439	
1679	7176	A	1805	776	1376	GAPWAFGGLPWVHGLAKEGVTA VI

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						AEHGLWNIGVHEGHGTLQLQHMH HYAVALRRHPFIQAQAQRGVLAG GGMGTRRE*VRARGQPRVHSNNCH TGQNRYTSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVFVHFPGLSHIGEEHGL RGQLSTV
1680	7177	A	1806	420	508	
1681	7178	A	1807	735	841	
1682	7179	A	1808	796	1123	IQWICHNTISAPKNYLEISPHINNKQ F*KKI*KHFPPA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS
1683	7180	A	1809	137	303	
1684	7181	A	1810	122	385	YPALEHILKAQAIQSRCGDSCLPPS APWDHPGPTTP\SPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG
1685	7182	A	1811	77	1181	PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQFTLTADV*RSPKKSRSRPRE SPKKAKKLEVIIGKPGSSSF*QRIR KRERTPATRA*SQ\KREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSDR KGDRDRDREREKENERGRRDRD YDKERGNEREKERERSRERSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRERSRERKHSRERSR NAGKRSRERSKEKSSKHKNESKEKS NKRSGSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND
1686	7183	A	1812	1	585	PLKRSDDGNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEKSAVTAL WGQA*TWKVGKGALGK/RCWVV LPWDPKRSFEVLWGNLSQLPDVAVN GANP*R*KASMAKEKVLGCPLVNG PWLTHWTTLKGHPLPHEVSLHCD KLHRGSLKNFRAPGATVGLGCCLA HSLLAKEFNPNKLQGLPIQEKLVGW VVG
1687	7184	A	1813	505	671	QKNKVYFFFETYEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPCLC
1688	7185	B	1814	277	480	GTGHFYGRTPSDTNCQEYTHRKL CQIKSKADLVLMKNSKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ*
1689	7186	A	1815	32	1386	VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSSRGVYSAYQAP DIHECCHFRSASFFLDKMATPAVPV SAPPATPTPVPAAPASAPASVPAPT PAPAAAPVPAAPASSSDPAAASAT TAAPGQTPASAQAPAQTPAPALPG PALPGPFPGGRVV\RLHPVILASIVD

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						ISYERRNEGACPS*SGTLFGKLVDK/ HSVE\VTN\CFSVPHNESEDEVA\VD MEFAK\NMYETGIKKVS\PNKLILG/ WYATGHDITEHSVL\IHEYYSREAP NPIHLTV\DTSLPGTGRMSIKA\YVST LMGIPLGRT/LWGVMTPLTV\KY/ AAYDTERIRRLTLIMK\TCF*PPTRV WTSQVDLQQEGGGIQLRNPMPPLS TSVANMPEGCTCLGKVSADNTIRK VGHFLMSL\VN\QVPENRKPMTFET MLNSNINDLF\MTYLANLTQSR\IA LNEELVNL
1690	7187	A	1816	273	748	VIQNLFNKMDVGTGQVRVVHACNP RHFRRRLRQEPKSGVQDQPDQHGET PSLLKIQKLARR/GGVVHL*SQLLRR LKQENRLNPGGGGCSEPRSHHCTPV *VTQ*DSVPPAPRKKKMYVVLTKK FHIWHISFTLPNIKRSDSLRNRKVT NFSCYCSKVS
1691	7188	A	1817	1	406	LCQLETYPPISQCTASDFPGPVTAS WAIQEAARSQAKAGA/GSATLS/M AYAGARFVFS\LDAMNGKEGVVE CSFVKSQETECTYFSTPLLLGKKGIE KNLGIGKVSSFEK\MISDAIPELKAS IKKGEDFVKTLK
1692	7189	A	1818	1	1222	FRQRAGAGQCGRWWSHFRVTSSCA CYVDAPPAPAMLSALARAVPSACS/ LARSFSTSA\QNNAKVAVLGASGGI GQPLSLLLKNSPLVSR\LTLYDIAHTP \GSGPQDLS\HIETKSR*KA\YLGTV NSLP\DC\KGL*WW*VIPAGVPTKP GMDRD\DLFTTNATIVGTLTAACAQ HCPEAMICVIANPVNST/ISPITSKK VFKKA\WGQHPQKKSSGVTTLNIVR AKTFVAELKGLDPAGVNVPI\TGGH AGKTIIP\ISQVHAYDPVRGFECTPK VDFP\QDQLAALTG\RIQEVAGTEVV KAKAGA\GSATLSQCRNAGARFVF SLVDANELEKERCLWEC\SLPLSPQE TECTYFS\TPLL\LGKKGIEKKKAKT/ LGIGKSLPFEEK\MISDAIPELKASI KKGEDFVKTLK
1693	7190	C	1819	876	1124	MALGLRQRGIVSLAASITGPCPMSP APSHPGTQVLLPTKRHPQVCLSHTC VEMRQVTKRLSAFKVRNKPDRFY SALLCSTE*
1694	7191	A	1821	103	483	
1695	7192	B	1822	1	798	MAFLDNPTIILAHIRQSHVTSDDTG MCEMVLIDHDVDLEKIHPPSPMGDS GSEIQGSNGETQGYVYAQSV\DTSS WDFGIRRRSNTESPKEPEQLRNLFIG GLSFETTNEKRS\HCEQWGTLPDCV VMKDSNTKRS\GGFGFV\TYATVEEV DAAMNARPHKRRKYP\LLGKNTN DKQLDLGPEKGRKHALNCHRMKP ALFSVLCEIKEKTGGATQAFAKENN QKAYKETYGVSHITRHDMLQIPKL AQNEKSQVPSIRSIQRLKII*

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1696	7193	A	1823	3	545	
1697	7194	A	1824	1	440	VYLHLHSSQDRLLPMTVVMTASAR VQDLIGLICWQYTSEGRKPKLNDN VSAYCLHIAEDDGEWTHDFTLLDS NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVRINAAHGFSLIQVD\TQKVT MKEILLKAVKRRKGSQKVSACD
1698	7195	A	1825	293	2142	GNWPTERMAFLDNPTIILAHIRQSH VTSDDTGMCEMVLIDHDVDLEKIH PPSMPGDSGSEIQSGNGETQGYVYA QSVDTSSWDFGIRRRSNTAQRLER LRKERQNIQCKNIQWKIERNKQS AQELKSLF*KKNLSKEKPPISGWKQSI LSVRLEQCPLQLNPNFNEYSKFDGK GHVGTATATKK\TDVYLPPLHSSQDRLL LPMTVATMASARVQDLIGLIC*QYT SEGREPCLKDNVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVRINAAHGFSLI QVDNTKVTMKDILLKAVKRRKGFQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPISIDSDLLCACDL AEEKSPSHALF*LYL\SNHDYKHS TFESDAATANEIVLKVNILAESRAS TAR\ADYFAQKQKLEQTVRAFSEFQ KEKEIPGSIEQLAFQPIQILVPVASEP ACPGPSALRSPPGVLKSFGGEAHPL GPLGTGAGGLFGEGVGGPLRREAA GDIA MGRKFALAMGF
1699	7196	A	1826	436	917	RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARDCNPNTVRLKWEDHLSFG I*DQPGKQ*DL/PSLQKNKKLPRHGG WTLWSQLLGRLRWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA WVF CFFVEMQVSLFS RLVSNWAQVILPLQPHSVGIAVTS HCTQPYVIL
1700	7197	A	1827	46	573	SQTPMGHFTEED\KATITSLWGK\N NVE\ DAGGE\TPGKGS LVVYP\WTQ RFFD\SFGNLSSASAIHGQTPKVKAH G\KKVLTFLGTMP TKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNPIFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP
1701	7198	A	1828	1	388	
1702	7199	A	1829	75	520	TPERGSAYPRLLCGAPPGEATVIM SDQEA KPSTEDLGDKKEGEYIKLV IGSGFSEIHFKVKMT\HLKKL*ES YCQRQG\VPMNSLRFLFEGQRIAD\ NHTSNKNWGMEEEDVD*SFFREQT GGSFQQFRIFLFFFLSKSFFIF
1703	7200	B	1830	78	236	MSYIPGQPVTA VVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT

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						DK*
1704	7201	A	1831	67	587	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALGQ IGDKIMQVNGWDMTMVTHDQA RKRL\TKR\SEEVVRLLG*RGSRMQ K\AVQQSMLFLRQPPSCDSCPLPLC TVTPLPHSGPHLASADRWAPASEGL
1705	7202	A	1832	3	420	HSLSGTSEVINKLLVQTPMGHFTEE DKATNTSLWGK\VNVEDAGGETLG RLLVVYPWTQRFVDFSFGNLSSASAI \MGNPKVKAHGKKVLTFLGEMPLK HL\DDLQGAFFAQA*SELALVDKPA MWD*GTSKLLGEMLLG
1706	7203	A	1833	3092	3227	ERQ/WPGTVAHACNPSTLGG*GGG AGIT*GQEFKTSANTVNPSSL
1707	7204	A	1836	3	1088	SMAA VAAESACICRWRRCSTGQF EELLRLKAKSLLVVHFWAPWAPQ\ CAQMNEVMAELAKELPQVSFVKL EAEGVPEVSEKYEISSVPTFL\FKNS QK\DRLGWVHMPQELTKKVQADM HLSGLLPTQALMEHL*RKILQPFGL EGNLTSWLAPLAWLFYWKGELPSK EPR\CGFSK\QMVEILHKHNIQASSF DIFS\DEEVRQGLKAYSSWPTYPLA\ YSGGELIGGLDIIKELEAEELDTICP KAPKLEERLKV\TNKASVMLFMK GNKQEA\CGFSKPNKGYLNSTW C*NLETFRILEDERKFGQGLKSLTP NWPNIPLSLYVKGEVLVGGGLDIVKE\ LKRKLGEFAAL*LRGEN
1708	7205	A	1837	3	703	VEFFSSQRAELYATPLTPAPGPNGGI PGWTLWLALPRPGNLRKGPGLSL QEVDEQPQHPLHVTYAGAAV/DDE LGKVLTPQVKNRPTSISWDGLD/S KGKLYTLVLTDPDAPKQGDPKY RE\WHHFLGWSTLKGQMTSATGTV LS\DYVGLGGLPKGTGLHR\YVWL \YEQ\DRPLK\CDEPHPSATRS\GDHR GKIQRWASLPVKK**SSRAPGGWAP CYPQPEVGMNQCAPKL
1709	7206	A	1838	717	1390	ASTTTSSVHCARTYMGSVYNTPAR VRLRVGWRAADQLLLAASSTSAAI VSTRALECAKMQNAEADATLVFI GYVVPALATLYAAGATLPRSAGKD TPPGTGDHGPAGALGTQAAGGHRV HAVWALDATLSDPAGAHGHHLAR EARGCTLPGGYCTL*RISPNSWPSA AL*HHFSTAT*TRASPASNG**KSC PAG/APALLPGPHGGAAGAGVGGP ALLGET
1710	7207	A	1839	1	310	RTSPHSPRNILLLS/EPENADSLMLV DFEYSSYNYRGFDIGNHFCEWVYD YTHEEWPFYKARPTDYPTQEQLH FIRHYLAEAKKGETLSQEEQRKLEE DLLCM
1711	7208	A	1840	3	375	HYLAEAKKGETLSQEEQRKLEEDL LEMYSLKDEMGNLRKLLSTPSPV

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						VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPPESETE VQETGLFLSLSRSPWLAGQSPVLCM
1712	7209	A	1841	94	429	
1713	7210	B	1842	96	979	XVGEEPREVLLRLYGAILQGVDSLV LESVMFAILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLLPKAPPPNPT PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVL SAAIATKMAQFHG MEMPFTKEPHWLFGTMER*
1714	7211	A	1843	5	1463	PEKPRPAGRGAERGRKEPSPSESG AHPGLGPGRRARAMAAEATAVAGS GAVGRCLAKNGLQQSKCPDTPKR RRASSLSRDAERRAYQWCREYLG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSL VLESVMFAILAERSLGPQ LYGVFPEGRLEQY/IPTSWVQSRPLK TQELREPVL S/QAIA TKMAQFHGM EMPFTKEPHWLFGTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDE\MGN LRKLESTPSPVVFCHNDIQEGNILL LSEPNADSLMLVDFEYSSYNYRG FDIGNHFCEWVVDLYSSEE/WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPPRRSQKNWKE\DLL VRKSSRVMFQSHFLWG\LSILQ\A ASMSTIEFGYLDLCPSLRFQFLLPS KKGQA*PSVHSCILDSTLPLLGFLLE PPGQGPWRGGTTSRRPWRLG
1715	7212	A	1844	143	762	CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLP GMYPALMYQ MYKSRRGLKRSEDSKETYELPHRLI EKKRRDRINECIAQLKDLP EHLKL TTLGHLEKAVVLELTLKHVKALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKYIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNNFFFL
1716	7213	A	1845	203	1507	CRQERAVAPARRAMERIPSAQPPPA CLPKAPGLEHGDLP GMYPAHMYQ VYKSRRGIKRSEDSKETYKLPHRLIE KK\RRDRTNECIAQLKDLP EHLKL TTLGHLEKAVVFE\TFEH/V*KALT NLNLSSSRQKIAL\QSGLOAGELSG RNVETGQEMFCSGFQTCAREVLQY LAKHENTRDLKV FASLSTHLHRV VSELL\QGGSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTD\DSGYGGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQEESEPPTKKNRMQLWDD\EGP FQLASDLNQLPPFGPTPQHQPFFCL PFYLIPPSS/ATAYLPMLEK\WYPTS VPVLYPGLNASAAALSSFMNPDKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD
1717	7214	A	1846	628	1061	AHRKSLYLCEACFPRSRASQETSGL

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						KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPKNSREQGFNDPVGQSV EPLEQLFPWEWQWPAQAQDREL
1718	7215	A	1848	88	953	FQAPQLCYDSAFMISSVPSPHILRV EFPCFHAHLRVCEFPFHAHLVCVE FPCFHAHLVCVEFPFHAHLVCVE PCFHAHLRVASVNFRAHLVCVE FPCFHAHLRVCEFPFHAHLVSVN FCFHIHLVCVEFSCFHAHLRVCEFP FHAHLVSVANFRVFTPTCASVNFV FTPTCVCEFPFHAHLRVASVCEFP CFHAHLQVVEFPFHAHLRVCEFP FHAHLRVCEFPFHAHLVCVEFP HAHLVCVEFPFHAHLVCVEFP AHLRVASVNFRAHLVCVEFP HAHLRVCEFPFHAHLVSVNFCFH IHLVCVEFSCFHAHLRVCEFP HLCVSVAN/CPCFHTHLCVCEFP HLCL*ISVFSRPPASVCECL/CN/CPC FHAHLQ/CL*ISVFSCPPAGL*ISVFS CPPACL*ISVFSCPPVCL*ISVFSCPP ACVCEFLCFHAHLVCDFPCFHAH QSATVLV
1719	7216	A	1849	1	254	
1720	7217	A	1850	3	308	
1721	7218	A	1851	1	380	IPTPLIGNFGPRGPRIRHERPQKRDD RREPSSFGRKRRQ*DGTLRCRRCGS/ KA\YHLQKSTCGKCGYPKRKRKY NWSAKAKRRNTTGTGRMRHLKIV/ YRRFRAWDFREGTTPKPK*GSLQHS SSSS
1722	7219	A	1852	41	544	APSPRRPWGHFTEED\KAT\NTSLWG K\VNVE\ DAGGE\TPGKGSVVYP\W TQRFDSFGNLSSAF\AHGQTPKV KAHGK\KVL\TSLGDAIK\HLDLKG TFAQA*VNLHL*QSCNVDP\ENFQA PGEMLLVTR/VLAIHF\GK\FTPGGC KASWAEDG*LAVGQWPCSSRYH
1723	7220	A	1853	145	705	SWRNRTVSNGSAVSASSVHLCFAE CKALCGERILTDGSDVSRPTIAAGG CNGTVKYL*QEV\KTAPL\HDGP SHVGIPRSCPKPLDKRAHLVCLAS \NCDEPTMYVKLVEAL\CAEQNQ *LRVD\DNKKL\GEWG*GLLLKFDR GGGKPRKSWL\GSCFS*FKDY\GK ESQAKDVIV\EFKCKK
1724	7221	A	1854	110	776	SLASGPYL\THQQKVLGLYKRALRH LEISWCVQRDKY\RYFACLMRAR/ EEHKK*KRIWAKATQ\LKEARGKN FWYPVKHPKSQYILPLTSPGGHPP Y*EDHD/CAYKVPRIGCL\DWHP EKAMYPDYFCQRREQWKENLRR GKAWGTEGLSSLQ\ETP\PG\GPL TESFAPWPEKGD\LPLW\WYIVT RPRERPMLEERPHLSCLQVKYVT EHGTCP

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1725	7222	A	1855	1	858	
1726	7223	A	1856	165	856	PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIW\FFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGKRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGPNPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKCAREPLQCGFPGN LDPLSSILLGRREGIQMV\LCANQV\ VNGPPWGTLCGGTCQCCGCCGG\D GPVLNLRA
1727	7224	A	1857	163	1322	PGPYCGPVATMSLHGRRKIEIKYE APWTVYAMNWSVRPDKRFRWALG SFME\EHNNEGYLDGLDEERS*VVS KNILDRPYPTNKVMWIPDTKGVPY DLLATSGDYLRVWRVGETETRLEC LLNNNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDKIEVYDIAF SRAGGGGRDMFASVGADGSVRMFD LRHLEHSTIYEDPQHHPLLRLCWT KQDPNYLATMAM\DGMEVVILDV RVPCTPVARLNNHRACV\NGHLLW\ APHSS\CH\CTAAG*PPGFSSWD\NQ QMPRA\IEDP\ILAYTAE\GEINN\Q\ W\SNSAPNWESPIC\YNNCPWRYS ECSVGGAVPHEAGAFVFPASAPPK
1728	7225	A	1858	1	420	REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTL EEQG VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQRTYRGL* ILAKRAAETVVDPEMTP
1729	7226	C	1859	28	156	MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPKPGLV*
1730	7227	A	1860	1	315	
1731	7228	A	1861	1	119	
1732	7229	A	1862	1	1477	
1733	7230	A	1863	3	1866	PLQSGHSAGRGGSGVAQGW HKKK YLQAKMTKFLREERIQWKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPPRLKK\DRKNLLET RLHITGRELRSKIAETFG LQENYIKI VINKKQLQLGKTL EEQGV AHNVKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQRTKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKLNLAQKCFKNICYGENHQ RLVHIKGNCGKEKVLFLRLYLLQGI RNYHSGNDVEAYEYLN\RHVSSLKS YILIHQKWTICCSWGLLPK HRLGL RACDGNVDHAATHITNRREELAQIR KEEKEKKRRLENIRFLKGMGYST HAGQ\QILLSNPQMWWLND SNPET

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						DNRQESS\SQENIDRLVYMGF\DALV VAEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEIIIAEYLSYVENRK SATKKN
1734	7231	A	1864	1	727	MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTTLFSPGGGGGAKAT AAAGAGLASPGMKTNGGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPGQWWSGRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGATIEVF LPPRLKKDRKNLLETRLHITGRELR SKIAETFGQLQENYIKIVINKKQLQLG KTLEEQGVAHNVKA\M\VLKQSE EDARKNFQL\QEEEQNEAKLIEERL QRTKRGLEILAKRAA\EPVVPEMT PYLDIANQTGRSIRIPPSERKALMLA MGYHEKGRAFLKRKEYGIALPCLL\ DADKYFCECCRELLDTVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKNCYGENHQRLVHIKGN GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLNHRVSSLKSYILIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAATHITNRREELAQIRKEEKEKK RRLENIRFLKGMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVA\EAALRVFRGKVPVAAQT PAYNGGSL/PFPELPLSAEDSLSPAT \SPSDSAGTSSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEIIIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQHQCLAP RFPVRLGTSPGQWWSGRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGATIEVFLPPRLK KDRKNLLETRLHITGRELRSKIAETF GLQENYIKIVINKKQLQLGKTLEEQ GVAHNVKADGCLN
1735	7232	A	1865	1	513	PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPRNLAAAVEE QYSCDYGSGRFFILCGLGGIISCGTT HTALVPLDLVKCRMKVDPQKYK GIFNGFSVTLKEDGVRGLAKGWAP TFLAGYSMQLLQVLAFYEVFKVLY
1736	7233	A	1866	2	1296	ALCEPQPFQSGSCVAILGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG TTHTALVPLDLVK\CRMQVDPQKY KG\IFNGFSVTLKEDGVRGLAKGW APTFLGYSMQGLCKFGFYEVFKSL\ YSNMLGEVENTYL*RTSLYLAASAS\ AEFFADIALAPMEAAKVRIQTQPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTVE A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSP\PEFLG*P VLD*GKKVSCFLWVLQRDLGFK\ GV\WKGLFARI\WIGTLTALQWFI YYSVKGYFR\LRP\PPP\EMQES\LK KKLGVNSVVR\KANCGLNLLVDPV FEESAKGTFIYLTV
1737	7234	A	1867	127	433	RPLESWIGLVRCNICRSPIAEAVFRK LVTDQNISKNNWRVDSAATSGYEIG NPPDYRGQSCMKRHHGIPMSHVARQ DLNRKSNRVKTKAKIELLGSDP QKQL
1738	7235	A	1868	2	535	
1739	7236	A	1869	551	1299	PADPPRPSYYRHRTTPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVTDQNISKNNWEGRQRG NFRWVIDSGAVSDWNVGRSPDPRA V\SLRNHGIHTAHKARQITKEVFP TFDYILCMDESNL\RD\NRKSNRVK TCKS*KFELPWEL*SPQKQLIEDPY YGE*LWTLETVYQQ\CVR\CCRAFL EKAH
1740	7237	A	1870	85	563	SSF\DIVHVCNTPNVKKMVSGSSHK VIQEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSETQIYLGWQV KIGFPNF*NPVAGILDRTKYRIFP*AP GIHKLKGYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK
1741	7238	C	1871	604	804	MKRLRHLRXINN\AKITQPLSKTAL NLSPTQGGSKSRAILEFQLSRGPVN PTLNWPSLNPFREPE*
1742	7239	A	1872	64	73	AFL*RWGSPPCCPRAGLK/PP*P/PSI CPPRPPK\GAGITRREPPGQAYFLII*F PSI*L
1743	7240	A	1873	47	225	NSHHVRGRPRCADSSSPSGDRGQPE AQPAPDSSAPEHAQEPGRAAVKRP DL*SHMTRRP
1744	7241	C	1874	101	232	MTMITPSSKLT\TKGNKSWSTAVA AALELVDP\PGCRNSARGF*
1745	7242	A	1875	66	723	AILI\LLSSEGLWSSDQHRLVGVDQS PPQGS\LCCHFSAMATSEQSICQARA SVMVYDDTSKKWVP\KPG\QQGFSR INIYHNTASNTFRVVG\VKFQDQQ\V VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTFSNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEF\ERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPVPPPTGA\TPPPPP\PL\PAG GAQGSSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGLMEEMNKLLAKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKAASQSDKPAEKKEDESQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAKGPR KLRAFPSQQPHSRMKPAGSVSDMA \LDAFDLDRMKQEI*KEVVRELHK GERKEIIDVAIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPRLM
1746	7243	A	1876	1	668	GERGVARHDRPRGTLREYKVVGRCLPTPK\CHTPPL\YR\MRIFAP*SMSSL SPRF\WYFVSQLKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRL\YDS RSG\THNMY\REYRDLDPHPQAPVHP SCLTRDNGVAPAPAA\HEAHFHFRI ERLEE\AGQQDCRRPGCSKQFPRI RKFPAAPPGLRRQDKPRF\TTKRP KTFLKVQGPSSGVCQNKQTETPR
1747	7244	A	1877	1	1059	
1748	7245	A	1878	87	260	
1749	7246	A	1879	1	1254	
1750	7247	A	1880	160	615	PSLNTYVTSPLSENFSARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSVNIHTACIIDVFGVW HRESIMNVNVKGRVAWGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFSFIDEKTRT EQ
1751	7248	A	1881	53	1338	CPLQGHPRVTLESDDLPSIFCFLVSD SCYFGLATMGWSCLVTGAGLLGQ RIVRLVVEEKELKEIRALDKAFRPEL REEFSKLQ\NK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIQNG HEEEPLENTWPAPYPRSKKLAKKA VLAANGWNLK\NGGALYTALRPM YIYGEGRFLSVSINEALNNGILSS VGKFSTVNPVY\GNVAWGHILAL RALQDPKKAPSIRGQFYISDDTPH QSYDNLNYTL\SKEVFPPLDSRWAS FPLSLMYWIGFLLGNR*GFL\RIY TYRPPFNRISSHCSN*ALFHLLFIKE GFSEILGVLRLP\TAGGGKAKAGKR VGSWWVPFVDPAQGRNLEVPRIQ
1752	7249	A	1882	3	575	HSLFGTSEVINKLLVPDAMGHFTEE D\KAT\ITSLWGK\VNVEDAGGETP GKGSLLVYP\WTQRF\FD\SFGNLSS ASAI\MGKPPKSAHGK\KVLTFGLT MPTKHLE*FSRGTFCPSLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP
1753	7250	A	1883	1	960	GRPAPEGGPLSLPNAAMARGPKK HLKRVAA\PKHWMLDKLTGVFAPR PSTGPHKLRECLPFII\LRNLKYA LTS\DEVKKICMQRFIKINDGQVR\TD ITYP\AGFMDV\SIDKDGREFSVL/Y LIDTQGVRFCL*HRITP*GRAKVQSC AKMRKILLWAPKGIPSSWVTHDAR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NHPATPDPPSSKVN*YHFRLDLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITN\RRERHPGIF*PLVHVK \DANGNKLLATSDFSNIFWLLGKGN KPWISL\PRGKGIPPHLLLEERDKRL AAKQSSWVKWGPWVTWSDLLVP
1754	7251	A	1884	1	1218	FFQNSARGAGAGWQLPWTRFVWT SGLLEINEVLVIQQRGVRIYDGEKI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQIVFIEEQ\AAGIGKSAKI VVHL\HPAPPNKEPGPFQSSKNSYI KLSFKEHGQIEFYRRLSEEMTQRRW ENMPVSQSLQTNRGPPQGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHM\QAKQLA\WNIA RVPLEERGIMSLTEVYCLVNRARG MELLSPEDLVNACKMLEALKPLR LRVFDSGVMVIELQSHKEEEMVAS ALETVSEMGSLS*EFAKLVGMSVL LAKERLLAEKMGHLCRDDSV EGL RFYPNLFMTQS
1755	7252	C	1885	179	361	MPKVCFVHNLKTSSERDLFALMN TVGKKHSIMSEKGRSKKFLHLIDSK KNEDPHLDGTL*
1756	7253	A	1886	2	913	RRLLLFGWARGAVSLGSAGVSSS GFLTAPHSSRLTAAAAAAGGAWRF EAERHRGWGAEEEQPEGGAVCPG TERPCAMAYAYLFKYIIIGDTGGGR\ SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIKLQI\WDTAGQES\ FRSITR\SY\YRGAAGALLVYDITR\ DTSTHLTTWLEDA\RQHSFQHGGS LCLLGNKSD\ESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSCKNCFPM* KEAFINTSKRNFIKIQ\EGVFDINNE A\NGIKIGP\QHAATNATHAGNQGG QQAGGGCC
1757	7254	A	1893	138	426	FIHSHCCIVFRLFIHFSLHPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFV*V YTFPF\GINPKKGIARL*GVYIFSFSIY CQTVFQSDCKKAPF
1758	7255	A	1894	45	1057	FLVFLVETGFHHVAQAVLELLASSD PPALAPPKCWDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFSCLSLSS SWDYRCMPPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA/FPKCW DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKTTSHLPTKEALT W/VSHATAKHLWILVSILMEF*VA LIS/SFFLPGGK*T*VTAPQCPSLGQ DTLS*FLHAACRSVPYPGLA/CGPS LWLTRVLLPTPP*QQHNP/DTLEKT SFPGPHWIL*/TPQPSLSETPAPKVPP FFAFGSIPTHEEPGLP
1759	7256	A	1895	2	289	

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1760	7257	A	1896	1	397	
1761	7258	A	1897	1	410	STMISPVLILFSSFLCHVAIAGRTCPK PDDLPFSTVVPKTFYEPGEEITYSC KPGYVSRGGM\RKFCPLTGLWPIN TLKCTPRVCPFAGNLRKMGAVRLIT DFLNYSPTRFSSLLTWGFILEWAL DS\AKCIEGG
1762	7259	A	1898	19	1215	CQCDSSSTMIFSRCSLSSFLCHVAI AGRTCPKPDDLPFSTVVPKTFYEP GEEITYSCKPGYVSRGGIEESLSCPL \TGTVGPFNTSGNVTPRVCPFAGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSCTGGKGK\WAS P\ELPGLVAPI\CPP\PSIP\TG\ATLH VLLRPFRLGNNSPPIGDTAVFECLA HNAMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFPHQDPDNGIW*TYP CQNPNTLFTRVKAPHLGLPHDGIFS GMGPRKE\NEC*PQTW\GKPGSWPLA PSW*KPSLVKGT\PKRPTVV\Y\PQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\DA\SDVKPC
1763	7260	A	1899	58	446	
1764	7261	A	1900	1	954	MGEVSGTSDCTDDQCRQVKKALEG GKAARGHRSKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA VIERLLNGHAKILEVDLKNYGFVE FDDLRLDADDAVYELNGKDLGGERV IVEHARGPRRDGSYGSGRSGYGYR RSGRDKYGPPTRTEDRLIVEN\LTSR CSWQDLKDYM\RQAGEV\TYADAHK GRQKMKGVIEFVSYS\DMKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRSRHSRKSRSRSGSS KSSHSKSRSRSRSGSRSRSKSRSRSQ SRSRSKKEKSRSPSKDKS\RSRSHSA\ GKSRSKSKDQAE\EFQ\NDNV\GK PKSRSPSRHKS\SKSRSRSQERRVEE GRKRGSF*QGQ\EAQEKSLRQSRSR\ SRSKAGSR*PVDRSRSKSKDKRKR KRSREESRSRSRSRSKSERSRKRGS KRDSKAS\SCKKKKKEDTDRSQSR PSRSV\SKEREHA\RSLESSQREGRG ESENAGTNQEDPGPGPRSN\SKSKP NLPIRMHRSKIKSQASKTPISGPM SR\ASRSP\SRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP
1765	7262	A	1901	3	180	
1766	7263	A	1902	227	440	GMHNVCIYAVNE*FCGFIIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMA\$PVAGSWSHFPEREF
1767	7264	A	1903	2	438	HEELDTSERKIEFDSASGTYTLYL\I GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLFTPK\QEIQWIRI GA\NV\NFTFAP\STIIFH\LGHA\AM LGLMYVYWTQLNMF\QTLKYLAIL GSVTFLAGNRMLAQQA\VKRTAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1768	7265	A	1904	1	1660	
1769	7266	A	1905	156	2369	PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFGLRRDLLGGMAPP SSTVFLALTIHASTWALTPHYLTK HDVERLKASLDRPFTNLESAFYISV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYAAQA\SQGLSGCEISISN ETKDLLLA\AVSE\SSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQKQKTVLA\TVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQFEEGLETTALFVAATYKA /LMDH\VGTEPSIKE\QVIQLMNAI FSKKNFESLSEAFSVASGAAVLS HNRYHVPVVVVPEGSASDTHEQAI LRLQVTNVLSQLTQATVKLEHAK SVASRATVLQKTSFTP\VGIVFELNF MNVKFSGG*CDFLVEVEGDNRYSIS NTVELRVQDPPTVEGITNVDLSTV DKDQSIAPQTRVTYPAKAKGTFH SAGQATRNFGVLSSW*DVNTGAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSEKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVIKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPPWCP NTFTAPESFFGPLL/LCFLRLWIRD WVPKCLPTFTFCFLSTHIFHPWDM AYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH
1770	7267	A	1906	37	404	PQLSRCRSECMYVNPTVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1771	7268	A	1907	271	1086	YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAAVALLQPFLV TKEAFDR*ACEGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVARGLIARGVPTGPS*NVSSQC FPAGQ*TNHSVLLPTKGVPDMLD QG*WAL\ELGPHKLSRCSGVNA\N NPHSGG*RSMGPGPPWSDPHKAKI MLNRIPLGKFAGESEVEHVNAVL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT
1772	7269	A	1908	2	305	AREGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHE\ECMPYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A
1773	7270	A	1909	2	529	GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSN FYSVFEGELSDTIPVVHASIACRIG RMCVGVTEILADV LKVEVFRQTV DQVLVGSYCVFSNQGGLVHPKTSIE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DQDELSSLLQVPLVAGTVNRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE
1774	7271	A	1910	18	889	GVQGTVAACGACYWLLGLMAVRA SFENN\CEIGCFAKLTNTYCLVAIGG SENFYSVFEGELSDTIPVVHASIAG CR\NGRMCVGNRHL\VPNNTTD Q\EL\QHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWEVFRQ TV\ADQV\LVESYCVFSNPGRWVP SPRPFQ*RPRNELSSISFKVPLVAGT C*TKGSEVICLLGMGGMNWC\FC GPGTPNPAQSCQVVEECLQS*NEAP ALAPIANRACGNSL\IDSLT
1775	7272	A	1911	132	440	
1776	7273	A	1912	149	389	FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYNYNVLMVPKPQGGLP NTALLSLVLMAGTFFFAMMLRKFK NSS
1777	7274	A	1913	3	153	
1778	7275	A	1914	94	593	LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYNYNVLMVPKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKNS SYFPGKLRRVIGDFGVPICLIMVLV DFFIQDTYTQKLSVPDGFKVSNSSA RGWV\HPLGLRSEFPIWMMFASAL PALLVFILIFLESQITT
1779	7276	A	1915	115	3015	TTGHSGPRHGGAAGGCSLASAVLP PGGSGDLVLD SYLRWGKSPSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPA AHDTEATATDYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAAPLR\QDENLGENGAW GRPHLSHLTFWSLLELRRVFTKGT LLDLQETSLAGVANQLLDRFIFEDQI RPQDREELLRALLLKSHAGELEAL GGVKPAVLTRSGDPSQPLLPQHSSL ETQLFCEQDGGTEGHSPSGILEKSP PDSEATLVLVGRADFLQPVLFVGR LQEAEELEAVELPVPIRFLFVLLGPE APHIDYTQLGAAAATLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDDPL QQTGQLFGGLVRDIRRRYPYLSDI TDAFSPQVLA AVIFYFAALSPAIF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL VVGFSGPLLVFEE AFFSFCE TNGLA EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFIS\RYTQ EIFSFLISLIFIYETFSKLIKIFQDHPL QKTYNYNVLMVPKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGVPI SILIMVLVDFF IQDTYTQKTSQVPDGFKVSNSSARG WVIHPLGLRSEFPIWMMFASALPC LLVFILIFLESQITTLIVSKPERKMKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GSGFHLDLLL VVGMGGVAALFGMP WLSATTVRSVTHANAL TVMGKAST PGAA\AQIQEVK\EQRISGLLVAVLV GLSILMEPILSRIP LAVLFGIFLYMGV TSLSGIQLFDRILL LFKPPKYHPDVP YVKRVKTWRMHLFTG IQIICLAVL WVVKSTPASLALPFVLILT VPLRRV LLPLIFRNVELQCLDADDAKATFDE EEGRDEYDEVAMPV
1780	7277	C	1916	20	202	MAAIKYLGISAILYYKYKCPRGQGN QPEELGTGSILCGNFSLGMLFPVQM YTVKKAYRAV*
1781	7278	A	1917	1	493	
1782	7279	A	1918	214	612	
1783	7280	A	1919	287	847	SDRPTMAPGVARGPTPYWRLRLG GAALLLLLIPVAAAQEP PGAACSON TNKTCEECLKNV SCLWCNTNKA CL DYPDTSVLPPASLCKLSSARWGVC WVNFDA LIITMSVVG GTLLLGIAIC CCCCRRKRSRKPDRSEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\ YGLFKEENPYARFENN
1784	7281	A	1920	61	515	
1785	7282	A	1921	1	2175	
1786	7283	A	1922	3159	3441	
1787	7284	A	1923	36	387	
1788	7285	A	1924	64	408	
1789	7286	A	1925	1	10514	
1790	7287	A	1926	64	601	VNNILGLGHTFWALLASPKMEHKE VVLLLLLFLKSGQGEPLDDYVNTQ GPSLFSVTKKQLGAGSREECAAKCE EDKEFPAGAFQYHSKEQQCVIMA ENRKSS\INRVRDAVLFGKGKCILF RVQDLGMERTTEGRC PKQKMASPC QKWEFHFS PADLGQTFPFIFVFIYCK VVPLCL
1791	7288	A	1927	173	491	AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQQVWREPPGPASK APHSPVGYSSPGHESHL L PGDDPA KDGSCPP\PFPLGIEAPVPGPRKRIR TCCCMN
1792	7289	A	1928	1	735	
1793	7290	B	1929	1	1026	MRARRLPWALT LVAELGWD TQGG DQTSPGGNDRMSMEAEC ESTTVSP LSCSIPTGCGQ TREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVLLL WPFHSSTLAKHKRIHTGE KPYKCEE CGKAFSR SSTLAKHKRIH TGEKPYKCECGKAFRQSSTLTKH KJIHTEEKPYKCECDKAFKRLSTL AKHKIIHAGEKLYKCEE CGKAFNRS SNLTIHKFIHTGEKPYKCEE CGKAF NWSSSLTKHKRIHTREKPFKCECG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFSR SSTLTKHKTIHTGEKPY KCECGKLLSTPQPLLNIK*
1794	7291	A	1930	1	2832	

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1795	7292	A	1931	98	3867	PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQNLYR NVMLENYRNLAFLGIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLLRKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKVFQCGKYL KVIFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TQHKCVYITEKSC KCKECEKTLWSASTLTNHKEIHTE KPYKCEECGKAFLWSSTLTTHKIIIC AKEKIYKCEECGKAFLWSSTLTRHK RIHTGEKPYKCEECGKAFLSHSSTLA KHKRIHTGEKPYKCEECGKAFLSHS ALAKHKRIHTGEKPYKCEECGKAFL SNSSTLANHKITHTEEPYKCKECD KTFKRLSTLTCHKIHHAGEKLYKCE ECGKAFLNRSSNLTIHKFIHTGEKPY KCEECGKAFLWSSSLTKHKRFHTR EKPFKCKEKGFIWSSTLTRHKRI HTGEKPYKCEECGKAFLRQSSTLT KIIHTGEKPYKFEECGKAFLRQSSTLT KHKIHSREKPYKCKEKGKAFLQFS TLTTHKIIHAGKKLYKCEECGKAFL HSSSLSTHKIHTGEKSYKCEECGKA FLWSSTLRRHKRIHTGEKPYKCEE CGKAFLSHSSALAKHKRIHTGEKPY KCKEKGKAFLSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTCHKIHH AGEKLYKCEECGKAFLNRSSNLTIHK FIHTGEKPYKCEECGKAFLWSSSLT KHKRIHTREKPFKCKEKGKAFLWSS TLTRHKRIHTGEKPYKCEECGKAFL RSSTLTCHKTIHTGEKPYKCKEKG AFKHSSALAKHKIHHAGEKLYKCEE CGKAFLNQSSNLTTHKIIHTKEKPSK EECDKAFLWSSTLTEHKRIHTREK PYKCEECGKAFLSQPSHLTTHKRMHT GEKPYKCEECGKAFLSQPSSTLTTHKII HTGEKPYKCEECGKAFLRSSTLTTEH KIIHTGEKPYKCEECGKAFLSQPSSTLT RHTRMHTGEKPYKCEECGKAFLNR SKLTTHKIIHTGEKPYKCEECGKAFL SSSTLNGHKRIHTREKPYKCEGCG\ KAFLSQSFN/TLTGHKRLHTGEKPYK CGECGKAFLKESALTCHKIHTGEK PYKCEKCKAFLNQSSILTNNHKIHT ITPKIHTREKPYKYKECGKSFNRSS FTKHKVIHTGVKLYKCEECGKSFF WSSALTRHKIHTGQPYKQEKFG KAFLNQPSHLTTR
1796	7293	A	1932	590	891	
1797	7294	A	1933	1	1527	
1798	7295	A	1934	13	1668	PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFL\GPHLVQSDGTVPFWA HAGIAISSDQIRVAPSLKSQSGSV WTKTK\AAFENWEVEVTRVTRGRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RJGADGLAIWYAENQGLEGPVFGS ADLWNGVGIFDFSFDNDGKKNPA IVIIGNNGQIHVDHNDGASQALAS CQRDFRNKPYPV\RAKITYYQNTL\ TVMIANNNGFTPDKNDEFCACKVEN MIIPAQGYFGISAATGGLADDHDVL SFLTQFQTEPGKEPPTPDKEISEKEK EKYQEEFEHFQQLDKKKEEFQKG HP\DL\QWQPAEEIFESVRDRELRLQ VFEGQNRIHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRGAGMPGQHG QITQQLDTPVVKTQHEILRQVNM KNSMS\EPVRLVSGMQHPGS\AGGV YG\TTQHFIDIK\EHLHI\VKRIDIDL VQRNMP\SNEKPKCELPFPFSCSLST VHFQ\IFVVVQTVLFIGYIMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV
1799	7296	C	1935	238	360	MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGPL*
1800	7297	A	1936	1	1656	
1801	7298	A	1937	83	260	
1802	7299	A	1938	1	678	
1803	7300	A	1939	1	1097	
1804	7301	A	1940	1	1706	MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSSRLDSLKRDIYAGKPQPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWWPCIME TLSNASGTFAIRLLKILCQDNPSHN FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLLEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIYFKGKWNEPFD ET YTREMPFKINQEEQRPVQMMYQE ATFKLA\HVGGLRAQLLELPYARK ELSL\VLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFE VNEEGTEAAAASSL\WVVAECCME SGPRFCADHPFLFFIRHTRANSILFC GRFSSP
1805	7302	A	1941	3	428	ETLERIKNNDPKLEEVNLLNNIRKIP IP TLKAYAEALKENS YVKKFSIVGTRS NDPVA YALAEMLKENKELKTLNVE SNFISGAGILRPGEALPYNTYLVEM RSDNQSQPPGNKVEMEIVSML\EKN ATLLRVR*HFSQQDAR
1806	7303	A	1942	1	1258	ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQTQTS SSTMSYRRELEKYRDLDEDEILGAL TEELRTLLENELDELPDNPALLPAG

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						LRQKDQTTKAPTGPFKREELLDHLE KQAKEFKDREDLVPTTGEKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSSIMNKEGLNSVIKPTQ YKPVDPDEPNSTDVEETLERIKNND PKLEEVNLLNNIRNIPIPTLKAYAEAL KENSIVKKFSIVGTRSGDGVAYAL AEMLKENVLKTNLVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHHFLKFGL PPYPSKEPRLRIASTAMMNTIALVR EURLAAPDLGPSFPKCRSGV
1807	7304	A	1943	2	382	EIAHQIEQQMG/EG*NFVAIESVV*K IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTPDAAGVNQLFFTPDLSAQ HLQDVIMGAVTCEGCKGFFKRSIRK N
1808	7305	A	1944	240	454	
1809	7306	A	1945	1	1851	
1810	7307	A	1946	128	512	TAPLAAGRPRGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYRRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL
1811	7308	A	1947	1	705	
1812	7309	A	1948	124	1583	IMATIEEIAHQIEQQMGIEIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTPD AAGVNQLFFTPDLSAQHLQLLTD NSPDQGPKNVFDLCVVCQDKASGR HYGAVTCEGCKGFFKRSIRKLVYS CRGSKD\CIINKHHRNRCQYCRLO CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLDSGMFMNIHPSG VKTESAVLMTSDKAESCQGDLSL ANVVTSANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLSD SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALGQEK QP*SLVKAYWNELFTLGLAQCWQV MNVATILATFVNCLHNSLQDQAKV IAALIHFTTRAITDL
1813	7310	A	1949	6	2028	KILRTLTPQKYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRSGRTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGIEIVTEQQTGQKIQIVTALD HKTQGKQVILTNDGSTPSKVILAR QDSTPGKVFLTPDAAGVNQLFFTP PDLSAQHLQLLTDNSPDQGPKNV DLCVVCQDKASGRHYGAVTCEGC KGFFKRSIRKLVYSCRGSKDCIIN KHHRNRCYCRLOQRCIAFGMRQDS

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						VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDSTLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNGDVSRAFDLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTDKEGPLLSDSHVAFRLTMP SPMPEYLVNHYIGESASRLFLSMH WALSIPSFQGSRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILATF VNCLHNSLQQDKMSTD RRKLLME HIFKLQEFCSNMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTPDDTYRLSRLLL RLPALRLDGCTITEELFFKGLIGNIR IDSVIP\HILKMEPADYNSPIIGHSI
1814	7311	C	1950	65	286	MDYCNTFLPSNPETVFGDIMPRVNK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIYP*
1815	7312	A	1951	15	82	
1816	7313	A	1952	2	1934	CVQAATSLSVGICPLPGPGSPPPWY PGVSVNVWIFKQIDDEGDLRLINK EVLSGVVVISSKDSVQHOGVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQQEG SEEAGGLSGAEALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGKVLVYETYHGVFVNIQYTLRC DMKRSLAKDLTKTCEFIVHSAPQK GKFTSPVDFTITPETLQNVKEHSQ TEAGQQRAFRFRSALRGGRLTAR ADNSSSNVAQGSQKSGHPCSRPSS VLPQQRQVCRVKRALLPKFLL/RRT SQLNKLCHHAATNGRAGGGELGSR HQKRGAAAGARGDPGQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCR\SYARDATEIQNIQIADGDVCR GLSVPIYMVFPRLFTCPTLETTNFKV GKWHSPSPHGPMPGRAAQROGLL WVTELRTCRPSVPQCQGLPQAIQLR ACCPSAQQNLVKELLCRTGDTPT GSPGACGTSTVTWGNTQTHISVDM GRPQPQVGTDSKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQGSPIAEESVEKESCLLK EFEVNIVVLLHPDHLITENFLKLKR I
1817	7314	A	1953	262	1274	ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMGTLDIKSKR ANKVYHAGEVLSGVVVVISSKDSVQ HOGVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFPS GKTEIPFEFPLHLKGNKVLVYETYHG VFVNIQYTLRC\DMKRSLAKDLT KTCEFIVHSAPQKGKFTSPVDFTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK

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						RGAAAGARGDVRVCR\SYARDAP\EQNI\QIADGDVCRGLSVPIYMFPR LFTCPTLETTNFKVEFEVNIVVLLHP DHLITENFPLKLCRI
1818	7315	A	1954	2	236	DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQPRAVPPRSM S
1819	7316	A	1955	760	925	HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRGGRITGGQEFKTSVANIT KPCLY
1820	7317	A	1956	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSASAIM GNPVKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAHFHGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLM MQSFQG
1821	7318	A	1957	41	638	APSPRRPWGHFTEEDQGLLSTSLWG KVNVEKWCWEKTPGKGSLLVYP\ WT\QRFFD\ASFGNLSAFAHHGQTP KVKAHGK\KVLTFGRCCQSTLDD LKGTFAQLSELHCDKLHVDPENFK LLGNVLVTVLAHFHGKDFTPGGC RASW\QKMGD*SGQCPVLQIPLSS LAPMMQSF\SRIRLLFLQAITNNKSISA KRSP
1822	7319	A	1958	3	227	
1823	7320	C	1959	171	366	MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEDVPLYPEW CMLWRYPASRPNVKRP*
1824	7321	C	1960	332	421	MEEKIFSQPGMVAPTCNPSTLGGQG RWIT*
1825	7322	A	1961	322	1145	RFSKSPD\SGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRAASADSSLPG CGRREVCGSRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEAADDSYGVVA GRWGRPVQDSRLGTAGEGIAGRES WGSVTSWVLGSHMVKFLVAELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML
1826	7323	A	1962	30	2814	LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSPRSPLEPM ARPRRAREPLLALLPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQGVRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALSFFVQALIRGRG DGDEVGVRCPPGVPLRPAPPERV VAVVGASASSVSIMVANVLRIFAIP QISYASTAPELSDS\TRYDFFSRVVP DSYQAQA\MVDIVRALGWNVYSTL ASEGNYGESGVEAFVQISREAGGVC

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						IAQSIKIPREPKPGEFSKVIRRLMETP NARGHIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAILPKRASIDGFDQYFMTRSL ENNRNIWFAEFWEENFNCKLTSSG TQSDDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDAFGRY DIFQYQATNGSASSGGYQAVGWQA ETLRDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCCWHCEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPPLL LAVLGIVATTTVVATFVRYNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGAAVCAARRLFLGLGTTLSYSA LLTKTNRIYRIFEQGKRSVTPPFISF TSQLVITFSLTSLQVVGMIWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDSLIGCLGYSLLMVTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGTAQSAEKIYIQTTLT VSLSLASVSLGMLYVPKTYVILFH PEQNVQKRKRSRKATSTVAAPPKG EDAEAHK
1827	7324	C	1963	334	387	MKCYIYIMTLVLLIV*
1828	7325	A	1964	1	489	
1829	7326	A	1965	152	717	VESIEDVGNHRTDHGADMISIHVEE ENAFILDTLAKKQWKGPDDILLGMV YDTDASFVWDNSNMTFDKWD QDDEEDLVDTCAFLHIKTGEWKK GNCEVSSVEGTLCKTAIPYKRKYL DNHILISALVIASVTILTVLGAIIWFL YKKHSDSRFTTVFLTGPQLPYMEN CVLVVGEENEYVPVQFD
1830	7327	A	1966	3	614	LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCYAYL QMKGNR\EM\YDCTSSSFDGIAM MSPED\SWVSK\WQAKSSNFKP\GV YA\SVVTGRLAPKGIR/VRELKSR\G VALQIPGDTANKDLAKMQGCQHL SPPPCLCIISCSWNLNEQNFQILPTLQ FRLSSTVERAAHHFIILSSLDYRWG GRDLGWVD
1831	7328	A	1967	66	407	
1832	7329	A	1968	2	1272	CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRGVEHGPAIREAGLM KRLSS/LGDLTSPEIEVLFTDIKVR THCPKSLPGTETVQIHELSSFFLNILG GKKKKQSWEQEGCHLKDFGDLST PVPKDDLNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDLCCVVWVDAHADI NTPLTTSSGNLHGQPVSFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVDPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPIHLSF

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						DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI
1833	7330	A	1969	212	460	
1834	7331	A	1970	1	1223	TVVECLSPA WHEESSGGRWRS LPA SNRAEPLPWRFSVL RIMSLRGSLSR LL\QTRVRSILKKS VHSVHVIGAPFS QGQKRKGVEHGPA AIREAGLMKRL SSLGCHLKDF/GQDLSFTVPKDDL YNNLIVNPRSVGLANQELAEV VSR AV/SQDGYSCVTLGGDHSLAIGTISG HARHCPDLCVWV VDAHADINTPLT TSSGNLHGQPVSFLLRELQ\DKVPQ LPGFSWD/IKPCISSARIVYIGLRDVY PPEHFILKGTMDIQYF\SMEEILDR\I GIQEGHNGTFDLLIGKRQRPIHLS YDIDAFDPTHAPAHRTVPVGDITYR EAMYIAEKIH\NTG\LLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTREGGAYWSYDPTFPT\SSP\ DESENQARVRI
1835	7332	C	1971	162	425	MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVGNIGRQLAMGVPEK PIVIESSKPXILEXGRFLEENLXLVD YXKGLSFFLK*
1836	7333	A	1972	89	308	
1837	7334	A	1973	2	454	
1838	7335	A	1974	570	1418	PMPLRLHDHFWSCSCAHSARRRGPP RAIAAGLAAKVGEMII VFVSGPSLM AVLSASDADPAPRGRSAVKSGPY GSPYPNTWHHSLMQKSLVLFVGE VLALVLNLLQIQRNVTLPFEEVIATI FSSAWVVP\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGQVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSGLG LGITIAFL ATL\TQFLVYNGVYQYTSPDFLYIR SWLPC\IFFSGSVTVGNIGRQLGYG VFLEKPHSD
1839	7336	A	1975	1	287	KFQERGIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQTP/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSSPKEKDV RPATSTTSCSMLLSILFIG
1840	7337	A	1976	1	166	
1841	7338	A	1977	37	448	GGCTCPCSRWQGSPQAPAGLPPL ASGPAPSASASPQPSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPVLGP CAESPGHRGWV ASPWSSGWSP
1842	7339	A	1978	45	249	
1843	7340	A	1979	77	3801	KGGVFAHDLVPLPFQGTDSPPSRAP PGRGVPLPPGALTMNTRDTPRVAE TSHHLKIFLPKKLLECLPRCPLLPPE RLRWNTNEEIASYLITFEKHDEWLS

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						CAPKTRPQNGSIILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLVQ GMECLYGCVVHSSIVPTFHRRCYW LLQNPDIVLVHYLNVPALEDCGKG CSPIFCISSDRREWLVKWSREELLGQ LKPMFHGIKWSCGNGTEFSVEHL VQQILDTHPTKPAPRTHACLCSGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPPELPA HTSPSSSSSSSSGFAEPLIRPSPTS RGGSSRGGTAILLLTGLEQRAGGLT PTRHLAPQADPRPSMSLAVVVGTEP SAPPAPPSPAFDPDRFLNSPQRGQTY GGGQGVSPDFPEAEAAHTPCSALEP AAALEPQAAARGPPPSVAGGRRG NCCFIQDDDSGEELKGHGAAPPISP PPSPPPSPAPLEPSSRVGRGEALFGG PVGASELEPFSLSSFPDLMGELISDE APSIPAPTPQLSPALSTITDFSPESY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLRVCYCPAHEV GLVSLQVAGREGPLSASVLFYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQGPGEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDPNLVDHFCTPLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRPLPSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPPSSSPDTGLSSVS SPSELSDGTFVTSAYSSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSTTPSELPERGRLAVPSA PSWAEFLSASTSGKMESDFALLTLS DHEQRELYEAARVIQTAFRKYKGR RLKEQQEVAABVIQRCYRKYKOLT WIALKFALYKKMTQAAILIQSKFRS YYEQKRFQQRRAAVLIQQHYRSY RRRPGPPHRTSATLPARNKGSFLT KQDQAARKIMRFLRRCRHRMRELK QNQELEGLPQPGLAT
1844	7341	A	1980	1	4333	MQVQDDGVNLIPFAKCSRVSRSPP PRLPSQSLRPMPQRYGDVFWKNLN QRPTPTWLEEQHIPPMLRATGCSQL GLYPPEQLPPEMLWRRKKRRPCLE GMQQQGLGGVPARVRAVTYHLED LRRRQSIINDTDSPPSRPLRPGVTLP GALTMNTKDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPQNG SIILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLVQGMCECLYGCV VHSSIVPTFHRRCYWLLQNPDIVLV

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						HYLNVPALDCGKGCSPIFCSISSDR REWLKWSREELLGQLKPMFHGIKW SCGNGTEEFVSVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLSIPHAHPPE PPPLIAPLPPELKAHTSPSSSSSSSS GFAEPLEIRSPPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPQRGQTYGGGQGVSPDFPE AEAAHTPCSALEPAAALEPQAAAR GPPQSVAGGRRGNCFFIQDDDSGE ELKGHGAAPPISPPSPPPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTQLSP ALSTITDFSPEWSYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGERLAHGSPPFR GMSLLHLAAAGGYARLIETLSQWR SVETGSLDLEQEVDP LNVDHFSCPT LMWACALGHLEAAVLLFRWNRQ ALSNPDSLGRPLPSVAHSRGHVRLA RCLEELQRQEPSVEPPFALSPPSSSP DTGLSSVSSPSELTDGTFSVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQIIEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYL\ENVDFHPSSTPPSEL\PFER \GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTL\SD\QEQLRELYEAARVI QTAFRKYKGRRLKEQQEVA AAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYYEQKRFQQSRRAAVLIQQH YRSYRRRPGPPHRTSATLPARNKGS FLTKKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS
1845	7342	A	1982	1	145	
1846	7343	A	1983	1	419	
1847	7344	A	1984	3	532	PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTLLLNNEGSLLA\YS GLRGTTDAPGSPAAIA\SNIAWA\YG PETGTQAFNEDNLQI\IILHGTCMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS
1848	7345	A	1985	2	555	
1849	7346	A	1986	90	323	

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1850	7347	A	1987	1	4695	
1851	7348	A	1988	81	523	SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\W SSDSWEVWGLASTNRNSNSDGV GGEGTKKAVPPAVPTDDGWDNQNW
1852	7349	A	1989	1187	1720	QNQSRDKMRDLREGQMEPPKSELI GWGGGETSRWVRGGASPPPALSP LFLITWSGHKDLK\DLKVRGLRGLE APRVNVWETEANQAGLQPLGPPAT IGLRPRRPGPRVGREGGPAWPLG EFGIPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGQPGQAPGADG RAARSRG
1853	7350	A	1990	738	1086	GTASENLGCKILKHRQQLRKVYP VVLHILSYRGSHSSRKNWGRKNI LKTFFFLGGGGDGSCWQRPGWELQ WALFSGSLQSPPGFKQFSCLSLLS SWEYRCTPPCLANFCIFQ
1854	7351	A	1991	1	340	LGEGGRTAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLLGRRLPKA WPPPPSSLPVLTDEQKSR/YPGHEAH DQGG\WDARQSIIRKVVDPETGRTR WGAFLTYTTGSGSVG
1855	7352	A	1992	1	142	
1856	7353	A	1993	58	328	LKKKGKEKAEAAQQVEALPGPSLDQ WHRSAGEEEDGPVLTDEQKSR/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLLKGDGEGPKRKS
1857	7354	A	1994	120	416	LFFGESSRLTVLEDLKNVFPQVAV FEPKAEIFHTQKAPLVFLATGFYPD HVELSWVNGKEVHSGVSTDPQP LMEQAALNDSRYCLSSRLRVSATF
1858	7355	A	1995	1	977	VKLPSCPDPAMGTSLLCWMALCCL GADHADTGVSQNPRHNITKRQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLSDRFSER PKGSFSTLEIQRTEQGD SAMYLCAS SIGAGLPSSNPQHFGDGTLSILED LNKVPPEVAVFEPSEAEISHTQKAT LVCLATGIFPDHVELSWVNGKEV HSGVSTDPQLKEQPALNDSRYCLS SRLRVSATFWQNPRNHFRQVQFY GLSENDEWTQDRAKPVTVQVSAEA WGRADCGFTSV\SYQQGVLSATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF
1859	7356	A	1996	2	883	FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICRGTSV KIECRSLDFQATTMFYRQFPKKS MLMATSNEGSKATYEQGVKDKFL INHASLTSLTSTVSAHPEDSSFYCS ARESTDPKNEQYFGP\GTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATGFFPDHVELSWVNG

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						KEAHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSATFWQNP RNHFRCQV QFYGLSENDEWTQDRAKPVTQIVS AEA WGRAGEWGLGRCLLEEIR
1860	7357	A	1997	195	1133	PQHGGHFPRIKSCSWQARPLEDEA TLGQCGVEALTTLVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEAVVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSPYIEYT PASPAYAQYPPATYDQYPYAASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH
1861	7358	B	1998	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
1862	7359	A	1999	1	437	DPRATEGMVVADKTCQKSTGR LPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISK NKLD FLRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDTS
1863	7360	A	2000	2290	2481	
1864	7361	A	2001	3	860	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKL\PRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAA DTAMT\TQLISS\NLKLHSLASTGR\LP RV\VTAN\NRMLKQMLFRYQGYIGAA LV LGGVDVTGPHLY\SIYPHGSTDK VP\YVTHGFLAPLA\AMAVFEDKFR PD\MEEEEA\KNL\VEDSPPPQFP PPS WRIFND\LGSGSNIDLCVISK\NKLD FLRP\YTVPNKKGTRLGWRYRCEKG \TTAVLTEKIPLLWST
1865	7362	A	2002	1	340	RQGTIVAISSIQGKMSIFRSAYAAS KHATQAFFDCLRAEME QEIEVTVI SPGRSC/VEVAQDVLAAGKKKKD VILADLLPSLA VYLRTLAPGLFFSL MASRAR*ERKSKNS
1866	7363	A	2003	56	385	RPWTSPPPQSPCCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLA AVGKKKKDVI LADLLPSLA VYLRTLAPGLFFSLMA SRARKERKSKNS
1867	7364	A	2004	2	409	
1868	7365	A	2005	1	1092	
1869	7366	A	2006	50	1101	LTMVSPATMKSLPKVKAMDFITST AIL\PLLFGCLGV\FGL\FRLQWV\R GKAYLRNAV VVITGATSGLGKECA KV FYAAGAKLVLCGRNGGALEEL\

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						RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNAGISYRG\TMDT\TVDVDKR VMETNYFGPV\ALTKALLPSMIKRR QGHIVA\ISSIQGKMSIPFRSGICQPS KHATQ\AFFDCLAVPEMEQ\YIEIV TVISPGYIHTNLS\VN\AITADGSRYG V\MDT\T\SPGPESPVEGGPRMFLAC LWGKKK\KDV\TLADLPALPLAVY\ LRTLAP\GLLPSSLPCLPRAQKRAGN PKNSLV
1870	7367	A	2007	75	461	
1871	7368	A	2008	3	426	DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYDLA GGAGPIDAEKGGSLVVGDFEATKY VCRTLETQSQSPFSCMDLTYVSL LQEVGFPRSKVLKLRKIDNVYTT WAPGAIFHYIDSLNRQKS
1872	7369	A	2009	3	421	QALGNRGVVSRGWRRPGWRPGRG SPKDRLPAPRKRALVSVGVAERA VHETPTLTHETFKALKPGLSAYADD VEKSAQGIRELLDVAQDIPDF*K ATPLILK/ATAGLRLLPEKKAQR*LA K\GKEVFKA\WLFEGNDW
1873	7370	A	2010	337	769	PLALCLAPAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYDLA AGVGLIDAEKGGSLVVGDFEIAAK Y\VGVTWSVKGRVSSPVCRTLETQ QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLRKIDNVETSWALGAIF
1874	7371	A	2011	2	486	
1875	7372	A	2012	176	1643	MKKGIRYETSRKTNYIFQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVFIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFGIMFDAGSTGTRVHVQF TRPPRETPTL/TAHETFKALKPGLSA YADDVEKSAQGIRELLDVAQDIPF DFWKATPLVLKATAGLRLLPGEKA QKLLQKVKEVFKASPFLVGDDCVSI MNGTNE\GVSAWITINFLTGSLKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KDGKELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHVDFYAFSYYD LAAGVGLIDAEKGGSLVVGDFE AAKYV/CVRTLGETQ\QSSPFSCMD LTYVSLLLQEFGFPRSKVLKLRKID NVETSWALGAIFHYIDSLNRQKSPA S
1876	7373	A	2013	21	119	PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK
1877	7374	A	2014	1420	1627	IGLNPSSVPSTFFSYSPQFTEGVPP/P GMRP/PFPWEQRPTGWSFFSPCPQ TPSPPTSEHGTPPNWPKC

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1878	7375	A	2015	447	775	QIPKEHLHHP/PQTSHSNRPLR/P/GN RPNPESPTGSPPECCSCLAPRGS WGDPNPLQRTPGAGKVAGGPFPPP TQQSPPGKALCINLKGKFAAIKLLD NVLQPSSALGFL
1879	7376	C	2016	49	519	MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPFM SPRYPGGPRPPLRIPNQUALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTTPRGMVP*
1880	7377	A	2017	1	1155	
1881	7378	A	2018	56	1416	WVDRCVTVGAALGTSMYGKGKS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLEIRWEKNITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEH\SSEAKAFHDYSAAAA\PS VLG\NIPPGRWACQLGPVTRGSFQ PFMFTFGYPG\GPRSPLRV\PNQALG GVPPGGQPLLPSGMDSTRQQ\GHPN MGGAMQR\MTTPRGMVPLGPQFLT PWLSQLNYGGA\MRPPLNALGGPG MPGMEQGSRCGRPW\PNPTNA\NSL PFSSAFSWNLLGPPG\GGGPPG\TPI MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNF\PMGP\GSDGPMGGLGG MESHMHMNGSLGS\GDMAISKNSPN N\MSLSIQP\GIPK\DDGAMGANFLN PFQSESYSPSKPYKCVFPFPGLFMKP TVSQPFPELRTEENYSSTSVPVKQR NLSHTKPTFLFPALSPLL
1882	7379	B	2019	162	349	LEELEEEELDLVLLRAFCLLLSW DVEAEQFLEVSLFFFLFSDPRPRD RLRLLERLREPT*
1883	7380	A	2020	2	353	SSSDGRKKRGKYKDKRRKKKKKR KKLKKKGKEKAEAQQVEALPGPSL DQWHRSAEEEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKVV DPETGRTRWGAFLTYTTGSGSVG
1884	7381	A	2021	1	142	
1885	7382	A	2022	404	946	PVCACPRPEQGTKVYLFPSWLSLT FSLHHREKQAEGRGEEEDASSASS SSSSSSSSSSSSSSSDGRKKRGK YKDKRRKKKKKKRKKLKKKGKEKA EAQQVEALPGPSLDQWHRSAEEEE DGPVLTDEQKSR/YPGHE\THDQGG\ WDARQSIIRKCGGPLRRGAPGLLKG DGEGPKRKS
1886	7383	A	2023	3	634	
1887	7384	A	2024	131	546	VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLDSFHLEMIHPR CESWKMPGALPM/YCSP/CCLLVLL KDQGGGASTGVRRRKESWLPAPHS STVQVTQEGWREQSRELPKTECQL GWFLFLLQPYSRSFY
1888	7385	A	2025	363	578	RPYPCLSPPRSSTNPLSS**LNKIPS

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						LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK
1889	7386	A	2026	166	191	KNVIHQSKNCVFVKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYQPAPARQAPADHRQWPVPQ RGPEASG
1890	7387	C	2027	358	405	MSSREGARDGGEGRLS*
1891	7388	C	2028	306	347	MSPGRGPGMEGRG*
1892	7389	A	2029	2	358	QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRHLQASSCPAHPPLP PTQSCSSCQGWLCPPQGCPPGPRT A/CIVPWPSPFVASAATQERGQCPPL DPLSPNQTRALHLSGTSGK
1893	7390	B	2030	1043	1146	MPSSVSWGILLLAGLCLVPVSLAE DPQGDAAQKTDTSHTDQDHTFNK ITPNLAEFASFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTETPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACLTSSHX *
1894	7391	A	2031	2	402	SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKL RVD PVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
1895	7392	A	2032	9	509	NSARATDSETHHGARLLPDKTNV KAAWGVGAHAGEYGAELERM FLSFPTTKTYFPHFDLSHGFAQVK GATAKKVADALTKA VAHV DGH A QTALSALSGPATAHKL RVGPGSTF KLLASHLPCWLT LGRPPSPA EFQPLA VARLPWNKVPGLLVEAPLLEPSK
1896	7393	A	2035	413	674	CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGLSLQRPPGP/SD SPASASRAWPQTAH
1897	7394	A	2036	2525	2734	LTNGTESTPPRPTPSRCSRQCPES VGPPFCSPFCVPAHFKLLPWFQFQ TVISSPQIISSSVCAFF
1898	7395	A	2037	168	392	NKSFFPPSSFDLSILNTFSFPLTLSSL RSGPTHHTHTHAN/THHTHTHTHT HTPSSPDPAHPHTLTDNWWVSTL
1899	7396	A	2038	216	528	AGEKLGAGDTSWRVVWPAACT PGRVERVGWCRVGPADPSGGLTPG VACGASWQGPFWSAKDLQGPWSW WPVWPTRPFLDLGSSGLLIWVHK WPWGVVCVYV
1900	7397	A	2039	37	424	RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPAP*PQTGC WSPDGSRLFTVLGEPLIYSLSPER CGEGKGVALEVQSQQRLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL

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1901	7398	A	2040	1	442	PEFRVDDFVLRYPsAYESSPGTELRECGL/WPFRPGVCRLQTSCEPWINLPVLQLTKDPLKTPGRLDHGTRTAFIH HREQVWKRCINIWRDVGILFGVLNEIANSEKEVFEWVKTAGSWALALCRWASSLHGSLFPHLSLRNEDLIAEF
1902	7399	A	2041	722	1395	CLCLGLWACQS\CILIWTLADPTSLFTRPSSG\CAQVLSHPGHTPVTSLAWAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLWSPDGSKILATTPSAVFRVWEAQMWDLWRRWPTLSGRCQTGCWSPDGSRLFTVLGEPLIYLSLSPERCGEKGVALEVQSQ QRLWQICLRQQ/YTRHQMVRGLGERLTPWSGTPVGNVWLCFMKGKAAQGLPGW
1903	7400	A	2042	1	418	MPEQEPTAEQLS*IAAENEDEHSVNYKPRQAQSIQEIQLDKDDESLRKYKRALGRVAVSADPNVPNVVAPGRVRLLPQALSATTPGRPSLTQPGTNKGPSAHIAESRLCLPRPIPLRVVSARLRQRRLSLLLF
1904	7401	A	2043	1	525	LSQQASLESF*KHFFCLKEVVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYIVGSYWPRAEYEFLLTPKSPRWTASPTPSVLQSGAPLGHQYLLP PSVPSSGHWPGVCSPRLLVPPLLGRPSLTLPGTNKGPSAHIAESRLCLPRPIPLRVVSARLRQRRLSLLLF
1905	7402	A	2044	354	487	
1906	7403	B	2045	61	516	KSIQEIQLDKDDESLRKYKEALLGRVAVSADPNVPNVVVTGLTLVCSSAPGPLEDLTGDLESFCKQSFVLKE GVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGVSYGPRAEYEFLLPRPIPLRVVSARLRQRRLSLLLF*
1907	7404	A	2046	11	328	
1908	7405	A	2047	1	507	LTFVCSFRPVPLYDLRSNLD SKNQ SFLFKEAVDYRIKISFRFHPKYISLI* YIQHTYSK/GVKIDKTDYMLGSY/GPRAEYEFLLTPVEEAPKGMLARGSYS IKSRFTDDDKTDHLSWEWNLTISIY CLRPCRWPATGLAPVPPGSQCHHPR QAFDPARNKQGTKCTHC
1909	7406	A	2048	1	327	TAEQLAQIAAENEDEHSVNYK/PPAQKSIQEIQLDKDDESLRKYKEALLAPLAVSADPNVPNVVVTGLTLVCSS/APGPLEDLTGDLESFCKQSFVL KEGVECTVGPH
1910	7407	A	2049	1	452	
1911	7408	A	2050	3	868	SHFVLDVIPGVGHLLTPQRMPLSRNRGGGEERRCPPWSPFGAPLQPTLLL RSAPPLGIQVQGLSPSRPQVSRPRLSLMAEQEPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQLDKDDESLRKYKEALLGRRWPFSADPNVPNVV

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						VTGLTLVCS\SAPGPLELDLTGDLAE SFKKQFVLCLKEGVEYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMVGSYG\PRAEGSFELTPVE\EA KGM\LA\RGSYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD
1912	7409	A	2051	1	618	TLLVPQDSERTHPWLLSPADK\TNV KGPPGGKVGAAHVSRMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV KGHGKKVADALTNAAHVDDMP N\ALSALSDLHAHKLRVDPVNFKL LKPLACLVDPGPAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFELQIPV KLGS LGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS
1913	7410	A	2052	3	398	
1914	7411	A	2053	1773	3913	FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLLE MVKLTSMRGQFLEAQIPTGISLTQ YQLYQKQTNKNMSYSFVFLKWV ALGQGRRAGYPSLEDADSRRFNGS RSFLITVIGITLTVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRRAVEAQPKDRTWDVGKG QGTGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLLLAGLCCLVPSLVED PQEDAAQKTDTSHHDDQGDWEDLA CQKISYNVTDLAFDLYK\SWLIYHN Q\HVLVTPTSVAAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKEQINNYVEKRTGRKV DLVKHLKKDTSALVDYISFHGKW KDKFKAERIMVEGFHVDDKTIIRVP MINHLGRFDIHRDRELSSWVLAQH YVGNAFFILPDPKKMWQLEEK TYSHLENIQRAFDIRSINLHFPKLSIS GTYKLKRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVL TIDEK GTEATGAPHLEEKAWSKYQTVMFN RPFLVIIKEYITNPLFIGKVVNPTQK
1915	7412	A	2054	3	409	PGPVVVSNNSSAHGSQRTSGPESSM K\YCCPEMVEYQKKGKSLDSEPSVP SAAKPPSPEKTAPVASTPSSTPIPAL PPTKVPEPNENVGDAVQTKLIMLV DDFY YGRDGGKVAQLTNFPKVATS FRCPHCTKRLY
1916	7413	C	2055	235	366	MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG*
1917	7414	A	2056	3	484	STTPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWVVE NR*L\SLGHR\APSFPSPA\VSIAFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG

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						PESSMKGTIT*KTLSSQSFKNINKVF VVSELYTQK
1918	7415	A	2057	2	4256	FVHGSMADTDLFMECEEELEPWQ KISDVIEDSVVEDYNSVDKTTTVSV SQQPVSAPVPIAAHASVAGHLSTST TVSSGAQNSDSTKKTLVTLIANNN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQANHVTSPPV ASQPIFITTQGFVRNVRPVQNAMN QVGIVLNVQQGQTVRPITLVPAPGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTNTFTTVIPATLTIRSTVPQ SQSQQTKSTPSTSTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSFSPSP AVSIASFVTVKRPGVTGENSNEVAK LVNTLNTIPSLGQSPGPVVVSNNSS AHGQSRTSGPESSMKVTSSIPVFDL QDGGRIKIPRCNAQFRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSTPIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHMKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHMKDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNGNAFQQHYM RHQKRNVYHCNKRLQFLFAKDKI EHKLQHHKTRKPKQLEGLKPGTK VTIRASRGQPRTPVPSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYLALFKNSVSGI KLACTSCTFVTSVGDAMAKHLVFN PSHRSSILPRGLTWIAHSRHGQTRD RVHDRVKNMYPSPPTNKAATV KSAGATPAEPEELLTPLALPSPAS TATPPPTPTHPQALALPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKKLRVVLALCC NTEQAAEHFRNPQRRIRRWLRRFQ ASQGENLEGKYLSFEAEKLAEWV LTQREQQLPVNEETLFQKATKIGRS LEGGFKISYEWAVRFMLRHHLTPH ARRAVAHTLPKDVAENAGLFIDFV QRQIHNQDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSILLEAKESGYSDDEIME LWSTRVWQKHTACQRSKGLVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQPLDVCIKRTVKNFLHKK WKEQAREMADTACDSVLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPGPDGNINSPTRNADMQKELIA SLEEQLKLSGEHFESSTPRPRSSPEE

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						TIEPESLHQLFEGESENE\SFYGFEEA DLDLMEI
1919	7416	A	2058	3	824	
1920	7417	A	2059	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\SCMAALT\VTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVYPAKTQPLQHHNLLVCSVNGF YPGSIEVRWFRNGQEEKTG\VVSTGL IQNGDWT\FTLV\MLETVPRSGEVY TCQVEHPSLT\SPLTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS
1921	7418	A	2060	2	867	GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLT\VTLMVLS\PLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQEEVRFDSVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVYPA\RTQPLQHHNLLVCSVSGF YPGSIEVRWFRNGQEEKTG\VVSTGL LIHNGDWT\FTLV\MLETVPRSGEV YTC\QVEAPRA*QAPLTVEWRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPRGFLS
1922	7419	A	2061	3	940	RNFRVDPRVREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RTVSLMVLS\PLALAGDTRPRFLW QPKRECHFFNGTERVRF\LDYFYFN QEEVRFDSVGEYRAVTELGRPD AEY\WNSQKDLLE\QRRAA\VDTYC RHN\YGVGESFPVQRR\VEPKVTY PSKTQPLQHHNLL\VFCSVSGFYPGS IEVRWFLNGQEEKAGVVPQALIQN GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLPLGPGLFIY FRNQKGHSGLQPTGFPELKCR
1923	7420	A	2062	25	384	EFHRLRENPPMVA\VSCTKTNVKG PPGGKVG\AHAVRSMCAEALERMFL SFPT\TKTYFPHFDLASHG\SAQVKGP RQRRWP\NALTKRRGAPLDDMP\NT ALSALSDLHAHKL\RDVPVQLSSS
1924	7421	A	2065	47	353	AGRVRI\WDCVEVDLTEL\GAGQSV EASRHAWEVVRNRNCHWAPQLFSL FAPGWGG\GEGRVGDGGAVGWFPS PQPPSSPPGV\MPCPHRRGTEPGRD LVPAQ
1925	7422	A	2066	3	692	KRLPKMAEVQVLVLADGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVV\RC G\NISGNFYRNEVKVPWLFPSKR\IM NTNPSRRPLTTS\GAPSR\I\FWRTVRG MLP\HKTQAEAKAA\LDRLK\VFDDGI

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						PPPYGQEKSGMVVPAALKVVRLLK PTRKFCLIFFSFGGALAHQ\VGWK YQAVTAP\LEE\KRKREKPRFHYRK KENSIMRLARKQAREETWRKKIDKY TEVLKTHGLLV
1926	7423	A	2067	1	2091	
1927	7424	A	2068	384	4189	ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETEVEKGRIRGRPRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFQICSGCRGTVRIEMFRNM QNAEIIRKMTTEEFDEDSGDYPLTMP GPQWKKFRSNFCEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLMTALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRYRDAIAEIRAICIEIGV WMKMYSDAFLNDSYLKYVGWTLH DRQGEVRLKCLKALQSLYTNRELP KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEELSNEDCENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEELAKRRGRNSPNGNLI RMLVLFLESELHEHAAYLVDSLW ESSQELLKDWECMTELLLEPVQGE EAMSDRQESALIELMVCTIRQAAEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADAEK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVESDVLEACS KTYSILCSEETYIQNRVDIARSQID EFVDRFNHVEDLLQEGEEADDDDI YNVLSTLKRITSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQCLSNVNTP VKEQAFMLLCDLLMIFSHQLMTGG REGLQPLVFNPDGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLIYDIVDMHA AADIFKHMYKYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNELVQ EQGPNLDR TSAHVSGIKELARRFAL TFGLDQIKTREAVATLHKDGIIEFAF KYQNQKGQYPPPNLAFLEVLSEFS SKLLRQDKKTVHSYLEKFLTEQMM ERREDVWLPLISYRNSLVGTGEDDR MSVNSGSSSKTSSVRNKKGRPPLH KKRVEDESLDNTWLNRTDTMIQTP GPLPAPQLTYTVLRENSRPMGDQI QEPSEHGSEPYFLHNPQMISWLG HPKLEHLNPKDITGMNYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDMN\EEF\EDTM\VIDLPPSRN RRERAELRP\DF\DSA\IIEDDSGFG MPMF

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1928	7425	A	2069	1	2661	
1929	7426	A	2070	1	1454	
1930	7427	A	2071	1	2364	
1931	7428	A	2072	1	1368	
1932	7429	A	2073	114	1473	VKGDRFGALRFNDPCAGIKLPMTFF TELEKTTLKFIWNQKRARIKSIQS KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTPGPSEITPHT YNYLIFDKPEKNKQWGNDSLFNKW CWENWLAICRKLKLDPFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPALPLGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVGTWMKLEIIL SKLLQEQKTK
1933	7430	B	2074	1	1890	MDKFLDITYTLPRLNQEEVESLNRPI TGSEIVAINSLPTKKSPGPDGFTA YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASIIIPKPGRDTTKIENFRPIS LMNIDAKILNKILANRIQQHIKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMIIISIDAEKAFDKIQH FMLKTLNKLGDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVMELLARAIQEKEIKGI QLGKEEVKLSLFADDMIRIKYLGIQ LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTEPSEITPHIYNLIFDKPD KNKQWGKDSL FNKWCWENWLAIC RKLKLPFLTPYTTINSRWIKDLNV RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHWPSEKCKSKHNEIPSHTS*
1934	7431	A	2075	1	2676	MKAEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHNRKQERPKI DTLTSQLEKEKQEQTHSKASRRQE MTKIRAELEIEIQKTLQKINESRSW FFERINKIDRPLARLIKKKREKNQID AIKNDKGDITDPTEIQTIREYYKH LYANKLENLEEMDKFLDITYTLPRL NQEEVESLNRPI TGPEIVAINSLPTK RSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASIIIPKPG

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						RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQG WFNIRKSINVVQHINRTKHKNHMII SIDA EKAFDKIQPFMLKTLNKL SID GTYLKIIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTAWYWYQKRDIDQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKTLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIKKSGNNRC WRGCGEIGTLLHCWWDCKLVQPL WKT VWQFLRDLELEIPFYPAIPLLGI YPKDY
1935	7432	A	2076	1	3045	MDKFLNTYTLPRLKQEEVESLNRI TGSDIEAIINSLPTKK\SPGPDGFTAE FCQRYKEE/LEKEGILPNSFYEASIILI PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIPG MHGLFNICKSVNIIQHINRTNDKNH MIISIDAEKPFDKIQHFMLKTLNKL AQNLLKLIGNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLG IQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLP CSSAC RRPVIGLQLVMINSGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTAPL GSTPQAAVCRGPRGRELRAAPADS

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						HLFQRDLPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWR SLSNNKGTGRLYEQVA
1936	7433	A	2077	1	2142	
1937	7434	A	2078	1	1551	MRFKEKIHLHNIKEPSEAASADGGA VASYPDLAKIVDEGRYKAEVMQLR CGWRAPASDCVHSVAVVGVDVSL EVLARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPTVSAQNLLKLIS NFSRVSGYKINVQKSQAFLYTNNK QTESQIMSELPFTIASKTIKYLGIQLT RDVKDLFKENYKPLLNIKEDTNK WKNIPCSWIGRINIVKMAILPKVIYR FNAIHIKLPMTFFTELEKTTLKFIWN QKGVHIAKSILSKKNKAGGIMLPFH KLYYKATVTKTAWYQYQNRDIDQW CNRTEPSEIIPHIYNHLMFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPK PIKTEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKLSFCTAK ETTIGVNRQPTTELEKIFAIYSSDKGLI SRIYKELKQIYKKK\NNPIKKWVKD MNRHFSKEDIYAVNRHMKKCSSSL VIREMQIKTTMRYLTPV
1938	7435	A	2079	1	1458	GLSGDLLGAHQLPDVLGCVQPLPD LLLPPQNLLALQSLQDDLLWALDP AAAAPWAMDRGAATQWAVGPVV SDPWVMEAVASLPSAMDLDAAQP TWLLGAASLLVTDQPMQPSADQL AEFPDLLSKVSQSLRIKYLGIKLTRN VKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFN APIKLPMTFFTELENTTLKFIWNQK RACIAKSILSQKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWN GTEPSEIMSHIYNLIFDKPEKNKQR GKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIKT LEENLVNTIQDIGMGKDFMSKTPKA MATKAKIDKWDLIKQKSFCTAKET TIRVNRQPTTEWEKIFAIYSSDKGLIS RIYKELQQIYRKKTNPIKKWAKD MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPV
1939	7436	A	2080	1	2028	
1940	7437	A	2081	2	1547	
1941	7438	A	2082	3	1945	
1942	7439	A	2083	1	2124	
1943	7440	A	2084	1	2250	
1944	7441	A	2085	2	2483	GKYYKLSSGTAPTCVSLGWGLARG

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						DSAAPALGSRTSACAPCSHGTWKL SLEPSDRLSPCDRSSEEAHTHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKGAGGPVI CRSLPESRGFLWASEGRKCMIGSW AAMGRRLRKSTISSRFGPQTLAGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPTQTHWEFILS EDYNKMTPVKNYQVLEVLARAMR QEKQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQIISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCSWV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWY.WYQNRGVDQWNRIEPESEI PHIHNLHIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLDPTPTPT KINSTWIKDLNVRPKTIKLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLIPRIYKELK QIYKKKSNNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIHKSGNNRDM DEAGNHSEQTARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPVIG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIY QPAPKS
1945	7442	A	2086	1	2622	
1946	7443	A	2087	853	2831	YPESTMNSNKFTRKKQTTPSKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRSLK SQDRKD*QSTLLAILIKKGQKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDITYTLPT LKQKKEVKTLNRPITGSEIAIINSLP T/KKSPGPDRTAEFYR/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR* HHCIFRKPHHLSPKSS*ADKQLQQS LRJQNQSAKITSIPHQ*QTNREPHE *TPIHNCFKENKMPRNPTYKGCEGS LQGELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDFHRIKKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT*LQ TILQGYSNQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLRQT*TNLQDKNKQPHQK

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						VGKGYEQTLTKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN
1947	7444	A	2088	1	4954	MVFSIDAQKAFDKIQHFRMLKTLN KLGIDGTYLKIIRAIYNKPTGNIILNG QKLEAFPLKTGTROGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSQYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLFKENYKPLLNEIKEDTDK WKNIPCSWIGRIHIVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIKSIKLSQKNKGGGITPPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSGNNSEGLNPGYKGFPTIHWAPL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGQVFISSASQAF TKKARIYARLRVSQALTKLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFLLEL NQKSQQYQKQEQTHSKASRMQEIT KIRAEKIEITRKTQKIDESRSWFF ERINKTDRPLARLTQKREKNQIDA IKNGKGDITTDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVDSLNRPTGAEIVAIINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKGR DTTKKENLRPISLMNIDAKILSKILA NRIQQHIKKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFMLKTLNKLKIDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNNDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFK\ENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEK\TTLKFIW NQKRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHS LFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK

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						SFCTGKETTIRVNRQPTWEKIFAIY SSDKELISRIYKELKQIYKKK\TNNPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMA\IKKSGNNRCWRGCGEVGTLL HCWWDCNLVQPLWKS\VRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTMEYYAAIKND EFMSFVG TWKLEIHL SKLSQE QKT KHRIFSLIGGN
1948	7445	A	2089	93	225	
1949	7446	A	2090	133	849	PVWPKWSGWPLL MRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STPDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVLP/LARIAT VVIGGVVAMAAVPMVLSAMGFTSV VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTPDPKATELTRAGMEASALTSSA VTSVAKVVRVASGS\AVVLP\LAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRCGPMAGC ANGCSSAMGLQLRAGIALVLP
1950	7447	A	2091	161	1344	TCPVLRHYSTMSSHKGSAVAQNGG APASNREADTVELAELGPLLEEKGK VRVIANPPK\AEEEQTCVPVQEEEE VRVL\TLPLQAHAMEKMEEFVYK VWEGRWVIPYDVLDP\WLKGND\ YLLHGHRRPMPSPFRACFKSIFR\HTE TGN\WTHLA/LGFVLF\FLGILTML RPNMYFMAPLQ/EKKVVFGMFFLG AVLCLSF\SWLFHTAYCHFGGVFSTF PQRELFKG\LLLNMGELWSPGLYY SFYCSP\QPARLIYLSIVCVLG\NSANV AQWDRFATPKH\RQTRAGVFLGLG LSG\VVPTMHFTNRWRALSKATTV GQ\MGWFFLMAVMYITGKLAFNAA RIPERFFPGK\FDIWFQSHQ\FHVL\ VVAAAFVHFYGS/VSNLQEFPLTGL EGGL
1951	7448	A	2092	2	1419	RLRDPYRSSRLCRRGASRTSSAARS RSRSPA VEGCNRSPGAPQAPARRR RPSRGAPGRAMVKVAFNSALAQK EAKKDEPKSGEEALIIPDVA VDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIK\DDVILN/ESPSADAP AALYQTIE\ENIK\IFEERRSLNFISVP VPEFADSDPAKIVQDFMRKLTAYL DFNLADKCYVIP\NTSMCYATPKTL LELLIN\IKAGNLFALSPYLD SMRHM GYLLDR\ENIDHLGF\FIYRLCHDK\ ETYKLATRRKLFKGIQKREGQQLF SAISGIFENKFAVETLICSW

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1952	7449	A	2093	1	669	
1953	7450	A	2094	267	550	GRTMMFGAKRRQEEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQELRGTVSNCKNMVVRGLDEDET TFLDEVSRQQELIEKQPKRRRT
1954	7451	A	2095	1	418	
1955	7452	A	2096	272	383	
1956	7453	A	2097	118	379	RSGGGRGRRGPPEVLHLKHPMLKRP DFLYRKPFPSRGWEHGPPSRKSHLL/ GAPPPFPKFCHLC*APSPFRVLSFY QKRIHLVPPTQLH
1957	7454	A	2098	1	276	
1958	7455	A	2099	1	341	
1959	7456	A	2100	1	450	ACPYLALNSSMFCPDLILPTCLISST GFVGEKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLPCHAHYHSRCVDPWLQ TRKTCPIK\QPVHRGPGDEDQ\EE/ ETQGQEEGYEGE\PRDQ\ASERTPF LG
1960	7457	A	2101	238	525	
1961	7458	B	2102	178	373	XLPQPLRGPLAHS DPERPAPFASSLF IGVLGKTKRKKLKGKEGDERGS KGTNPALRKDPTFGF*
1962	7459	A	2103	634	1940	SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQLSSRCHAPLQPFPLPV VVA AVLWGSGPDGASFRATS\DH NCQHGFADLPALF\GATLSLEGPQG LALGEPHPDNACSPIAPPPAPVNGS VFIALLRFD CNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGERSSEYLRALFVYE KGARVLLVPDNTFPLGYLIPFTGIV GLLVLAMGAVMIARCIQHRKR/LQ RNRLTK\EQLNQIPTQTNQKRDQ\Y DVCAICLIEYEDGDK\LR\VFPGAHA YH\NRCVDPWLQTR\KTCPIK\Q PVHR\GPGDEDQ\EEETQGQK\EGDE GE\PR\DHASERTPLL\SSPTLPTS\ FGFLRPKFPLVFSLGP\STDPPLSPPS SPCYPLITPHTYTFG
1963	7460	A	2104	25	527	EFHRLRENPPMVA VSCPTKTNVKA\ AWG\KVGHAHVRSMAEALERMF LSFPT\TKTYFPHFDLASHG\SAQVKG ATGKKVADALTNAVANVDDMPN VAVRPEATLHAHKLRVDPVNF\KL LKPLACLVDGPAHLPRPSFTPGGA TSSLGQSFLGFLKHRCLNLPNYR
1964	7461	A	2105	262	364	
1965	7462	A	2106	3	1265	PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLDGDKARPAQLRRESG GAESVTRPLRAASPAPPPRAARAA MSEKPKLGRRAPASLSARCRAPR CCSCRARRPRIPQQCPRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSS

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						AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPCAPTPTHRAP CAPTASIASPGVRPPLPIAPPGVRPR LPITPPMEGVKTENDHINLKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRF\RFDDGQPNQWKDDL STAGDWKDED\IDVFPSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCGNSRTFTT MIFLSLMYFKLQLKTISAGMNL
1966	7463	A	2107	4	408	
1967	7464	A	2108	1	465	PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCPLGLGPAI*SPHPHQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQTANQCILPQASSTLCC*LHPQ NLVCP
1968	7465	A	2109	126	488	
1969	7466	A	2110	1	5586	
1970	7467	A	2111	68	310	TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETLQHRELDKTRARGPE*GS VVLTSPWSPCRKCATGTYHGSPH CQSSGGGR
1971	7468	A	2112	2	630	FFFFFDLLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSSFSRISFSVSGICPWWSR DGEVGTTFPSQFAKGRKGLIRGGP QHPLRLSPGPIEEQ*GLVSPKARLG ISPCQLCPGFWSYL\DSVSPPPGGSC SGCTVPGSSHNVPVSHPSGPACGV RTALSSA
1972	7469	A	2113	331	754	NFLKTNNVWSKWTHVLSQFWYQG FJLFCGLSIVKCTEIDSSICTE\PSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQKDNMGEMGNGTT TTKTFCFIFMPGEDQGCSSCVSTRIT RKSQVQKSRGTISR\YFHK
1973	7470	B	2114	110	225	XLGRPQLAGSLRSRFPISGMERGEFT QDCQRNAGREELQGRLSIQSFSPILA LGPDDSCETKTGMDKLS*
1974	7471	A	2115	83	287	SLLLKCSGVIVLRRPLGYGQVMK* PGAA*Y*GRTG*SHPFSTDWSTDG VRKSIWCHRNCRWESPS
1975	7472	A	2116	167	397	EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWGDEGHWPTPNRS CLL
1976	7473	A	2117	1	540	FCHLQIYYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRRKLLNLSLGLSLLKFLGSVPGGT AGMGKSVPLSPSQVCCGFRSFNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWWVTYPALSLSFNKSQCPWVFP LPTMPPG

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1977	7474	A	2118	1	3121	RQEAE LARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYLVTS IAKACALDPGTRATGGSLSGTGNDT SEACDADFSSLTACSGVESTAAPQ KLLILDARSYTA AVANRAKGGGCE CEEYYPNCEVVMGMANIHAIRNSF QYLRAVCSQMPDPSNWLSALESTK WLQHL SVM LKAAVL VANTVDREG RPVLVHCSDGWDRT PQIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLANNPCEREKRNI YKRTCSVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTAVYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDL SACTS SPLTRTSSDPNLNNHCQEV RVGLEP WHSNPEGSETSFVDSGVGGPQQTV GEVGLPPPLPSSQKDYL SNKPFKSH KSCSPSYKLLNTAVPREMKSNTSDP EIKVLEETKGPAPDPSAQDELGRTL DGIGEPPEHCPETEAVSALS KVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTP LDPSTDF\LNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLENPRFGKMPLELVRKPISQSQI SEFSFLGSNWDSFQGMVTSFPSPGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSSHSNGH CTGPGGKNQMWLSSH PKQVSSTKP VPLNCPSVPPLYLDDDGLPFPTDVI QHRLRQIEAGYKQVEVEQLRRQ\ VRE FQ\ MRLDIRHWCAPPAEPPMDYEDD FTCLKESDGS DTEDFGSDHSEDCLS EASWEPVDKKETE VTRWVPDHMA SH\ CYNCDCEFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS
1978	7475	A	2123	3	259	FPHRAGPILSSFQVPQRWL VGGFGR NCIAGGESV VWDRTNKYTRN* AQE WGMFWSLDGHLGESIIRGRSNTG ALSCPWPLGHL P
1979	7476	A	2124	1171	1784	KLYSLSVLYKG EAKV VLLKPA\YDV SSFSFF\QRPTVQE\ FMTFTS QLIVER S\SRKGTASVKEQDYLCHVYVRN DSL AG\VVVIADNEYPSRGGPF TLL\ EKVLDEF SQAKSHRIDWPVGIPWL TIHYPALDGHLSRYQNP READPMT KVQAELDETKIILHNT PWESLLERG EKLDDL VSKSEVLGTQSKAFYKTA RKQNSCCAIM
1980	7477	A	2125	2	262	RGNWVFLHTTEFSLTRSLISFN SCFI TRLECSGAITAHCSLDLLGSS/QSPTS

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						PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV
1981	7478	A	2126	36	376	PFDPAVLTAKA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALILVHLSRGGAEVQIFAPD VPQMHVIDHTKGQPSEGESRCGGGI GTCFLSTSHGAFF
1982	7479	A	2127	3	724	LAAASAFPTLCPVCRTPSQRALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGAEVQIFAPDVPH MHVNDHTKGQPSEGESMNVLTES ERIRRGKITDLANLSAANHDAIIFP GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSKDLPGH CPGRPLKWSLRKRCLRAPEGGPC CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREPMALSSVTD
1983	7480	A	2128	172	1020	PSDPAVLTA MA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALVLSGCGVYDGTIEHESA\ ILEHLSRGRAEDHIFAPDVPHMHVI DHTKGQPSEGESRNVLTESARIARG KITDLANLSAANHDAIIFP/GEGFG AAKNLSTFCRWTGKICKVNKEVER VLKEFHQAGKPIGLCCIA PVLA AK VLKGVEVTVGHEQE EGKWPYAG TAEAILALGAKHCVKIEVVEA\HVD QKNKVVTTPAFM CETA LHYIHDGI GAMVRKVLELTGK
1984	7481	A	2129	1	416	IQYRSDELHSITMKKGGVLFLLGII LLVLIAAHGTPVVRKGRCSCIITNQ GTIHLQSLKDLKPFGPSQCKIDIIA TLKNGIQTCLNPDSAD\VKELIKKW EKQVSQKKKQKNGKKHKKKVLK VRKSQRSRQKKT
1985	7482	A	2130	2	81	
1986	7483	A	2131	2	130	
1987	7484	A	2132	1	524	RPRIRHEPQTQREPTMVLSPA\DKTK AQRPPRLKLGATPGEYGGEPLERM VLFPPPTPKPYFPH\DLSHG\SAQVK GATAKKVA\DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHLPCLGEPWAGPPSPA EFHP LAVARLPWQSFLLGFLKHRCLNL PNYR
1988	7485	A	2133	388	654	GLFFVLQFFFLFCFVFLRSHSVSQAG VHWCRHGSAAST/SPGSSDPPTLAS\ KVLGVTDMSHCTWAESYFTKMG SPVVACACSSSYLGG
1989	7486	A	2134	384	622	INAPPRCPQLCTSEVCAME/CPQRV PAGPCPGCPGNLLIHAPSNRPGTTS QINDPQFLRICFWGSPKTPSHRHKS FFF
1990	7487	C	2135	44	340	MKCSQPXRCHFQSD FQKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGVVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV

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						P*
1991	7488	C	2136	2413	2829	MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCACLLPSPEPTGSVNVI FYVPLPSGLLTSAPGSRASGVGV LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGDQEALVQGALGW GQRAWTPAQCSVDNG*
1992	7489	A	2137	69	332	YQVLKTDKNMSRISFFPFLRKGLAL SPRMECSGAITAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS
1993	7490	B	2144	73	358	XVPGSRGPETKLWDDFSMSQATKR KHVVKEVLGEHIVPSDQQQIVRVLR TPGNLHEVETAQQQRFLVSMPSK YRKNIWIKRGDFLIVDPIEEGEK*
1994	7491	A	2145	80	201	
1995	7492	A	2146	498	748	FLPRRGDNDSSYPQ/WTKACRRRRRT CW*T*TWWIRSGQRKMWSCGRRL TTCMPRTRTAARLMACGSGSWRR SGPSCGCRISP
1996	7493	A	2147	1	1764	MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLDTCGANAK QSRDCFGCLRE/WCAKSRPAAEVSE LKADSKEGPQAQGPEQERTGL
1997	7494	A	2148	842	1186	FLPRRGDNDSSYPQ/WTKACRRRRRT CW*T*TWWIRSGQRKMWSCGRRL TTCMPRTRA WTTWRSKNLALSCP SMTKSLKSGHIPSASWRAARLMA CGSGSWRRSGPSCGCRISP
1998	7495	A	2149	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMKTSFREWLG DTCGANAK\QSRDCFRMPFEKWCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD\CYC\RTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWVSWVTYQLFLEWDFP GPIPHPHPHFQSV
1999	7496	A	2150	150	446	HEGLLLKLRLSDVYFLLFFETRSCF VAHAGVQWHHYNLS/T/PPGTPMF PLLASQVAGSTGMNHQAQIIKKT FGENMILLCCSGWLSGIFVLYSLY
2000	7497	C	2151	203	427	MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQAD LLNGQCGFQQSSEPQPHVHTTSS*
2001	7498	A	2152	1	1065	
2002	7499	A	2153	597	1292	QTFSNTIFLLTRHKQHSMILVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVR\VPATNLILGEGRGFEISQG RLGPG\RIHHC MRTVG\WAERLLQI MCERATQRIAFKKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMDTL GSAGAKKEIAMIKVAAPRAVSKIVD WAIQVCGGAGVSQDYPLANMYAI TRVRLADGPDEVHLSAIATMELRD QAKRLTAKI

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2003	7500	A	2154	1694	1886	ASDSRV P A P G I S / P S A P F P T Q L S P R R S P P S P P P P P Q S P L G I F S P K A S P V G I L H L F K T L F C I L N V
2004	7501	A	2155	1002	1480	M L L L K T T E R F E V S V C M A C T Y V \ S N L G K K Q R S V S F L A S G L M R V S T G P E L R L H H S F V L T G D V G R R I C R L L V G L F T K G D T S S K R V \ H P F S P G P \ C F L L C D L A R \ V G S S P K I N R V P H F T R T Q T S T Q R S C T V F V W Q R C S L V G P F Q V T V F T M \ Y F H H S L R S I S R F S S G
2005	7502	A	2156	1	1623	R L P F V D V D A R V Y A D A P A K L L L P P L A F W E L A V R L R G A E A A S E R Q V Y S V A V K L L L L H P A F Q S C L L L T L L G L W R T T P E A H A S S L G A P A I S A A S F L Q D L I H R Y G E G D S L T L Q Q L K A L L N H L D V G V G R G N V T Q H V Q G H R N L S T C F S S G D L F T A H N F \ S E Q L R I G S S E L H E F C P T I L Q Q L D S R A C T S E N Q E N E N E Q T E E G R P S A V E V W G Y G L L C V T V I S L C S L L G A S V V P F M K K T L Y K R L L L Y F R A L A I G T L L L K R L F Q L I P G A V W F Q P L E D Y Y V S K S A V V F G G F Y L F F F T E K I L K I L L K Q K N E H H H G H S H Y A S E S L P S K D Q E E G V M E K L Q N G D L D H M I P Q H C S S E L D G K A P M V D E K V I V G S L S V Q D L Q A S Q S A C Y W L K G V R Y S D I G T L A W M I T L \ S D G L H N F I D G L A I G A S F T V S V F Q G I S T S V A I L C E E F P H E L G D F V I L \ L N A G M S I Q Q A L F F N F L S A C C C Y L G L A F G I L A G S H F S A N W I F A L A G G M F L Y I S L A D M F P E M N E V C Q E D E R K G S I L I P F I I Q N L G L L T G F T I M V V L T M Y S G Q I Q I G
2006	7503	A	2157	1	604	M G T R W E P G W R A P G L A P A A Q A R S S G R A A P A A G S E R A R E R E R D G G S V G G G G S S A I P S E R A A D A H G E D S G A Y R W E R A N R P F S N N C C C L A F Y L G M E E A R W L Y A G L F C V Y G A S L I A I A T H V P L F G S Q I K A E / D P S G D S A P A A H L P P Q P A Q / P H L P Q A Q L M L T G S Q L A G H P L G M R W S M A T Q H A G C V S Q R C G L F P M T V G C S Q G N I L W S L
2007	7504	A	2158	22	1358	V H F S M G A P E I R M S K P L E A E K Q G L D S P S E H T D T E R N G P D T N H Q N P Q N K T S P F S V S P T G P S T K I A E D P S G D S A P A A P L P P Q P A Q P H L P Q A Q L M L T G S Q L A G D I Q Q L L Q L Q Q L V L V P S H H L Q P P A Q F L L P Q A Q S Q P G L L P T P N L F Q L P Q Q T Q G A L L T S Q P R A G L P T Q P P K C L E P P S H P E E P S D L E E L E Q F A R T F K Q R R I K L G F T Q G D V G L A M G K L Y G N D F S Q T T I F R F E A L N L S F K N M C K L K P L L E K W L N D A E T M S V D S S L P S P I Q L S S P S L G F D G L P G R R R K K R T S I E T N V R F A L E K S F L A N Q K P T S E E I L L I A E Q L H M E K E V I R V W F C N R R Q K E K R I N P C S A A P M L P S P G K P A S Y S P H M V T P Q G G A G T L P L S Q A S S S L S T T V T T Y I L S C G D A P P Q P D S W R G W G R G R G C A P P Q F H P L C H S P T P G H

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						HQQHKPQLKAAATRLSACQA
2008	7505	A	2159	3	452	
2009	7506	A	2160	9	633	NSARATDSERTHHGARLLPDKTNV KAAWGKVGAGHAGEYGAELERMF LSFPT\TKTYFPHFDL\SQRSAQVKG ATGKKVADALTNAVA\HVD\DMPPQ TALSGPEATLHGAQSFGVDPVQLSS SLSHWPAWLT\GPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFGASPGQP SLSWNPYPYRWSFE
2010	7507	B	2161	55	372	MERFLMDGFQPPQQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSLPLYFVSAADGTNVVVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN*
2011	7508	A	2162	552	1809	QLRGRGASRKWSALRRELGRRAWF ESAQSPDWRQGPKGPTSRVPLSSP HSEPHPEMAEDKTKPSELDDQGYD ADDNVKIICLGDSAVGKSKLMERFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHFPVPAAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVTYRNLSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAIRLAVS YKQNSQDFMDEIFQELEVGVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMGGQASPATLFTNF SLEQEEEDVPDQEQSSSIETPSEEAA
2012	7509	A	2163	807	1389	EPMAENKTKPSELDDQGYDADDNV KIICLGDSAVGQSKLMERFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSA\ADGTNVVVKLFNDAIRLAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQSSSIETPSEEVASPHS
2013	7510	A	2164	3	923	RAARTRAEPEVECAAAAGPAGVV RERAESRHGGRARGADPQRPWSLQ PSLGTARDNTLPSLGPGLSTARS QWAKNKTTPSELDDQGYDADDNV KIICLGDSAVGKFKLMERFLMDG\ FQPQQLSTYALTLYKHTATVDGRTI LVDF\FHTAGQERFQSMHASYYHK AHAICIMVFDVQRKVTYRNLSTWY TELSGSRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAA\DGT NVVVKLFNDAIRLAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQSS SIETPSEEAAASPHS
2014	7511	A	2165	1	2715	
2015	7512	A	2166	1	2256	
2016	7513	A	2167	339	1086	IQMNRFL\LM\SLYLLGS\ARGTSSQ

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						PNELSGSIDHQTSVQQLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSSEH GSSKHTVAEHTSGEHAESEHASGEP AATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQKGKCLRGEGETCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLFSHGTRMQIICCRNQSFCKNI
2017	7514	A	2168	2	425	
2018	7515	A	2169	2	169	GRVGDTLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVLDPYLGFQTHKMNTR*FG S
2019	7516	A	2170	2	227	
2020	7517	A	2171	177	1400	LNAPGSQSLVGMKGLGESKNMVV NGRRNGGPLSNDHQQNQSKLQHTG \KDTLKAGKNAVVERRSNRCNGNSG FEGQSS/RYPVSYGMTAKELCENDD LATSLVLDPYLGFQTHKMNTSAFPS RSSRHFSQSDLSHNNPVRFRPIKG RQEELKEVIERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLKE HVFYILRMFATDSGFEILPCNRYSS QNGAKIVATKEWKRNDKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDRCRPNCK FVSTGRDTACVKALRDIEPGEEISC YYGDGFFGENNEFCCECYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK
2021	7518	A	2172	3	114	
2022	7519	A	2173	328	471	
2023	7520	A	2174	1	190	
2024	7521	A	2175	2	132	SGLGRLPGPWQEAGSSRGPSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIFHAISPIPHF IAKRVTYDSDATSSACRELAYFFT GIVVSCLVISPVILARVALIK/WGAC GLCV/VAGNAVIFLTIQGVFFPIFGRG DDFSWE/QWGYWTDfs
2025	7522	A	2176	191	479	NTSLPNPSEVSHSSLRLDSGGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM
2026	7523	A	2177	1920	2524	TQYPPAEQRSQTLMQDVFALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTIQTAFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQK PFVGGGTGVLKKPEGAGPAAPTSG WRPRGEAPHRTGTAPPTAVPSGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRKLKLDAGRRLRSGSKPHVK HL
2027	7524	A	2178	239	380	
2028	7525	A	2179	34	202	EPTTRQTLYMLITFTPHNHLVRETSS

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						VPFEQMKN*GSERFNTLSKALQTISAKTRI
2029	7526	A	2180	1	1566	
2030	7527	A	2181	574	1949	KSKCRFPEGLSEGFGPMRKEALSSG SVQAEAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIVQVAQAMSLTE DVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPSKSHDVYWD IEGAVRRYVQPFNLALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNLLYVPELAHSPLYIQDKDGAP VATNAFHSPRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFLGIAQPHLPPKCLLSGPTSEGL MTWELDRLLWARSVENLGQATTT LTSLGAASWARSATLFIKGRRGHLE VLQRLAPVQKSAEELASGHL\DLPL LSPAREAVTSSELAFFDPSLLHLLYF PDDQKFAIYIPLFLPMAVPILLSLVKI FLETRKSWEKA
2031	7528	A	2182	76	419	
2032	7529	A	2183	71	350	AFIPAMAELIQKKLQGEVEKYQQQLQ KDLSKSMGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETLAQ LQQEFQRAQAAKAGAPGKA
2033	7530	A	2184	175	1032	GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHHLTRIVGIGGTFDV SKLPFLSSPDLSKSMGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFPF*PP FFSLPWISRFSTYLFLAFSTLHSESY* FLPFCLSPLSLLSKRYESQLRDLERQ SEQQRETLAQLQQEFQRAQAAKAG APGKA
2034	7531	A	2185	112	520	AFIPAMAELIQKKLQGEVEKYQQQL QKDLSKSMGRQKLEAQLTENNIV KEELALLDGSNVVFKLLGPVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETLAQLQQEFQ RAQAAKAGAPGKA
2035	7532	A	2186	635	1015	GGQKHPTGLLKPPANTAATMPKRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKASAKKGEKLP KGRKGGKADAGKGLGNPAKNPR LPLHFQFQKAE\GTGGLPSEMFIFES SGTYW
2036	7533	A	2187	302	471	TLSHRVLVEAQSREQLAALKKHHE EEI\VHHK\KEIERLQKRNL\SRHK\QK DSKLLKH
2037	7534	A	2188	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGRV\WGVRTM\QA VRGFGSDQSENFPTGPRAPHP/RKAG

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						GALGKREQAEEERYFRAQSREQLA ALKKHHEEE\VHHKKENERLAEKK FERHKQK\KMLKH
2038	7535	A	2193	2	406	ARAEMSRSVALAVLALLSLGLEAI QRTPKIQVYSRHPAENGKSIFLKCY VSG\FHPSDIE\VDLLKNGKE/RLKK VEPSDLS/FSAKDWSFYLA\LPYTEFH PQLKKDGVCPARVMHVTLSPAPRL VK\WDRRHVKQHQ
2039	7536	A	2197	319	393	WL/TPVIPTLWEAEVGGSFHRSSR
2040	7537	C	2198	84	290	MLPSKGLSFFSLQHLRDSRSLFPM SMITMLELECCRASSNHEVRWLKX HXVSQICSLICFPXMLTIRA*
2041	7538	A	2199	2	743	PRVRSEVS\YRSLADPEPTGRDGMT YADLFKYIIIGDTGVGKTCFLLQFTD KRFQPVHDL\SLGVEFGGSLCSTLME NQFKLHIWD\TAGQESFRSITRSY\Y RGAAGVALLVYDITRALKPFNHL\AS WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFAREVHGRIFR GTSAKTACNVEEAFINTAKRIYRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC
2042	7539	A	2202	20	222	
2043	7540	A	2203	1	458	RSSLTSLSNSAAAMAPVKKPCGEG GAKKKKQVLKFTLADCT\HPVEDGI MDAAQF*ASFCKERIKVKRKKLGT LSGGG/V*PIERSKISKITVTSEVPFS KRV/YLKYLTCKY\LKKNLRL\DLV CRVVA\YQPKRELNRNYSYFQINQDE GRREED
2044	7541	A	2204	2	321	FIFFSFSFFSFFSETGSCSVAQAG VQCHDHGSPQS/PNLPGSSDLPTSAS KVLGITGVRHSLPPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS
2045	7542	C	2205	46	234	MTLRXWITWPFLFLSPSSKCLHLII ASILLDLQLGSTHSSLSTIFFVVLAF RKIGLVCPP*
2046	7543	A	2206	1	243	
2047	7544	A	2207	144	479	RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDS\LYAPGKAAVMTRKQS GYGGQ\TKPIFRKKA\TTKKIVLKA LSALSPTCRSKRMLAFKRWQAFNL LGGDKKRKGPSASS
2048	7545	A	2208	75	540	GGSGSVRLRSESPREEAVEEEVAA VAVVVVAEEAGTNQLRAETMANI AVQR\IKREFKEVLKSEETSKNQIKV DLVDENFTELGEIAGPPDTPFERG RFP\LELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSVTGAICLADILKDQWG SWQWT
2049	7546	A	2211	1	2640	MYSGNRSGGHGYWDGGAAGAE GPAPAGTLSPAPLFSPGTYERLALLL GSIGLLGVGNLLVLVLYYKFQRLR TPHLLLVNISLSDLLVSLFGVTF VSCLRNGWVWDTVGCVWDGFGSGS

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						LFARPA PLPARPRAPRPTPPRSPLAS STLPDPSRMAGAF LFLRPLPPHAVQ DSIPVVSHLPPTCHQTLLLPKMADN LPTEFDVVIIGTGLPESILAAACSRSG QRV LHIDSRSY YGGN WASFSFSGLL SWLKEYQQNNDIGEESTV VVWQDLI HETEEAITLRKKDETIQHTAEFCYAS QDMEDNVEEIGALQKNPSLGVSN FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVT DVEESVEKEK YCGDKTCMHTVSDKDGDKDESKST VEDKADEPIRNRITYSQIVKEGRRFN IDLVSKLLYSQGLLIDLLIKSDVSRY VEFKNVTRILAFREGKVEQVPCSR DVFNSKELTMVEKRMLMKFLTFC EYEQHPDEYQAFRQCSFSEYLKTKK LTPNLQH FVLHSIAMTSESSCTTIDG LNATKNFLQCLGRFGNTPFLFLY QGEIPQGFCRMCAVFGGIYCLRHKV QCFVVDKESGRCKAIDHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQQTSILIVPPAE PGACAVRVTELCSSMTCMKDTYL VHLTCSSSKTAREDES VVKLFT YTETEINEEELTKPRLLWALYFNMR DSSGISRSSYNGLP SNVYVCSGPDC GLGNEHAVKQAE TL FQEIFPTEEFC PPPNPEDIIFDGD DKQPER/PLGTNN VVMAKLESSEVESKNLÆSPEKHPSK LEKSNLEMLFWTSFMASEFSLKDR RFPI
2050	7547	A	2212	328	583	
2051	7548	A	2213	1	416	PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVY WPLFVLIFHAI SPIPHFIAKRVTYDSDATSSACRELA YFFTTGIVVSCLWISP VILARVALIK\ WGACGLVLAGNAVIFLTIQGFFLIF GRGDDFSWÆQW
2052	7549	A	2214	1	180	AAATGAVGAATYPCAPNWK* RND EKTAADYKILGGSVLHLVLALRGG GGLRQ
2053	7550	A	2215	162	557	VASEHSPKIGASQGLDYEP LLVVAK VWYLTRPTG TKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEDIEP\ TDKVERNQRSVWEEK EG NPPPPQQQ RLHLQVAKQM\NDEK DSSLIYKILR WVQSFQT
2054	7551	A	2216	684	1496	LETSGLSENPLQAVGFGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVE EAPSGA\SYNPSFEDHQ TLLSAAHE VÆLQRQKEAEKLERQLRCPATEQ ARHPRSSTFQELCEGLLEESDGE PGQGE GPEAGDAEVCSTPARLATT EK\KTEQQRREKA VHRRLVTARA ALRAA\RLRATQELVFRVRGIQRPQ V\ALRLAÆLARRRRRRQARREAE \DKPRRLGT/RFKYQAPDIDVQLASSE LTDSLRTLKPEGQHPSRPVQELPRG

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						GI
2055	7552	A	2217	116	285	KLRNQRIQERHTDGGPEPLKSL*CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA
2056	7553	A	2218	3421	3698	AGRGPLRLQSHRFGRPSQVDCLSPA APDQPGQHKGKTPSPQKIQKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD
2057	7554	A	2219	381	1772	KMAESENRIQELSESSQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGGDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFLREFHDIERKFAEMY QPLEKRRQINAIYEPTTEEECEYKS DSEDC\DDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDPRGIPD FWLTVLKNVDLTLPLIKKYDEPILK LLTDIKVKLSDPGEPLSFTLEFHKP NEYFKNELLTkTYVLKSKLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LKTIKKKQKHRDL/WGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDDFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIYDNWMAAI EEVKACCKNLEALVEDIDR
2058	7555	A	2220	17	250	
2059	7556	A	2221	2	899	GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSCLATADLLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMTASLFKKKTVDVVIKEQNR ELRGTQRAINRDRAALEKQEKQLEL EIKK\MAKIG\NKEA\CKVLAKQLVH LR\KQKT\RTFAVSSKVTSMSTQTKV MDS\QMKMAGAMSTTAKTMQAVN K\KMDPQKTLQTMQEFPGRENMK M\EMTEEMINDTLDDIFDGSDD\EEE SQ\DIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\T\SKATISDEEIERQLK ALGVD
2060	7557	A	2222	3	586	ARAMGISRDNLHKRRKTGGKRKPY HKKRKYELGRPAANTKIGPRIHT VRVRGGNKKYRALRLDVGNFSWG SECCTRKTRIIDIYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPEEEIL NKKRSKKIQKKYDERKKNAKISSLL EEQFQQGKLLACIASRPGQCGRAD GYVLEGKELEF\YLRKIKARKGK
2061	7558	A	2223	2	727	LFPASAEQMGISRDNWHKPRKTG GPRESYPQAEAKSMSLGRPAA\NTK ILAPRRIQHSPVCRGG*QVNTVPLRF DIVGNFSWG/SKECCTRKTRIIDVV YNAI**PSWVRYPRPLVERICIVLID EQHPYRQWVRSPTYAL\PLGPQRK GAKLDSLKKEEIFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQQG KASLRICIAFK/RPGQC\GRAIDGYMT

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						RGHRVRSYYLRKIKARQSKINT
2062	7559	A	2224	298	408	CGII*ALNKKEHRGCDSPDPDTSYV LTPHTEEKYKKINEEFDNMMRNH KI APGLPPQNFMSVTVPTSPNALS Y TNP GSS
2063	7560	A	2225	1	1369	
2064	7561	A	2226	409	1944	LKMGRKKIQITRIMDERNRQVTF TK RKFGLMKKAYELSVLCDCEIALIIF N SSNKLQYASTDMKVLLKYTEYN EPHESRTNSDIVEALNKKEHRGCD S PDPDTSYVLTTPHTEEKYKKINEE FD NMMRNH KIAPGLPPQNFMSVTVPTSPNALS YTNP GSSLVSPSLAASS TLTDSSMLSPQTTLHRNVSPGAP Q RPPSTGNAGGMLSTTDLTVPNGA GSSPVGNFVNSRASPNLIGATGAN SLAGKVMPTKSPPPGGNLGMNSR KPDLRVVIPPSSKGMMPPLSEEE ELE LNTQRISSQATQPLATPVVSVTT PS LPPQGLVYSAMPTAYNTDYSLTS ADLSALQGFNSPGMLSLGQVSAW Q QHHLGQAALSSLVAGGQLSQG\SN L SINTNQNISIKSEPTSPPRDRMT PSGF QQQQQQQQQQQPPPPQPPQPPQ P QPRQEMGRSPVDSLSSFSSSYDG SD REDPRGDFHSPIVLGRPPNTED RESP SVKRM RMDAWVT
2065	7562	A	2227	3	168	PCPTHSRMLGSPQPKRQLPVA PVPT AQPPSPPKGRCQGQEPKPPRL PSP AQGPW
2066	7563	A	2228	272	416	VGRCFFLSSGGFFSLTSALPP PS/PSA HPGVLVTPFGAPTKPDRGRSRG
2067	7564	A	2229	109	866	DTRVG YFSSGAFAFFFLWARA ECRP LSKDSL VKPRATLPSIVGLGS VAVP RARRARRQERSRPRTGPGACLP PS LAPYGFARVERRARAMKAGFP VRR SGRKAPYGC GME\LA LRCLAE HG HSLGG\SAALGAS\AAAAARCKA AEA AADEPALCLQCDMND CYSRLRL LV PTIPPNNKKVSKVEILQHVIDY ILDQ LALETHPALLRQPPPA PPHHP AGT CPAAPRTPLTALNTDPAGAR\N KQ GDSILCR
2068	7565	A	2230	107	1073	
2069	7566	A	2231	23	538	LPEVPHSLRPRVKPHLCCAQPA VRV MARLPKLA VFDLDYTLWPFWV D T HVDPPFHKS/KVR*GQGR LGAR *DP ARAERTLALSSDGTVRDRRGQD VR LYPEVPEVLKRLQSLGVPGAAAS RT SEIEGANQLLELFDLFRCYLHSH PE WNESSNSKSRVRDICEGPNWAF EV QP
2070	7567	A	2232	685	1161	TFPLLPLADYTLWPFWVDTHV DPPF HNSR*GRDREDW/PAR*DPARA ERT LALSSDGTVRDRRGPDVRLYPE VPE VLKRLQSLGVPGAAASRTSEIE GAN QLLELFDLFRYFVHREIYPGSK ITHF

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						ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE
2071	7568	A	2233	79	564	SPTSAARSLRLRVMARLPKLAVFDL DYTLWPFWVDTHVDPPPHKSSDGT VRDRRGQDVRLYPEVPEVLK\DLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHR\EIYPGSKITHFERVA AE\TGISF\SQMIFFDDERREYCRRSA NWCVTCTSHPEW
2072	7569	B	2234	48	209	XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX*
2073	7570	A	2235	2	353	
2074	7571	A	2236	3	676	SAVEFPPLSHTTGTRPRTPIILLQQE NGYFIHTLWMGLALLGVLGDLGSGQ HRRPRSPCQPNFQQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APATDGG\FNLSTFLQEKTSVETR TMLLQPRGVPSASLQLTGVPHWGQ A/HYSVSVVETDYDQYALLYTRAS KGPGEFRMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDK CMTEQ
2075	7572	A	2237	1	1165	MGVTEVFLKDVITILLNLEELVQCRO TWGEARTRGKRVLGSLADEIVVRT QQPPSLEHKAWNATCKHWLAEEA ALEKYYSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTPLMLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFLTFISIDRYL IIKYPFREHLLQKKEFAILISLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLLGFS\PLF VMCLFYYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFSVLFTPYHV MRNVRIASRLGSWKQYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLLSFREK
2076	7573	A	2238	1	567	
2077	7574	A	2239	58	544	GKKMGSKAKKRVLLPTRPAPPTVE QILEDVRGAPAEADPVFTILAPEDPP\ VPFRMMEDAEAPGEQLYQQSRA YV AANQRLQQAGNVLRQRCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGWSATQAL PGGPSAPDWHSRGPSRGC
2078	7575	B	2240	1	1551	MCELDILHDSLYQFCPELHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLGNRHLHKERL AVYRWHASFICSGNTMPIVLVDWS DIREQKRLMVLRASVALHGRSVTL YEKAFPLSEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSRSKGRKNQRSTR HCHHPSPKIYSASAKEPVWLATNLP

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						VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFDC DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSDQHANEFGLS WILLGARTPTCKADLSRPYSCPHP QPQQRFLGDSGITTTSVPRYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLPNRSPTWQ ISIDKGPRQDTFMLFPPIKI*
2079	7576	A	2241	2	456	GTRSTRTARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLAAALLLL LLALYTARVDGSKCKC\SRKEPKIR YSDVKKL\EMKPKY\PHCEEK\MIIT TKSVSRYRGQEHCPHPKLQSTKRFI K\WYNA\WNEKAQRRVYEEAQGLR RRIG
2080	7577	A	2242	308	615	ETRVAVSGTGAAEV*GMVRLDISE GRAAVAAVVGGVVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG
2081	7578	A	2243	332	484	
2082	7579	A	2244	240	610	LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVAAVVGGVVAVGTV\ PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS
2083	7580	B	2245	158	2382	MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPP LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFMNMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN*
2084	7581	A	2246	753	1007	LAQGCSPGPSQDTALPGPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGNGSEGEKALTFHV CGDHPVKN
2085	7582	A	2254	188	833	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKL\VL\GLDNAGKTTLLHWLK DDQIGPTLFPPLPPTSEELTIAGMT\ FTTFD\LGGHGAKHVA\WKNYLPS QLMGFVFLVDCADHFSPSWNPKE LNALMT\DETILPMCPI\LGKN\IDR TDAISEEKLREIFGLYGQTTGKGNV TLKELN\ARPMEVFHVAVLLKEGK VYGRGFSAGLLPVLF
2086	7583	A	2256	333	621	CRKNSCYQAQNFNLRIPFSTTKLINL FHF*NDSQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFPSSL ESYIWHVKEKKYNPTAAAI
2087	7584	A	2257	29	659	LSVASFSFLS\NASAEDTMSRLSRLL WAATCLGVLCVLSADKNTTQHPNV

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						TTLPIVRETSAPVTPLPLVTPAPET CEGRNSCVSCFNVSVNNTTCFWIE CK\DESYCSHNSTVSD\QCVGNTTD FCSVSTA TPVPTANS\TAKTHSSSP LLQLPRQLLHQGTNTNTVNSVTSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK
2088	7585	C	2258	101	411	MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQIPIKXXXXXXXXXX XXXXXLF*
2089	7586	A	2259	2	575	
2090	7587	A	2260	1	265	SDALSKAQNDV MEMKMQSERLSK EYDQL\LKEHSELQHSSFGFLSKRS HKNGSIGKQTGSRKGSFRKRQKEK TVNFIKDTLQYTVSK
2091	7588	A	2261	47	906	RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIF\SFNVWGKIATFW NKAFLTIIILLIVLFLDAVREVRKYSS VHTIEKSSTRPDAYEHTQMKLFRS QKNLYIPGISLFFWLVRRLVTLITQ LAKEPVTORCALYLQAENTNKA K\FMEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLKTELKTS L\SKAQNDV MEMKMQSERLSKEYD QLL\EHSELQVPLGSFYLAFA PLHNPHSPSPRSGGFS AIDNPRGALPPCLV CVLFHHL
2092	7589	A	2262	669	995	KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHKSSKAIMTIPCKFISRKPSWEG DCSSLEPHGVSAFDIWPQLCIKKV LNHFSPRKN
2093	7590	A	2263	3	379	WPFLKLRLGTCGTCCSHEGRAAA WSAESSLQHSVVTMSLPLNPKPFL N\GLTGKPVMMVKLKWGMEYKGYL VSVD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNNVLYIRGVEEEED GEMRE
2094	7591	A	2264	68	268	QYLSLLLTQYSLVFICWLFICLALYV YLFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVPLFL
2095	7592	A	2266	190	554	HGVRSDLGRWPDHLCVCRHYHH LLHLLLLLPLQDVPPTTSWLSPPHP PLWCM/PPYPQPPSVPPSYPGPSLPG LPHHAASARECQHPYPIAVPHTLT HAHAHGPTRPTTRPLAGRSSRD
2096	7593	A	2267	2	445	
2097	7594	A	2268	200	894	TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLKSGTSLPHDHPG MHGMLKVLYGTVRISCMDKLDAG GGQRPRALPPEQQFEPPLQPREREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPAFLDILAPPYDP DDGRDCHYYRVLEPVRPKEASSA CDLPREVWLL\ETPQADDFWCEGEP

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						YPGPKGLPLKPLAHQERWAEDVPY PTTRAVSLPP
2098	7595	A	2269	257	781	QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPPIAFPFAFE AAQVEAKPDELKVTVKLKPRRLAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPLAEID/EFKSKE MGHFLKPDGPKIIGKVWHEKGM NDK
2099	7596	A	2270	271	404	
2100	7597	A	2271	2	5684	PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEGQN LGPQAIPQDGSITHQISRPNPPNFGP GFVNSQRKQYEWPEQTQQLLQ MQQKYLEEQIGHRKSKKALSARQ RTAKKAGREFPEEDAEQLKHVTEQ QSMVQKQLEQIRKQKEHAELIED YRIKQQQQCAMAPPTMMPVQPP PLIPGATPPTMSQPTFPMVPQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLPNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPPRVEFDDNNP FSEFQERERKERLREQQERQRIQL MQEVDQRALQQRMAEMEQHGM VGSEISSRTSVSQIPFYSSRLYLCDF VMQPLGLPQQSPQHQQMQGVVQ QQNIQQGSINSPSTQTFMQTNERRQ VGPPSFVPDPSIPVGSNPFSSVKQG HGNLSGTSFQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELPPQADQESVEPV GPSTPNMAAGQLCTELENKLPSNDF SQATPNQQTYANSEVDKLSMETPA KTEEIKLEKAETESCPGQEEPKEEQ NGSKVEGNAVACPVSSAQSPHSA GAPAAKGDSGNELLKHLKKNKSS SLLNQKPEGSICSEDDCTKDNKLVE KQNPAGEGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNSGNRLGLTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQQPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLSLVKE EPPEVPSPHPIPLSTAGKSSESRRND IKTEPGTLYFASPFGPSNGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHKVVILG

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						SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFKPPCEDEIDFL KKLGTSLKPDVPKDYRKCFCHEE GDGLTDGPARLLNLDLDLWVHLNC ALWSTEYETQAGALINVELALRR GLQMKCVFCHKTGATSGCHRFRCT NIYHFTCAIKAQCMFFKDKTMLCP MHKPKGIHEQELSYFAVFRRVYVQ RDEVQRQIASIVQRGERDHTFRVGS LI FHTIGQLLPQQ\MQAFHSPK\ALFPV GYEA\SRLLGGTRYANRRCR\YLC SIEGGRDG\RPVFVIR\IVGNKGHGR TGV LKVD\SPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFGLTVS AVARIAESLPGVEACENYTRYGRN PLMEPLAVNPTGCARSEPKMSAH VKRFVLRPHLTNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMKT EWKSNVYLARSRVSGGWGLLWL VRRLEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMFMRMDN DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKDFEDDQHKIPCHCGAVNCR KWMN
2101	7598	A	2272	1	2806	
2102	7599	A	2273	288	843	AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPIKSRK\GD VLHMHYTG\KLEDGTEFDSKPAPR TSPFVFSL\GTGQVIK\WDQG\LCL GMCEGE\KRK\L\VIPSELGYGE\RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKKTLSKPK
2103	7600	A	2274	80	308	VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWAH
2104	7601	A	2275	2	456	RSFFFFCEVGSWVGSMRVVMARL LSEGEQGIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLFL VSL LGTDLARGRNSASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QG WVSTSWGSSSPSPVQFFPKLLEF TGK
2105	7602	A	2276	2	81	
2106	7603	A	2277	325	485	ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLT KYR
2107	7604	A	2278	291	529	LFL LCKVGTWHQGPNHQKAPKAPG TPPTPSYPGTPSRQLLWQWVQRP PA\LP\PAVGTSTSPGRQCPGFS AQ HHLFP
2108	7605	A	2279	52	109	TVRLPR\HPGSRKNMASYCRIPACIA AERRYGTCTMYQGRWAFSS

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2109	7606	A	2280	3	452	
2110	7607	A	2281	26	526	NSTDSETHPWLLSPADKTTVK/AP AWGKVGAGHAGEYGSEALERMFLS FPTTKTYFPFHDLSHGFCPLRATG KKVADALTKRRGAPLDDMPNALV RPLASDLHAHKLARVGPSTFKLLKP LACLALTLGPAHLPRPSFTPGGCKAS LGQSFLGFLKHKRCLNLPNYR
2111	7608	A	2282	447	539	
2112	7609	B	2283	8	694	MQYNRRFVNVVPTFGKKKGTTFTK IFVGGLPYHTTDASLRKYFEGFGDIE EAVVITDRQTGKSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVIPAA PVPSLSSPYIEYTPASPVYAQYPPAT YDQYPYAASPATADSFVGYSYPAA VHQALSAAAPAGTTFVQYQAPQLQ PDRMQ*
2113	7610	A	2284	3	191	
2114	7611	A	2285	101	444	CSLFVPRPRSLQPLRRVTGQETGRP RSKAHVASTWRAFPEDQVLLAG APLEDEATLGQCGVEALTTLEVTG RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG
2115	7612	A	2286	2622	2881	KKSKDNKTFEEEEETESCSALQAGV QWCNLGSLQTLPGSNDSHASASR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGTPLDK
2116	7613	A	2287	41	655	TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAESTKIPR LRTDLFPKTRIQDLNRIFPLSEDS GSGFGSGSGSGSGS\GSWFPNGKW EQDYQLVDE\SDAFHDNLR\SLARI LASASRDWGQHGLAEFNVIKEDL PTLTTRQMVKQYFNVPVMNMIN WDKEFYRNF
2117	7614	A	2291	163	703	READMGTMKTQRDGHSLGRWSLV LLLGLVMPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDPRPT MDGGP\DTTK\PVSTVKETVCP\RP TQQ\SPKDGDFKRDGLLNRGMGTV\ TLN\QARGSFDISCDKDNKR FALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPRTES
2118	7615	A	2292	100	546	PPRTGQRQPLHSARRHGSPVS\ELAC I\YSALISARTDEVTVT\EDKINALIK A\AGVNVE\FPWPWLC\QRPLANV NIG\SL\CNVRGPVEPAPSSLVAAP AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL
2119	7616	A	2293	33	494	
2120	7617	A	2294	1	609	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVDVGGGALGRLLVVYPWT QRFESFGDLSTPDVAMGNPKVKA

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						HS\KKGLRGAFSDGLAHL\DNLKGT FATLASEL\HCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN
2121	7618	A	2295	1	338	AALAWAVSRLHFSRLSFPWPWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNG\ FFPVVDGFIRRVPLGSLNLPGIRS FVDKVGESNNMV
2122	7619	A	2296	67	283	LPFPGCFFLF*VLFVAGLAFVIGLER TFRFFQKHMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR
2123	7620	A	2297	3	209	
2124	7621	A	2298	3	544	TRAALAVAVSRLHFSRLSFPWPWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAFVIGLERTFRFFQKH KMKATGFFLGWVYLVVLIGL/WPLI G\MIFEIYG\FLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVG ESNNMV
2125	7622	B	2299	54	1731	XKLSRECEIKYTGFDRDPHEERQAR FQNACRDGRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLERA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERALAAAANKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDRVRKATQQAE QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEQVEQEAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNARVKQLKRQLEEA EEESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPQETSQ*
2126	7623	A	2300	1	2448	
2127	7624	A	2301	1	2655	
2128	7625	A	2302	5	605	VDPDSGQIQVPCTPRGLKWSPNMN PARKTDACGEDTHPSLLGVFPFSRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLSQRVPAPPPQE PKMPSLCCRNTSTTFSGRPSQSPTK KQRPR
2129	7626	A	2303	1	588	MGFCHVDQTGLELLTQPLLALIGAA

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						LEGGRAGGAADLAPDFGRALALQIK YTGFRDRPH/EERQARFQACRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPNLVTPPRYTP MVPCGGHHQAQRKRPLCTPPSSIQ QGSM SVKSMPTPVA AHKSFTSALC
2130	7627	A	2304	1	615	GLKGGKMPRVVPDQSKFENEFF RKLSRECEIKYTGFRDRPHEERQAR FQACRDGRSEIAFVATGTNLSLQF FPASWQGDQRTPIREYVDLERA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTQ QAFEEARRMTREFEDRDRSHRQEM EARVSQLLAVTGKKQLDPRPGSNL GGGDDLKLR
2131	7628	A	2305	73	168	
2132	7629	A	2306	322	671	RLWASPAAPGKKKEMGNSMKSTP APAERPLNPEGLDSDFLAVLSLYP SPDINPPIFRRGEKLRVISDERGWW KAISLSTGRESYIPACVARSYHGW LLRGP GK NMAEELLQLPD
2133	7630	A	2307	624	1581	KAATSENKIIICEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLNPEGLDSDFLAVLSLYPSP DISPPIFRRGEKLRVISDEGGWWKAI SLSTGRESYIPGICVARVYHGL/W LFEG LGRDKAEELLQLPDTKVGSF MIRESETKKGFYSLSVRHRQVKTY RIFRLPNNWYYISPRLTFQCL\EDL\V NHYSEVADGLCCVLTTPCL\TQSTA\ APAVRACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSSPPYFED
2134	7631	A	2308	52	454	SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
2135	7632	A	2309	3	452	
2136	7633	A	2310	26	502	NSTDSETHHGARLLPDKTKAQRPP RLKLGANA\GEYGFGGPWKGMFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DALTSQPCRNVD\DMPPQ TALSAP EATLHG\HKL\RVDPVNFKL \LSH\CLLG*PWP AHLPRPSFTPCGCT PSLEQSSW AFC
2137	7634	A	2313	43	595	LRNMWQLERNVIET\INTFHQYSVK LGHP\DTL\NQGEFKELVRKDLGQN FLKKENKNEKVIEH\IHEDLDTNAA Q\QLSFEEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGHSWWPRPQA TNHGGQATLPLPKPGPRGLLCQTVL AVLGGWGQIKSLP

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2138	7635	A	2314	3	419	SLYHNSSQKRHWTFSSSEQLARLRADANRKFRCCKAVANGKVLNDPVFL EPHEEMTLCKYYEKRLLFCFSVFKP AMPRSVVLTCAFLACKVDEFNVSN PQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN
2139	7636	B	2315	324	487	MQRVRAGRIVITTTARQRLPDALG FREIFSSEQLARLRADANPNDAK PWPTGS*
2140	7637	A	2316	1	1050	
2141	7638	A	2317	191	229	
2142	7639	A	2318	186	1232	CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRKFRCCKTRAH/GKVFNDPVFLPEHEEMT LCKYYEKRVI\FCSVFKPAMPRSV VG/SRACMYFKRFYLNNSVM\EYHP RL\IML\TCAFLACKVDEFNVSSPQF VG\NL\RESPLG\QEKALEQILEYELL PYTSNFFHLLVHNPNY\RPFEGFLND LRTR\YPILENPEILRK\TA\DDFLNRI ALTDAYFLYTPSQ\ALTAILSSASRA GITMESYLSLMLKENRTCLSQLL DIMKSVRN\L VKKYEP\PRSEEVAVL KQKLERCHSAELALNVITKKRKG YEDDDYVSKKSKHEEEWTDD\DLV ESL
2143	7640	A	2319	152	371	DVLLATSSSEPSLFCPLCLTASTPKP LPPPGVLPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS
2144	7641	A	2320	4	474	PQYPAWHEGERAEWLCGRVSETGS ACSMADQL/TLKEQIAEFKEAFLAF DKDGDGTITTK/ENLGTVNEILLGSN PTEAELQDM\NEVDADGNGTIDFP EFLTMMARKMK\DTDSEGRKL\EEA FRVFGRLRVGNGLYL VACRNFRHV DGQTLGGGSLPD
2145	7642	A	2321	291	648	LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHSPTSFTSTSP GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRAS\HPAGPPVPSGVLV SRRRPEPGQGKPPESDFDH
2146	7643	C	2322	155	316	MTGPVSGSFIHWVLFSGFSSMSSNA SNVFGLV RPSC TTGLSRMAADSAG CCSL*
2147	7644	A	2323	28	1323	PSGARVAGAGPCGGGGMFVQEEKI FAGKV\LRHLICASDGAEWLEEATE DTSVEKLKERCLKHCAHGLSKDPK SITHHKLIHAASERVLSDARTILEENI QDQDVLLLIK\RAP\SLPKMADVS AEEKK\QDQKAPDKEGILG\ATAN LPSNKLDRAAVQTNMRDFQTELK ILVSLIEVA\QKLLAL\NPDA\VELFK EGECNCWDEDGGMSVWDEACPA A FQREMGLFRENRA TKALQLNHMS VPQAIGSWL\NEHA\EDPTIDTLPAG QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRRKREFRADA

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						RAVISLMEMGFDEKEVIDALRVNN NQNAACEWLLGDRKP\SPEELDK GIDPD\SPL\FQAIWDRWVQLGLTN PKTLAFEDMLENPLNSTQWMNDP ETGVPVMLQISRIFQTLNRT
2148	7645	A	2326	307	412	SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE
2149	7646	A	2327	50	247	
2150	7647	B	2328	276	779	MRTLAILAAILLVALQAQAEPLQAR ADEVAAPEQIAADIPEVVDSFAW DERAPLQVSGKSSPVCARLLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMP HGMKVPLFRFPQDKIIVLSTLIPTGD YSPHNKKNLFMRMVTSP*
2151	7648	A	2329	3	333	
2152	7649	A	2330	35	717	RRSSPSLLPLAERGGRARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVS\SSR\HPDRWIVPWKEG MEARRKEAKCGKQVREVCEGRLG VKGTLGRLVGIFENQERKHRTYV YVLIVTE\LEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTP\VVVATTYSVSGFRA SMFRAFRWT
2153	7650	A	2331	104	381	IQGGSMTTSSFSSTICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS
2154	7651	B	2332	228	445	METSSRELQAAEYLEKHQIKEVVSY LTSALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX*
2155	7652	A	2333	3	1459	GSKQVSEGTDNGDLPSYVSFAFIEKE VGNDLKSLKKLDKLEQRTVSKMQ LEEQVLTISSEIPKRIRSALKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISSQIEIERHLAYLKWI SQIEELSDNIQQLMTNNVPEAAST LVSMALDIKLQESSCHLLGFMRA TVKFWHKILDKLTSDFEILAQLH WPFIAAPPQSQTVGLSRPASAPEIYSY LETLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTPLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGSV NARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMLSSEAAWVSQ YKDITDVDEMKVPDCAETFTLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK
2156	7653	A	2335	46	1146	
2157	7654	C	2336	17	196	MTTLVTTTTMDMVIIATSRVVMGR YPGEVVIKIATNHTKLFHLQLIPNSG NFIAGPVSR*

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2158	7655	A	2337	208	1504	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGA AAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSASEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEVESIELPMDNKTNRKRG FCFITFKEEPPVKKIMEKKYHNVL SKCEIKVAMSKEQYQQQQWWSR GGFAGRARGRGGGPSQNWQNGYS NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSMSQSGYGK VSRRGGHQNYSYKPHLNYSICNLAS PTGGEAVFSNLKIQFESGS/CH*LLI AVQTKFLYQVPEWKYD/VGSL
2159	7656	A	2338	208	1466	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGA AAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSASEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*GEEPVKKIMEKKYHNVL LSKCEIKVA\MSKEQYQQ\Q\QQW DSRGGCAGRA\RGSGGQ\QSGYG K\VSRRGG\HQNYSYKPYLNYSICNL SPTAGTSLQALCRADFRFSQARS MR TG*RDAPRSRMLPFGGEAVFSNLKI HL/NGGSCHLLIAVQTKFLYQVPE WKYDVGSL
2160	7657	A	2339	1070	1238	PQRDFQFFLLWPPGGEAVFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL
2161	7658	A	2342	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEAL/RMFL/SF PTTKTYFP HFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKL RVD PVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLT SKYR
2162	7659	A	2343	2	512	GLEFGTSHRLRENPPWCLSPA\DKT NVKAVA WGKVG AHAGEYGAEAL RMFLSFPTTKTYFP HFDLSHGFAQ VKGATAKKVA\DALTKAVHRGRT CPNALSALSGPATAHKL R VGPST FKLLKPLACLVDPGPAHLPRPSFNP WRLQGFLG TKFLGFLVEAPLLEPSK
2163	7660	A	2344	265	426	SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMHAHTWPLCLQDVLV ECCSQS
2164	7661	A	2345	56	341	IVTLDWSRNLKYNRCWSKCYILSSS DSSSFRDSFTNPAEF*FKSFILNFV

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						MYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV
2165	7662	A	2346	333	534	LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FL\HPM*LFSPGLYILSNFH
2166	7663	C	2347	117	386	MDILICTDFGSVNYFNVWRLPKSYL SLFYRIYIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREAEKYAK ESLKEEDESDDDNM*
2167	7664	A	2348	2	359	FEDGVLLCHPRLEGSGT\SAHCNL\S LPGFKRSSCLRLP\SSWDYRNMPY PGYFCIFGTNNTETGFHQASFKLL NSRDLPTLAPVKCWDYRHEHCTRP LKYIFYQRYSHCMLEQHLLN
2168	7665	A	2349	648	887	SWKLLLLLCLLKNEHLPTKPTGHS NIADQTLKKSFCLPFFHKV*KGLIF LTPRTTPSLHLPIAVLLFSTAFIAYS T
2169	7666	A	2350	306	449	EIKKKYLLPGVVAHACKPSTLGGR GGQIISGQEFET\SLTNMAKPCFF
2170	7667	A	2351	1	625	NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWKG\VNVE\ DAGGE TPGKGSLLVYPW\TQRFFDSFGNLS SAFCPSWPTPKVKAHGK\KVL\TSLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK
2171	7668	A	2352	1324	1671	IVQTLSTLSKSSCRSTEPCTSLPDL QVGTTCRPHGTCC\NRCHVGGLMN PLKPNC\GCRKCNCGYLYIYLGQR LHPRGKFQPGNNHRFSCTQSVHMDI THSGMFLSLCFPGSTMF
2172	7669	A	2356	8	564	SAQMAVTTADPRVVRPRVRTQLCSL ASLIQTLLVHLTPEEKSAVTALWKG VNVDEVGGKALGRLLVYPWTQR FL\ES\FGDLSTPNAVMANPKVKAHS \KKILGALLVVGLAHL\DNLKGTF HTEVSLHCDKLHVDPENFQAPGAT CLVLCAWANHFVQKNFTPPVQAC LFRKL VAG\VANALAHK
2173	7670	A	2357	23	679	GLLTSGGAHLSPSRVTQGIYMSAL SEMPKPPDYSELSDSLTAVGTGRF SGPLHRAWMM\NFRQRMGWIGV GLYLLASAAFYVFEISETYNRLA L\EHIQHPPEPLEGTTW\THSLKAQ LLSLPFWVWDSYFFWVPY\QMFF VSLYSCYKELDPQNSGGYCYPSPIW LWAVYFGNRHAF/VVKASNSDSA DLQLIDTVKSVTRFFPLRITKTGQS
2174	7671	A	2358	17	392	SFKMADQDPAGMSPLQQMVASGT GAVVTSLFMTPLDVVKVRLQSQR SMAS\DAFKIVRHEGRTLWSGLP ATLVMTVPATAIYFTAYDQLKAFL CGRALTS DLYAPMVAGALARREHR LGPLTS

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2175	7672	A	2359	1	725	RFTGTMDAFVKIVRHEGTRTLWSG LPATLVMTVPATAIYFTAYDQLKAF LCGRALTSPLYAPM/VAGALARLSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLEMR TKLQAQHVSYRELGACVRTAVAQGG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVA AELTLPY
2176	7673	A	2360	102	1573	SFKMADQDPAGISPLQQMVASGTG AVVTSLFMTPLDVGKVRQLQS\QRPS MAELMPSSRLW\SLSYTKLPSSLQS TGKCLLYCNGVL\EPYLY\CPNGAR CATWF\QDPTRFTGTMDIAFVKIGE ARGAPRTLWSGLPATLVMTVPATA IYFTAYDQLKAFLCGRALTSPLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVRNRELGIACVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPQAL\YWF\NYEL\VRSWLNG LRPK\DQTSVG\MSFVAGGISRTVA AVLTLPF\DVVKTRQ\VALGAL\EA VKSEPPCNDST\WLL\LRIR\AESG TKGTLLQASFPRIKGCPPSCA\MIQ HLIEFRQKAFFPRGLNPGTGFLGGL EKGPKEGKDPVSSQREWGRRQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSGRPSTSSRHNFLLLPVVG ITYPPPKFKTKSSELPFVFPCGLL
2177	7674	A	2361	1	215	QPVMSEEEEDQYLAVLTFPRCVLV MIHTHAQVLNHVCIYVCVHMSVAV Y/ISACRATDPDTHTCVYMIQTY
2178	7675	A	2362	3	543	TRNTLGWEVSSFSPLLSSCLNMVRT KADSVPGT\QEKVVAARAPRKGL\G SSTSAHLIRPSVSIEESLKNKYARRE PPFCVRP/TLPKWAKREIGEFRLSP KDSEKENQ\PEE\AGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTFLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG
2179	7676	C	2363	69	290	MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDQWQPFLLSAGER*
2180	7677	A	2364	663	793	DGDSVMVLPTIP\EEEEAKKLFPGKVF \TKELPFGKKYLRYTPQP
2181	7678	A	2365	1	726	MPGGLLLGDVAPNFEANTTVGRIRF HDFLGDSWGHFSFSQ/PGGFTPWCA PRSFARA AKLAPDFAKRNVKLIAS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLFPPIIDDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCFVFGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMVLPNPSPSEEA\KKLFPEKE SFTQKELPNLAKKYL\RYTPQP
2182	7679	A	2366	3	452	
2183	7680	A	2367	1	627	TLLVPQDSERTHPWLLSPADK\TNV

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						KA/AWGKVGGAHAVRSMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKLRVGPGST SKLLKPLACLVDPGPAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPPAPP LSCTRTPVVFEIKS
2184	7681	A	2369	1	467	GTSACGVASLSVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNYLCIRA ASSQHLKCHWVGGNKTCFGPDDL GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM
2185	7682	A	2370	131	406	EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATQRLANF L\HSSNNLGGILSSTNVGSNTYGK RNAVEVLKREPLNYLPL
2186	7683	C	2371	257	422	MQVCFRQGFITLPGHHGLIATLGA PQLYMFLVLRASLFLWLSXFXRSX KLXXXRN*
2187	7684	A	2372	621	1202	GVPEPRARPSTSGMNGDRIRLPCWR NDROK\THML\DVMDHFSRASSIH RRALSRDRFFFTREPQD\TYHYL\PFQ PCPHRRPHFFFPKSRNRPA*CPFSS \TKPLNFHAMFQPFLM\HEGSAGP WDIHFSHPAFQHPPTFEIREGD\DDR DCCAGEI\RHNSTGLPCGLKDQVVT K\CREDLVLWDCFHQQPLPG
2188	7685	A	2375	154	1702	IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAGIVSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIQAKTS PVDEKALQDQLVLVAAKLDTEDKL RAAMV\GMLANFLGFPYYMGHMS ELWGV\HGVATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSRDLAHKVLSAL\QAVTGLLVA PGRADKQAIQLL\STVVGVTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETID\RLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGKM KGFSLLAEPQEFWVDNSTSVSVP LSGMGTGFQHWSDIQDNFSVTQVPF TDSAFLLLIQPHYASDLADKVEGLT FQQN\SFNWMRKL\PRTIHLTMPQL VLQGSY\DLQDLLRPGSSCPFLHTE LNLGRISGNDRI RVGEVLNSIFFEL EADEREPTTESTQQLNKPEVLE\VPL TRPFLFAVYDQGATALALSWGRV GKPA
2189	7686	A	2376	181	353	VGDRCEGNGNEARGHWKREVCCP GARSGASV*GSSGRLGLCL*VGTR AG*PGYPASLVPT
2190	7687	A	2377	1550	1823	GRLLDEPQAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFFPNLEKTVTFQSLLGPLKIPKEPG

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						LKEIKLTNVKKSCTLP
2191	7688	A	2378	134	321	GCF*KGRDLFADKMQEHSQ*FTAL FQPTNQKISSWVC GPKVNFKAITG SRSGKAIQNVES
2192	7689	A	2379	1	602	RTRASTRPSRDYGNVAVLWTRTSHP RPLTEPEPRATMSHGKGTDMLEPIA AP\VGFLSLLRTRGCVSEQRKVF GALQEALTEHYNNHWFPEKPSRG SG\YRCIR\NHK\MTPIISRVASQV LSQAQL\HQLLP\SELTLWVDPYEV S\YRIGEDGSICVLYE\EAPLAASCGA SFT/CARNQVACWGRSSPSK\NYVM AVSS
2193	7690	A	2380	28	423	SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCKIV*M STSKTGKHGHAKVHLVGIDIFTGKK YEDICPSTHNMDVPNIKRNDQFLIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG
2194	7691	A	2381	1	930	
2195	7692	A	2382	171	695	NRQDDLDFETGDA\GASATFFM\QC SALRKNGFVVLKGRPCKIVEMSTSK TG\KHGHAK\VHLVGIDIFTGK\KYE\ DICPSTHD\MDVPNIKRNDQFLIGI QGWGTL\SL\Q\DSGEVREDL\RVSP EGDL\GKEIEQKYDCGEEILIPVLSA\ MTEEAA\VAIKAHGKITGSPGVAVV ASK
2196	7693	A	2383	789	1380	IPYFLMVYGLQTL MCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPIPPQKKDYWVLLSLGAPKFK GYLVLCCMLQEPCKQPGKSTGWI RNYPSPWMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWGSPGQEQVLGLQ
2197	7694	C	2384	248	433	MSGILVLNLF LTLG SVGPSSSVTLV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP*
2198	7695	A	2385	1	1108	
2199	7696	A	2386	1	1528	MGTRAARPAGLPCGAENPARRRLA LGARQQIHSWSPRTPTSTRLTAPAGP ARGVARPAMAPDPVAAETA AQGPT PRYFTWDEVAQRSGCEERWLVIDR KVYN\INEFTRRHPPGSRVISHYAG QDATDPFVAFHINKGLVKKYMNLSL LIGELSPEQPSFEPTKNKELTDEFRE LRATVERMGLMKANHVFFLLYLLH ILLLDGAAWTLWVFGTSFLPFLLC AVLLSAVQAQAGWLQHDG\HLS VFSTSK\WNHLL\HHFVIGHLKGAPA SWRNHMHFQHHAKPNCFRKDPDIN MHPFFALGKILSVELGK\RKKKFM PYNHQHKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRFF LTYVPLLGLKAFGLGFFIVRFL\ESN WVFWVTQMNHMPMHIDHRNMD

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						WVSTQLQ\ATCNVHKSC/AFNDWV SVG\HFNFQIEHHLFPTMPRHNYHK VA\PLVQSLCAKHGIEYQSKPLLSAF A\DIHSLKESG\QLWLDAYLHQ
2200	7697	A	2387	45	949	APWWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGRR SSAPAHGDESCSLRPLSLAHGEP GGRRRAEACSRLSRSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQQSRSEAQPDAMEQ PRKRW
2201	7698	A	2388	804	985	VGGDSQDLRDPVPPQTAPPPNSLS PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG
2202	7699	C	2389	258	461	MSVTFIAVARGKLFFENLGHSELPL SLEWQTS DGEVEARGSRGGEALPR PGSMQPCPADVTRRPPTRP*
2203	7700	A	2390	1	370	GTRVTSGGSRRPGMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQ\ILKRKVSRLQLIKVTDISGG CGA\MYEIKIESEEFKEKRTVQQHQ MAINQALKEEIKEMHGLRIFTSPVK R
2204	7701	A	2391	1	1107	
2205	7702	A	2392	1	1230	
2206	7703	A	2393	1	908	
2207	7704	A	2394	177	934	PGLSQEPGSGMETVVIVAIGVLATIF LASFAALVLVCRQR\YCR\PRDL\LQ RYDSKPIVADLIGAMETQSEPSLE L\DDVVITNPHIEAIL\ENEDWIEDAS GLMSH\CIAIL\KICHTL\TE\KL\VCHD NGALGAKMKTSASVSDIIVVAKRIS PRVDDVVKSMYPPLDPKLLADART\ TALLLSV\SHLVLVTRNACHLVTG\G LDWINDQSLSVAAEEHLEVLREAAL\ ASEPDKGLPGP\EAFLQEPVLQFSAY RPAA
2208	7705	A	2395	1	333	GTRGERKAGLARGQVCGLSPFPK TNKESFPNSQLNPFWNY\CGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDNDRLSRMTSMCSISR VPEHVEFPNPK
2209	7706	C	2396	7	279	MXKGS PRXNFLECEKKSGQNPWAG LLRPWWVGHPKAPLIPVFSSISFPL YNPHFPIXILCNKLKSHVCKKASKY TNNPISQQWTLFSIK*
2210	7707	A	2397	35	416	SRAVEFVRSCAGYGERKAGLARGQ VCGLSPFPKTNKESFPNSQLNPFW NYVWGLGPCGASLSLVSFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSRMTSMCSISRVPHEVEFP

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						NPK
2211	7708	A	2398	3	344	
2212	7709	A	2399	1	1359	
2213	7710	A	2400	1	463	LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCRVAGTEDEEEEE GRRETPEDREVRLQLARKREVRLLR RQTKTSLEVSLLKYPCKSFHAI GNNAVAFLSSFVMNSGVWEEVGC AKLWNEWCRITDTTHLSSTEAF CVFYHLKSNPSVFLCQCSCY VAEDQQYQWLEKVFGSCPR KNMQITILTCRHCTDIKTSE STGSLPSPFLRALKTQNF KDSACCPLEQPNIVHDLPA AVLSYCVVWKIPAILYLCY TDVIGLDFMTVEAFKPIL SYRSLKGLVKKNIPQST EILKKLMTTNEIQSNIYT
2214	7711	A	2407	160	441	
2215	7712	A	2408	107	691	RTAILSRMKIFLPVLLAALLG VERASLIMCFSCLNQKSNLY CLKPTICSDQADNYICVTV SASVAGIGNLVTFGWSL ASKTCFPCCLAPFPEGRS MLGVAASMGHSAFCQSFL VAIFSCGPMAGLRGKR SPLLGARACCLSLAGRALL RFGPLDRPEPCSPDPPA QEGKPSPFWIPQCMGAP DSSRALICALGPRSG
2216	7713	A	2409	2	432	GRPPPDVEVMTSLKVDNLT YHTSPDVYIPRDRYTKES RCFAFVRFHDKRDAEDAM DAMDGAULD/GSELRLQ MARYGRTPDSHHSRRGPP PRSYGCVGYGRRSRPRL RRMP/RSRSTRSRSR SRSRSTRSRSTRSRSTR SRSRSTRSRSTRSRSTR
2217	7714	B	2410	1522	2003	MAIIYGVFSASNLITPSV VAIVGPQLSMFASGLFY SMYIAVFIQFPWFSFY TASVFIGIAAAVLWTAQ GNCLTINSDEHSIGRNS GIFWALLQSSLFNGLY IYFAWQGKTQISESDRRT VFIALTVISLVGTVLFF LIRKPDSENVLGEDESS DDQDMEVNESAQNNTK AVDAFKKSFKLCVTKEM LLLSITTAYTGLELTFF SGVYGTCIGATNKFGE EKSLSLIGSGIFIGIGE ILGGSFLGSSKNNRFG RNPVLLGILVHFIAFY LIFLNMPGDAPIAPVK GTDSSAYIKSSKEVAIL CSFLLGLGDSFNTQLL SILGFLYSEDSAPAF AIFKFVQSICAAVAFF YSNYLLLHWQLLMVIF GFFGTIFFFTVEWE AAAFVARGSDYRSIM LKSFLDSGDI LAQLCRRQQPRAPLT IRTSPDTLRRVFEKY GRVGDVYIPRDRYTK ESRGFAFVRFHDKR DAEDAMDAMDGAUL DGRELRVQMARYGR PPDSHHSRRGPPRS*
2218	7715	A	2411	2	229	
2219	7716	A	2412	3	353	FPLPFFTLVIWPGIRKFK LVHADGSLCEIFLIGP FKNMAGWNISVPYWF DQSLSKYVPETETMCT LMEGKLNFFLFKPRC IGKQCKRRTWGKRTT *SIRRR

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						SPWNKQLGYLKRLFW
2220	7717	A	2413	18	282	DPLKSGPRNRS*TRWTPSPRSVARRS KSKLSVSRSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSPSP EEGAGVLLRK
2221	7718	A	2414	2	830	LRSPSVLFCGKAFPVSPRGRQLPER RGVAPPRAEEAGASSRGSGPPLRA MSYGRPPPDVEGMTSLKVDNLT\Y RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFHDKRDAE DAMDAMDGAVLDGGELRVQMAR YGRPPDSHHSRRGPPRRYGG\GY GRRSRSPRRRRSRSRSRSRSRSR SRYSRSKSRSTRSRSRSTSKSRAR RSKSKYSSVSRSRSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSSVEEGA VSS
2222	7719	A	2415	1	320	RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSHTAKEP YTRNECGKVFG/HIARHQIHHSTEKP YKCN/NTLKAFSKHSGLMAHLLIDR PEKLCHYS
2223	7720	A	2416	733	1005	NPQTPMKNCWPLEKKAEP RPFLGS SMPLGFCPHGPPCSCDFLETHFLDE \EVKLIKMGDHLTNL\HR\LG DPEA GLGEYLFERLTLKHD
2224	7721	A	2417	148	1057	
2225	7722	A	2418	87	241	EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC
2226	7723	A	2419	1	924	
2227	7724	A	2420	1	1004	MPVGAGRRAKGD PATLGALAVFTV GAKRSKGHSPKHPAGRLPPLPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLLMDCRPQEL YESSHIESAINVAIPGIMLRLRLQKGN LPVRALFTRGEDRDRFTRRCGTDTV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGFSKFQAEFS LHCETNLDGSCSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSDG SPLSNSQSPFPVEILPFLYLGC AKDS TNLDVLEEFRGSSPYMILFHYGEMG TSYVPITSHFRQKLAQGFPVSTGTP GFIYS AK
2228	7725	A	2421	686	1812	TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGFSKFQA EFSLHCETNLDGSCSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQSPFPVEALALPSYLG AKDSTNLDVLEEFGIKYILNVTPLN PNLFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCV LVHCL AGISRSVTVTVA YLMQKLNLSMND AYDIVK\KKKSNISP\NFMFG\QLL GLSRRDAGDSAGPCGQQGSRHSRL YFYHFPFTRNVLPGWDFLQSTWKD

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						PTPFLAGMCLALQQFLLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG
2229	7726	A	2422	66	187	WGGGGSAAAAAMEANWTAFLFQAH EASHHQQAQAQNSLLPLLSSAVEPP DQKPLLPIPIQKPGAPETLKDAIGI KKEKPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTSS SGTNPSSSASTTAMPVTQSVKKPASK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPICNQRFKRKDR MTYHVRSHGEGITKPYTCSVCGKG FSRPDHLSCVHKVHSTERPFKCQT CTAAFATKDRLRTHMVRHEGKVSC NICGKLLSAA YITSHLKTGQSQSIN CNTCKQGISKTCMSEETSNQKQQQ QQQQQQQQQTHVTISWPGKQVET LRLWEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSGTMSNP VTVAAAAMSMRSPVNVSSAVNITSP MNIGHPVTTISPLSMTSPLTLTTPVN LTPVTAPVNIAHPVTITSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSP\WRPTGPRSCSRPMKLPITNSR QHRTACCPs
2230	7727	A	2423	3	777	RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFGLSPTVVTLAEL LVLLAALLATVSGYFVSIDAHAEBC FFERVTSGTKMGLIFEVAEGGFLDI DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYKF\CFSN\RMSTMTPKI VMFTIDIGEAPK\GQD\METEAHQN KL\EEMINELAV\MTAVKH\EQEY MEVRERJHRAIQRTTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG
2231	7728	A	2426	89	136	
2232	7729	A	2427	1	916	MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQKEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSPQARE DQLQRKAVVL\EYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQQRY SLFLPLHELWKQYIRDLCSG\KPD\ TQPQMIQAKLLK\ADLHGGLFISVT K\SKWPLLMLGITGNPFYQETKHIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFPSLGQVNRISA KKFQSEGNRLTL
2233	7730	A	2428	2	484	PDSSGPHRLRENPPWCLSPADKTNV KAAWG\KVGAAVVRSMCAEALER MFLSFPTTKTYFPHFDLSHGFCPL RATGKKVD\EALTKRRGAPLDDMP NAL/SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSWVSC

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2234	7731	A	2432	197	332	
2235	7732	A	2433	1	1788	
2236	7733	A	2434	3	111	
2237	7734	A	2435	220	423	HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIKIPYPKKKKK
2238	7735	A	2436	273	499	RSGVRDQPGQHKGITSLLKIQKLAR RGGACL*SQLLRRLRQENRLNPGG GGCSEPRSCHCTPAWETEQDSISKIK
2239	7736	A	2437	1	1176	
2240	7737	A	2438	245	394	
2241	7738	A	2439	458	701	GPAPTRRGPAHPGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHPG SRASGTGPGPCQRRRRSDHSSAGK WPLREASL
2242	7739	A	2440	365	814	AALRSSENSRHRSLVKMSDKKAK DPVN\KSGGQGPKRKNWSKGKSSG TSFNNLVLFDKATYDKLCKEVPNY \NLITPAVGSERL\KIRGSLGQKPFQ ELLSKGFIPNWFSKHRASSYFTPGIT KGG\DA\PSLLGEDCMNRSNPPVHLE K
2243	7740	A	2441	41	565	APSPRRPWGHFTEED\KATIK\NLWG KGEMWKDAGGKNPWERLPWLSYP MGQQRFFDQLLANLSLCLPIMGNP PKVKGTWPRKVL\SLG\SAHKSTW DDLKGHLLPKPEVNLHC\DKPAMW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRA\SWGRKMGDLELASA LVPSRYH
2244	7741	A	2442	3	284	
2245	7742	A	2443	1	3339	VEGMTQCSCVSSIEGKVRKLQGVV RVKVSLSNQEAVITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGP DIERLQSTNPKRPLSSANQNFNNSET LGHQGS HVVTLQLRIDGMHCKSCV LNIEENIGQLLVQSIQVSLENKTAQ VKYDPSCTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIAIAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VVS E SCSTNPLGNHSAGNSMVQTT DGTPTSVQEVAPHTGRLPANHAPD ILAKSPQSTRGSGHRRKCFFTDSKG MTCASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEEAVMEDYAGSDGNIELTIT GMTCASCVHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKIIES KTSEALAKLSLQATEATVVTLGE DNLIIREEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADESLITG EAMPVTKKPGSTVIARSINAHGSLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTVAAQN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLGLDVATLPLRK VLAVVGTAEEASSEHPLGVAVTKYC KEELGTETLGYCTDFQAVPGCGIGC KVSNEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLGCMIAIADAVKQEA LAVHTLQSMGVDVVLITGDNRKTA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKVAMVGDGVNDSPA AQADMGVAIGTGTDAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGIPIAAGVFMPIGIVLQ PWMGSAAMAASSVS VLVSSLQLKC YKKPDLERYEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSSLTSDKPSRHSAAADDD GDKWSLLNGRDEEQYI
2246	7743	A	2445	14	503	NNDFIVIGTGTEFGIPGPTHAYEKT IYDDYNCL*QCELENTQNLQRQF YDKRKLEAMLQGMVTETTMKWEK ECERRVAAKQLEMQNKLVWKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV
2247	7744	B	2446	226	347	XGKIIVASCFFPFSSRKRRSSTVAPA QPDGAESEWTDVETR*
2248	7745	A	2447	8	2985	WIQYSSTLTPNDWNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/YYCRVRPLGFPDQECCIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVTGSGKTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMITVQEFCKAEVDEDSVYGVF VSYIEIYNNYIYDLLEVPFDPINPNL HNLNCFVKIKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKLVAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTRLTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPRRRYRNQPRGPIGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSENHM QGKLEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLLQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPRLRHRRSRSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAESWDRCR\NKVFCGL WEMR\AGSQLGTWISASRHNP SAKS HETDSPSTERTFSFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFYPYGSQKTTSIQ\QNVYSVCFA \SNINSRGRRLRVSS\AYEFFIMFFLK YISCILIN
2249	7746	A	2448	20	349	SFCLEFFPCRPGELLALQDSAQNSTF DKTALPLPCLAPCPPPLGPQS\THIQP CFPHGTGCPAFFTTDLLQGRLSLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP
2250	7747	A	2449	3	384	PFLSVVSSQVAGHGRIFQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKPQPADPPSLGTQCPPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA
2251	7748	A	2450	1	1503	
2252	7749	A	2451	1	855	NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRARRFL SQRPAAAAAAQAALMQAIKCAG GWKAEA VGKTCLLISY\TNAIFPGE YIPTVFDN\YSA\NVMVDGK\PVNL GLWDT\SGQKDYDRVTPPYPPA/Q ADVFL\CFPFVSPASFENVRAK WY PE\VR\HHCPN\TP\IILVGT\KLDLRD DKD/TRIEKLKEKKLTPITYPQGLA\ MAKEIGAVKYL\EC SALTQRGLKTV FDEAIRA\VLCP PPVKERGRENCLPV VNVSAPSFLGPVPLEPL
2253	7750	A	2452	41	556	APSPRRPWGHFTEEDQGLLSTSLWG KVNVEKCWKEKTPGKGS LVVYP\ WT\QRFFD\SFGN\LSAFAHHGQTP KVKAHGK\KVLTF LGRCQSTLDD LKGHLLPKPEVNCTVDK PAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWWT\GVASALVP SRYH
2254	7751	A	2453	2	454	RSFFFFFCEVGSWVGSMRVVMARL LSEGEQCIPTACAAFAQQPGRPRR GLAGVGEGGPQCSWVNRYRCTLEFL VSLGTDLARGRGNSATGPTAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QG WVSTSWGSSSPVPQFFPKLLEF TGK
2255	7752	A	2454	94	218	
2256	7753	A	2455	266	547	
2257	7754	A	2456	2	494	RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWLVL SLLGIQLAWGFYGNVTGL YHRPGLGGQNGSTPDGSTHFP SWE MAA\NEPLKNPTENKGRQQRVSKGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HWVCWLLHWVLLLPRPQGQPAGG SGLVAGSTQLPTGLGLILPS
2258	7755	C	2457	12	356	MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX X*
2259	7756	A	2458	764	1135	LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFETESCPVAQAGVQWR DLRSLQAPPPGSRHSPTSASRVART TGAHHYTRLIFVCLVETGFHHVSQ DGLDLQDQFLESFLCCLLVRLRT
2260	7757	A	2459	1414	1761	SAINFFFLFETESRSVAQAGVQWH DLRSLQAPPPGSRHSPAPASRVAGT TGTRHHARLIFFFFFFFFFVETGF HRVSEDDLDLFTSGDLPTLTSQSAGI PGMSHCAWRIDGI
2261	7758	A	2460	63	542	TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPGSASEPWVQLQSHH PLPPPTQSPGEGFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCLPR VPQFPHPPLPPSGRKRDRERGMEEGE GGWAAGERRGGKEETLGRGPFTQR ERPRNQEGEGG
2262	7759	A	2461	2341	2443	GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL
2263	7760	A	2462	28	403	NTTTCVKGLQTQSYKTPDGNTTK QTNKVKHTHTII*II*NAPPAVSTAIR NKFSKNGEQRFIEPYTNRPNIHSLK *RTIQQYASSKNLEIKDFSWKKLQ* FLENRNKHECFQLFPKVNVGAS
2264	7761	A	2463	727	1156	ETTLSEARRGRSAAASCRGSALRRG RFPSRRGREAAAPVCPRHVLL*GAQ SKQAAVAGKRSRTRHASRWPKSLF TPRRRRISLKRALHFWQQSADPSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGERQDWRK
2265	7762	A	2464	10	302	MERFEAGLSHISPWLC*CCSHCGD CCLGSRSWGLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFLL
2266	7763	A	2465	303	531	VLRICKVSEENSLFPLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRWD E
2267	7764	A	2466	6	100	
2268	7765	A	2467	2998	3570	QDRKQGSSAPATPSRA*AAAAARP RRPAGRWRG*DAQSPAEPAPRSPP WRRAD
2269	7766	C	2468	125	404	MMARPPPWLESHCTRVVRADGQV XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX ADAW*
2270	7767	A	2469	1348	1807	CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCCFLR

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						WSLALLPRLKCKGPISTHCNLRPLPG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVGQAGLELLTSGDPP ASASQSAGITGVSHRARPSVWFSNQ SMNP
2271	7768	A	2470	538	676	VKRNP EAGAVAHTCNPSTLGGRGG WIS*AHEFDTSMGNMTPHLYK
2272	7769	A	2471	40	336	EYLYRHFKNKLFLYANILCSSGIWR HYVLILRTVSELLD***GCRWGLSR FDYLSNTGWV*VLLDISSFAFTGP LIHGTGGLSAFDLHCEALSFYRD
2273	7770	A	2472	2063	2406	SQKKKIQWYLRMFRQFDIYVCFLFF SVVLLMIGGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF
2274	7771	A	2473	22	273	LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSNIYPLSIKS EIEPIETRCLNRSNASLVQK*YGHKT GLWWLP
2275	7772	A	2475	1269	1511	INFFFF*IIDRFSLCHPGWTAQAQR LTATLLPSRFKRLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA
2276	7773	A	2476	1411	1827	LHTCCLRRRPSGRGRSQGGHCSQSG SSPPRRPRSPAPEGPGFHAP*LCIPDL GHGSRKRGCVPPCGPRTGWADLV ASAQAACGCQGGPPPSGSCSL*GRG PVGGSGHGPCWPQLVELCGRCWSW PGVAGSTWQWRRHPH
2277	7774	A	2477	1345	1642	WQFTGAVIHLAYVVLVCLVAFS SVSLGLNFFHKNFSDFQRERCWLF SPFKGCC*RCFFTQSLYYCQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP
2278	7775	A	2478	113	584	WQDYIYKEVRVTASEKNEYKGWV LTDPV SANIVLVNFLEDGSM SVTG IMGHAVQTVETMNEGDHVRREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDAPRTLCVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ
2279	7776	A	2479	658	785	KTHGWVQWLTPVIPAL*KAETGGW LEPRSSRPAWATQRDLIS
2280	7777	A	2480	2	598	PLGKGKFTGQSAQLTTGTGRGLILA KGSHATLQKHRINHTLTHKNPFLEE FWESPPLNLALIKGLNGFCLGTEK LFEQMTYGGGLKKVKCPIGYFALQS WEFHPPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST
2281	7778	A	2481	253	286	NDDDP*LPCLGQPPRSCQPSLP*S LLWSKMTTTPAQRSG
2282	7779	A	2482	407	587	QAGRGRARGVSEEARNKPVPPPTET PQPTLSPQ*MGPAQDPAPQQDYRG KKSLNAWCGRS
2283	7780	A	2486	246	519	FQFGIHNTNYQRQGAKVFFKNKGV

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						WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFHITGDYSQH
2284	7781	A	2487	470	977	TPPPAGLRQRGYPPPGNRLEARNW ARAKGGKTSAGRVFTQP*FPEQQLP PGRPWWPRPGCPHGLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDGTG LLASRKL RAGGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSSPSA PAGHSLSHPSRTGKLALVPGH
2285	7782	A	2488	393	618	IREWVNIFWNIHTEEYTVIKKN*V CQTWWLTTVIPELWEADVGSLEP RSSKLR*AMILPLYTSLDHKARLSL
2286	7783	A	2489	308	626	IRGTSNMNRKNVEKAYYAEA*LSL
2287	7784	A	2490	1222	1374	AQQVKRLEGQRGWKLRGGRGRWL TPVIPAL*EAEAGGSLEARSSRPAA AKK
2288	7785	B	2491	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
2289	7786	A	2492	1	437	DPRATEGMVVADKTCQKSTGRLEP LVTAIRMLKQMLFRYQGYIGAAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTPVNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDS
2290	7787	A	2493	2288	2668	FGRGHYCRRSVSQEEEAKNLVSEAI AAGIFNDLGSGSNIDLCVISKNKLDL LRPYTPVNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDGVLVLSTLSTS SVPKSTSHDLRLVTCFMTVGCCQ V
2291	7788	A	2494	3	861	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLPKVRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAA DTAMTYTQLISSNLKLHSL\STGRNP RV\VTANRMLKQMLFRYQGYIGAA LVLGVDVTGPHLY\SIYPHGSTDK VPYVTHGFLAPLA\AMAVFEDKFR P\DMEEEEAKNLVSEDSPPQFPFPP WRIFNGPGLPEANIDLCVISKNKLG FSPNPNTQLPNKKGTRLGWRYRCEK GTTAVLTEKIPLWST
2292	7789	A	2495	466	607	KKKERSCLWCPS*SLKNYGLSCR KKKKGAVKKIILVQAWWLMPVITV LWEAEVGGLEARGLRPTRATW
2293	7790	A	2496	449	694	ILRILGTPISFPVNKISFLPFKCLFPDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETHLSELIQEQTKKHKFSLIR GS
2294	7791	A	2497	52	298	YNIEEQQNKRTQSNRHRPTPPPEPP NPEW/TPKPTPTK/PSSPQGE/PGW TGGPAPHAGAAPPFPSPANPTLFPS LTTGGKV

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2295	7792	A	2498	112	485	YNIEEQEQTYKTE*SAQTHPSPGT AESRMEPKPTPPTKRLPPTGGGGRG GTWGDGPPCWGGHPPVFSPCPTP TLFPIFDPLGGQSLAQLGSWMVEPT LQRATLSFLKMGRRKETVAPPQI
2296	7793	A	2499	32	392	RPTFGIWFYPQVFPELLLELKAKYIG KHCFSIHSLPDTGPLPGCP/SPPGRA ALGIIPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPGQ SYFPAHPPTSSLSLGGIY
2297	7794	A	2500	914	1417	PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFGKFSSLPDWT GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSTLVWRMLNSASTS PSPAPSYISPPFPGQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPPCAPLL TSPPLTFLKSPRP
2298	7795	A	2501	1120	1159	ERAVCGC*CIFVM
2299	7796	A	2502	1145	1367	IFFSFLHIYIHNTHTHMYIYYTLCVC VCCVYGMVCACVVSFSSKPKQVC VWIEGNLNY*LQVVCLWYLDFFHS
2300	7797	A	2503	155	454	GGFSVWHTETPPRMLMHQVQFNL EYLTPPESTQKGGPTPLCIYGYVFFK SDYLYSLSLFFRFLYFSSLL*YLML VNFLFRMLFSLFMSFCYLFHIL
2301	7798	A	2504	901	969	RWPGMVAHACNPSTLGG*VGDP
2302	7799	A	2505	903	1339	DKTVQSIRSMGGWKMDASDSKFV DLWIAEGIGTSWRNPGYQAPRPLH HGCWGDGKSPPLPKPVSHITDVGP WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLQGACSEGGAPFSIELFAGRS
2303	7800	A	2506	433	548	PSEYTLGFKNPKIKLTFNGGNSMSG VHF*TGFTFLFL
2304	7801	A	2507	637	906	RIKKLSDGSYFLPGVSQIA*GSNYF* SKLGPDDGASRLQSHHLGRPKVGV FHHVGQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL
2305	7802	A	2508	211	575	RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLLPAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPCSSS/CHGRSHS SPC/CL*SRTSSVVDGEVCSNTL
2306	7803	A	2509	274	488	SGDKTMQLRGPCGGWGSCPALGT CTAGSP*LCHHKGHCSIHSTSCFLA TVSPCAIFNSTSKAGRGAQP
2307	7804	A	2510	83	442	NFTMVMYTDHILRNAHLMYTSGR RLSVPKIACHITDHSLTHTCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFCELLAGRFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG
2308	7805	A	2511	2	270	ARLGLPKCFFCVFVKTAASRSVSQA GVQRCDHNSLQP*PPGLKRSSLASR VAWTTGSHHHAQLIWLICFKQYFV SSGFYLLLVALWWGG
2309	7806	A	2512	234	409	KGFYAHEKNARTWWLTPIIPTLSEA *GGKMA*ARSLRPAWATIRDPISAK

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						SKKKKKKS
2310	7807	A	2513	78	460	NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPPRHLQGEGLTSARKRVLR LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ
2311	7808	A	2514	67	279	SHRVSRLAACGAAPAAARLAGGQR NGRAISGRPGLSS*GAGGGNVFKVC LLLKNRNTGGGRGHGYLYSLQR
2312	7809	A	2515	683	933	YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRRGEDAHSWSQRGRQEFV FYLKSTRNW
2313	7810	A	2516	2	208	SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA
2314	7811	A	2517	426	601	PSFRIFTQYSSFLKNSLKRLGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL
2315	7812	A	2518	55	489	HSALIQASVWFRYKYPCGYLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCGSPGPDWLI LGKLGPLGCSKPKGSHFAFPLVVPIF HPCSKTKLFPREELFVVR
2316	7813	A	2519	52	286	MMPCLRQRQREREREREREREH MRTQRKQLK*WITRFKNSSKRQR TEKNSKKPPVPHRGAGHSNGKLN C FRPAAS
2317	7814	A	2520	3	296	TNTRYTIGDPALQDMNSRRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHPSLDR*SSGFWDPAGRGE LMQWEMPQPCSPQPLPKCRSSI
2318	7815	B	2521	83	241	SEWQKKLTPEQFYVTREKGTEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI*
2319	7816	A	2522	19	629	YFVLISPLLTSTHGFDCYLCINTV HKTPCVFRSLWDIQEVFSIKGSRSP SPSKGNGFDSEGPVRTIPGGTLVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDSVISSCSIVYVFHSSEKKYCSG TGWPSFSEAHGTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRFICINSVALKFKPRK H
2320	7817	A	2523	1	707	MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGLGAEAGSLATCELPLAK\SE WQKKLTPEQFYVTREKGTEPPFSG IYLNKEAGMYHCVCCDSP\FSSE KK\YCSG\TGWPSFSEAHGTSGSDE\ SHTGILRRLDTSLGSA RTEVVCKA /QCESSILGHVFP\DGPGPNGQRFICI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIFHNSLE
2321	7818	A	2524	303	743	TGAQWGRGLGHVCWSMGFVSWE

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						CSGNGLSQAGLVKLLIILHSTVQK GLTPRWGGMNTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPSSGSVPGPPQCPV KALPVL RAGWATQPPGSFLWPTPS D
2322	7819	A	2525	102	421	VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGAAVAGL*GAAGCRGRSRP LKSRDAGLKS
2323	7820	A	2526	225	448	TQEGRGIDFGPWWPQLLPSSPSPG L*SPATPPQAWVPPLPSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL
2324	7821	A	2527	43	390	GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPPITGQCPLIVSPSYTVLSPHYK VVSPVTR*CPPVTG*CPPIAGQCPL *CPQAISWSPVVTG
2325	7822	A	2528	525	635	HIQQQLWWMPVISALWEA*EGGL LDPRSLRPAWAT
2326	7823	A	2529	66	432	TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGFCG WKAGTDFPTSKKPCFLPHNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRSLSGRAE
2327	7824	A	2530	5	95	
2328	7825	A	2531	1	123	
2329	7826	A	2532	118	363	
2330	7827	A	2533	23	250	YLIVVWICISIGLYTY*LIRALYILR KLTLFKYIPISH*SLSFIVIFCSLVYIY MYIYIYVYIYIYIYIYIYIY
2331	7828	A	2534	346	611	TSVEAQDATDRLWPDSCCPAHGAC TRTVWPKKPPYFPVKKMESCSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFCQ
2332	7829	A	2535	267	682	HFSSLRMQARPPSFRPYLVLPKNC WIFILINDSWMVLFFEASLPTVPSLV QTTIFLLGILQQPLTDLPSSTSTPF*S LHLSAV*VVFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKKSR
2333	7830	A	2536	45	280	
2334	7831	A	2537	1560	1885	QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQRSG LPNPKLGKNPLGPIPSQKPPCGGPV KTSIVAHNYSALSLSLLPQPGSA PQALSL
2335	7832	A	2538	60	341	VTLHSLVILFSAHICRIKLNITINLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYRM*SEIIHYIFILS VVLNVNEINSIIQMY
2336	7833	A	2539	442	686	TSYNNLLNNLNKNIETFRKELSSLSHL CNRGQGILKSLIAWLGAHAHAGNP STLGGRGRIA*AQEFKTS LGNLRP VSPKK
2337	7834	A	2540	459	603	GFLLEIIDKAEGGAHACNPSAFGGQ

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						DGRTT*GQEFKTSLSNVTRPHLY
2338	7835	A	2541	1	188	PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY
2339	7836	A	2542	582	825	GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWP G MVAHA CNP GTLGG*GRRIT*GQEFKTS LAN MVKLC LY
2340	7837	A	2543	775	1019	DRSSPKKPPDDLPEFTEPQWFTLKHI KQCFS DISRLRVGPGMVAHAYGVA YLSTLGG*GRRIT*GQEFETSLANM VKLC LY
2341	7838	A	2544	303	429	AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPT WGSWKT
2342	7839	A	2545	853	867	NP*NLACFCV LLEFPSSF*RGFRR LG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY
2343	7840	A	2546	357	560	KGSLVGLSLEERIFVVA VQPSLFHK KCLWQGTVAHTSNPSTLGGQGRSV A*PQEFKTS LGNIVRPCL
2344	7841	C	2547	486	728	MWVG VWEV FSGVVLGWGVPV ML QSDG SWKLPVHLHELLPFHMSWYP PQDDPNIWSLKQLGLPGCP LLSLC DVS YMVSSA*
2345	7842	C	2548	240	332	MACFS TSAQLKDRLLRSPATH TPL LNAPL*
2346	7843	A	2549	2	603	SLPYLPQHPLEFGPLNLHRDQRAG AQTLTQPM SLCCSKSLQLPNALTDK RPCWVLFPA GLSSLLRND SAKLPFR NKGSPPAQGLCPGGSRLTTWHL SF HGLFLLHQ RSAQRSTS QIPSNHTLT *CPTVT TETVPCLK*PRLSVVSVCF C SGSP*RALQCTPPGKPSF LSQLSLT DLPSTNL L FHPVGT PRAPGWA
2347	7844	A	2550	132	419	
2348	7845	A	2551	1083	1563	PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPAFSLTSRWDCRRVPPRANFCIFS SDRGFSMLVRLVSN SRPQVIHLSQP PKVLGLQVETGPQKREWVPRELTA SGQWK GQEPDQGEDSGTEGRWLPL LPSAGHSGED
2349	7846	C	2552	173	501	MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSP T LSPRLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGV SXRP*
2350	7847	A	2553	174	364	YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE ISLANMVKLHLY
2351	7848	A	2554	61	283	GGRIA*TQHSILDNRVRLHLKKKKK KKQYLKKVHLP GAVAH/TYNPSTL GGQGGWIT*GQEFETSLANMAKLC LY
2352	7849	A	2555	1140	1313	HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETSLA NMAKPHLY

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2353	7850	A	2556	99	296	WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYN
2354	7851	A	2557	175	332	RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY
2355	7852	A	2558	667	772	ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY
2356	7853	A	2559	7155	7302	IMKLKMYIWPAGAVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY
2357	7854	A	2560	227	410	FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTAVR*CSLFQGSYGIFGI EGRIPYSEL
2358	7855	A	2561	275	685	LKPLFTPSPGPAGVPRGLCWKEAPT PGSLLGEEETELNVY*GPPPGSLRPA SHWAPPEGLRPTSPLFVAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL
2359	7856	A	2562	20	354	PLYSQSFPIIYPFITLLPE*SF*NNNYC SFVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLTVYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS
2360	7857	A	2563	374	585	GNLINC*LHTHTHTHTHTHTHTHTHT NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAIRNA
2361	7858	A	2565	918	1096	HCHSNSEFDTETLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR
2362	7859	A	2566	101	327	LVKNQQSTQKLAKHGWACL*SOLL ERLREENHLNAGGGGCSELR*RPCT PAWATETVDSLPIMLVLQPFSLSL R
2363	7860	A	2567	347	478	RDHCRLGTVAHAYNPSILGGQGRRI A*DQQLETSIGNTVRPCLY
2364	7861	A	2568	622	761	KSVEVFYLSIGQEECLPHIQFIFHAT IFIIGRAQWLTGPAPFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A
2365	7862	A	2569	70	316	ISHPSPSTRWEAVTWALG*LFPCPC HLQGGRAQLPLPYPPPLPIVVAPPLI SRLNPDGDLSAKTILDVTLYISSTTV GGSWG
2366	7863	A	2571	145	331	IFHSKMPISEWKL*TLWQFFKELKI ELPFDPAIPLLGI*PKFQRLKNTNGIC HYFYM
2367	7864	A	2572	918	1135	GFISASLCNWILTHLKFFKEMGSR VAQAGVQWLLTGAVMAHCNKLKLL GSSNPLASAH*VAGAICMYDHWHA
2368	7865	A	2573	590	936	QLAACGGSC*SQHFERPR*EDCLN PGVQDQPEQNRETPISKIILKSWA WWHIPVVPGTWRADVGGLEPSRP KATVSCDCATALQPGRRARLCLK NKYIKYSVQKCVIFFLF
2369	7866	C	2574	34	670	MXVFLSSAGNMPVTCWCWEAPRC

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						NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQGPVVQTDAAAXMVE VSVXVVLEGWGXPTTRRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRVSVGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLAGRRXSGSNLI*
2370	7867	B	2575	70	165	EQIEALLESLRQAQQNMDPKAAEE QEEKEE*
2371	7868	A	2576	1	390	FFFFGVLPVLFDFHVCLFVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LWFEPDVSWLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPFAFSRPLYP LGPPN
2372	7869	A	2577	435	861	RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPPEHGSRLQPS/CAAA SV*TTR GP*GTLCLS*WGKGTSPGCC\GIERP KAGGKCTGHSGVCPVTRKSNHSLC ARSPTSCRPEFAPAAGPRGGALPG RVILCSKAISGTGPPRPTPPEHGSRLP QPSWLRRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCVTRKSEGLGGGRLGLCISGCT AALPSTNM
2373	7870	A	2578	38	398	PVLFLDFHVWLFVFCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNKQA ESMSLCGFFLPDCFFLT YKRIYL
2374	7871	C	2579	42	443	MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCPGRVILCSEAXSGTGP PRPTPPEHGSRLQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCIE RPKAGGKCTGHSGVCPVTRKSEGL PAEDKKTNMKV*
2375	7872	A	2580	871	1253	PRLPPGLPGADRSPAGSQACA\GPA EHGPPQRRGGGRRGGGGGGPGLPHP PTCGTWTSEGA\SRRA PPPPAKGG AGPRCSPDSPSPEHFDTQKGKLHS PCCWLFPLFPSPISDLSKRKRLPK NCL
2376	7873	A	2581	222	754	YPP*HVAPHPAPLPWQVQGPPDW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPFSLPNLSDLGTS FPLPQTLPLCPAPQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHTLLV PTFSQSSQNPPLPSPSPIGAVKALFAS TMG
2377	7874	A	2582	2	431	PEGAAPAAMAVTALAARTWLGVW GVRTMQA\RGFGSDQS\ENVDRGA G\SIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSREQLAALKKHHEEEI\VHHK KEIERLQKRNL SRHK\QKDSKLLKH

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2378	7875	A	2583	1	232	RETACCGRDARGAAPAAVMTAL AARTWLGWVGVRTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR
2379	7876	A	2584	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGVRV/WGVRTM\QA \RGFGSDQSENFPTGPRAPH/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEI/VHHKKENERLAEKK FERHKQKIKMLKH
2380	7877	A	2585	3	316	LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLNDAHNDG RISFDEYWTLLIGITGPIAKLIEQE QSSS
2381	7878	A	2586	3	469	
2382	7879	A	2587	434	815	TQVDWTQRRARPGPWRHPHPFPDD DSLGGCTSHLPPHGD*L*NPSSNGA NPRLSPAPHPPREAQTPPGAGAHR TPLSRACLGLAFPAQPVRLRRDTRK DGRKEQRETVPPTFPDARGTRLIL RHK
2383	7880	C	2588	204	354	MWLQMTRAVLSSNLDPYVCRRA RGRSSPSGSLXXKGEESWGPRHCY SP*
2384	7881	A	2589	390	681	RERGRRAGRRRETAVRSREKERER EGLDRSSRKR*PELVKGSRSAH*PQ SGRWSHRPRPAIVPTSFQPCDVRA QPNGPSDLDPHLPTRRRKACDRR
2385	7882	A	2590	598	769	YPQCPTPCQAARVWWDShLAIPAL LGGRGRWII*GQEFETSLANMAKPH FYQKKKKK
2386	7883	A	2591	359	775	KKTQPLHQGYPKINFRSPSPPIPVV PLLALPK*GHSFVPSPLQKIPPKG SPHDPTRQRPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRTFSKRGKDGPFDAGQ LQGHLLKGTFFFF
2387	7884	A	2592	585	780	TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRIT*VQEF ETSLANMVKHHL
2388	7885	A	2593	436	1645	GMSALVQSRVSHLHRVSLTRLTA RAQETSSPNTVTPPNQTLSTAQNK RTIPGPARE*VTLTRLSKEPLLVEK AAPTPHPQ*GPAPRPLQASALPLYPE QHRRAPSSSEDPWRPLTPPSH*GVS TWTP
2389	7886	A	2594	1	373	TCSCPWLAPLTLQKNCPPHCHILSL LRKTKQNDAPKKSPPRGSLPAVSGM KQDVTVLGRMEKPPRSIPQRPQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS
2390	7887	A	2595	502	798	SPKVQRHSSQAALRQAGGALS CLPSQRRPRTVSSREGPHPGKGV* GGVQRSKGPPLPTCPQGLTCLTPT DPGSAWNPPTPT*NEKGNSEIRH

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2391	7888	A	2596	1	136	HPCVHEPMSFEWPWQYRFPFFT*G SDPKKHGWASLPSPGPWAQP
2392	7889	A	2597	429	1003	VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFSLYSIIPSDVLPSSPFE TRVSWEQFAYLLESAYLLVQAIE *ASSFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIIFRGRSHCSLQYDPGFL TSLNAPSITI
2393	7890	A	2598	367	463	SGHGAHAYNPNTLGGRGRRIA*SQE FNTRLN
2394	7891	A	2599	436	833	CLTSALLGCVYVYFFSPHPALFFLR RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLFVHLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY
2395	7892	A	2600	53	95	DSILLTQAGMQWCELGSLQP*TRP PIVCFCLFIYLLRQHLAPHSWNAV V
2396	7893	A	2601	432	825	NFKDTAKGFLHFDHQKILDPCPLG SRARFGTYPECPHPVPSVTEAQETGL SVPSFGFHFHFLTYFLLLEYFYFH*G TLYLHLDLHQB*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF
2397	7894	A	2602	83	111	
2398	7895	A	2603	1	71	
2399	7896	A	2604	215	758	LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSPRLGLQ GSISSASRGRPAQHVPGRPATLSP AGAGPSR*ERSRAGARGRWLLDH AGERPAVRELSRPDPRQVSFGPRNIS EIGQVLPETSSCELPGIGDLLWQL EVYDARKHSLVGPESLSHRELGSPA GGRRP
2400	7897	A	2605	211	323	LDSLIQHSASTLAQHSASKPWKPD FHTQFFHTVWKLQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNVCVWKLSGFHGFE AECCASVEAEC
2401	7898	A	2606	75	232	TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFLIW F
2402	7899	A	2607	325	566	FNDKYFYYPGRQIQCHITLFLNLKI TSDFFFCFKKTG*VAHTCNPSTLGD *GGGIA*AQEFKTSLGT**DPIYKN
2403	7900	A	2608	1114	1367	AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNS*RKYTFKCIRKFNNLSEPF NHVCKVF
2404	7901	A	2609	100	450	FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYK*V GNFDILYIHTCVCVCVCVCVCVF VCLWSTLRMTDTV

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2405	7902	B	2610	50	382	XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESL DSEDYSL EEGQELSD EDD EYVQVT VYQAG DTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWAHX*
2406	7903	A	2611	1665	1787	FFVLLVETGFHRVSDGLDLLTS*S AHLGLPKCWDYRHEPP
2407	7904	A	2612	1431	1553	FFVLLVETGFHRVSDGLDLLTS*S AHLGLPKCWDYRHEPP
2408	7905	A	2613	1	752	DL DAGVSEHSGDWLDQDSVSDQFS VEFEVESL DSEDYSPSEGGQELSDE DDEYVQVT VYQAGSDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGKDKGEISEK AKLENSTQAEEGFDVPDCKKTIVND SRESCVEENDDKITQASQSQES EDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVSSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE
2409	7906	A	2614	426	813	SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRHRLGYAGT AGPLAGYRPFROHRQSLWRAASAI CVD AISMRTRSRSTVRPLWPPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL
2410	7907	A	2615	1740	1862	FFVLLVETGFHRVSDGLDLLTS*S AHLGLPKCWDYRHEPP
2411	7908	A	2616	1174	1354	FFVLLVETGFHRVSDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT
2412	7909	A	2617	2271	2393	FFVLLVETGFHRVSDGLDLLTS*S AHLGLPKCWDYRHEPP
2413	7910	A	2618	1029	1197	FFFFFFFFFGFLVETGFHRVSDSLD LLTS*SSRLGLPKCWDYRHEPPRPA EEGI
2414	7911	A	2619	402	990	
2415	7912	A	2620	1326	1716	KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLKAGCSGSCL*SQHFGR LRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH
2416	7913	A	2621	148	420	LSLSLCRFLGRFCSGSSSFSSIFVLFHF SFL*FMFSFSLETQFKHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFILSEKWR
2417	7914	A	2622	565	916	VPRARTQHSREKGRAGAWFGLHY QGSII CGSNSTW*NPQRGP KLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT
2418	7915	A	2623	1132	1245	KWHLGKI QNYSTGKCNRIYIYIYI*I YLF*CHLSIGNC
2419	7916	A	2624	209	326	
2420	7917	A	2625	808	1010	EETEGRARWLTPVNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK

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						KKKRKKEIKPGMVATCL
2421	7918	A	2626	1602	1940	PSGNTSETSKGLNIRSHTRLFEDIKG VNRSSQLFQKKPKNRDRIFQERYV RSLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK
2422	7919	A	2627	2565	2748	KSLKLGMSLKIKFIFLIKGLGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY
2423	7920	A	2628	1032	1292	MYIPLNNGTVGVDSQMHLDVQIDY RVLFSDYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL
2424	7921	A	2629	1640	1815	NSKGESSAPFLPDSHLEKRKSYGT HPLYISLLKNEYK*NNSNLKAVIFK ALLKNKQT
2425	7922	A	2630	1089	1226	IQIQNKLLKECPSWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT
2426	7923	A	2631	197	430	SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCLRFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRRTAL
2427	7924	A	2632	343	596	GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DNGKQM PCYYRAASEG
2428	7925	A	2633	1143	1553	QCRRVPRGKRLELGVHSSTG*QAPL LPSASATSSGFLADRRVGTGLRTPL RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAAASAAISARSSPPSAAGS GPDWRRPGKRHSRPTAAASAHTS PSQSPAIPAGGR
2429	7926	A	2634	158	585	ALTWVHLSSVSFFPDLKLTPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLLVPKAKLW SHVGRMEGDLQCPLCLWLHPILW FFGGSCFPQTEHSPVQSPDGLIAWN CPASDAGIKDCLPKYFC
2430	7927	A	2635	1348	1540	SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTIHVHLMGYVKIKQ LFNACDSMEHLQAH
2431	7928	A	2636	263	615	LVNSEGNIVVKLCHELQHGPLNSSP FLILLSHSEKINRASIMLKRYKLIN NYILSAFNPPPGKIHTHTHIHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE
2432	7929	A	2637	270	665	KLGKVAHVYPYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KTQTPGS GF*PSPHPSCKSGPKPLMGCPTPGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK
2433	7930	A	2638	54	311	SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQKLAGHGATHL*SOLL GRLRQENHLNLGGRGCSEPEIVPLH FSLGKQSEALS
2434	7931	A	2639	26	229	CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPPSPWPASPECCRDRH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ICPHPVGP GPPPSLALPAW
2435	7932	A	2640	133	586	THVMLCAQVGSHHPALPWASPEEC CRDHICPHPVGP GPPPSLALPAWDT HTHTHTHTHTHARTRATHAHLPS HAVFYFDFVQSGSLAGSPYPRGGG GGWFLGGAKKGRECPGG*MGGPP MTPSSFQKQLLLPPSQGPTPKPPEGG PCLQ
2436	7933	A	2641	186	609	RVGHHPPSVRHPHQGHGWL RDPV QLHLWSSCVAFP GGAPAGLP PSDQ DPGPPLAISPTHWPPCGQPKTIAA HGNHTRTGGR*RPRL*SRPAEWP SAPKGRSGGLPGSFQEPADSYPGCG TWCSSACKGRQPSYS
2437	7934	A	2642	989	1790	NYTPFLPCSASAEFCELWGRPLV FCYFYFQPPLAVEPFNVIVICCWVR VKVGPGAFPRGLRRDVQRADFSRS SEGLLMGWVRDFDNHQSTCALDPF SGGIGSLLVPGGSDLQIGCFQKS FQA LIEN*CLNRHNSLG*TPKRSIKILWA E*ISRAGLCNSSPEHPACGHPPR*G QWEAGPTAARTCFSPPTSNPPNSG PQAHEAQVSGDHS HIGGS*GSPSPPL AYNLSTRKAQPKCGKKCMVLPSTC KNCTYCKPFALWNCMP
2438	7935	A	2643	92	330	RQVCLPPSERNVASLRTPHPRRGAQ KSQEGPPGRQSPSELKSRYWCVENS TWVSRAPQGTGWPGWALPFPHQG* GWLGP
2439	7936	A	2644	1137	1290	HGQINQMEVNLPMDRKV*THHTHT THHTHTHTHSSTCPYTLKRNVK S
2440	7937	A	2645	96	357	
2441	7938	A	2646	2648	2953	DWGYLPFKTLTYPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHL YQNISPQYLCQKTPQTKMPILKKG VFFPFRM*APQESGTNVFCMFLCPS TL
2442	7939	A	2647	201	377	QTVFVKLCVYTHIYN*VYMLIHI*A PLSVY*YAYI*AHILSYIYVHLVIYI TEKYDF
2443	7940	A	2648	1917	2056	QSHAKEWIFLLTCFIF*KLLRNIYIYI YIYTHTHAYIYIYIYIFQ
2444	7941	A	2649	246	717	KRQSEEGVFSCCQGWNESLLKSK VLEYP*FLHFPSFSDLYLFNYVFIY LFIYFCSIQSQTQSKAERAYIYIYLY MCCRQNTVNFTTTTKQLFCHLNH LRRRNEKRWGCHFLVYAFEARSMF IYFFSLCINENDPEWRLAERSMYWS KHHKSC
2445	7942	A	2650	191	657	SGGERRNSSAPSAMSPSGSATTSPG T*PRIIDSERTPAFHARASTVKPPAGI NTREHPPLPCTPKPCTKTHFTAPP PQRCTHTSSPPRNLIQIFTRDTHPPPT HTHRHTHTQEPGWWSFDWVGCLR GFSFECTHFHFPQNKGTFFKMSYIA TY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2446	7943	A	2651	1108	1282	PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKKKTETL LRRPVFGAAN
2447	7944	A	2652	2	479	FIIAHPDPTVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIYIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLNVIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF
2448	7945	A	2653	341	622	YQNRLFPNQCFCTCLLVWLWDSPAP PPRPWQPPPQGF AHT*DRKEEGDPI GIWAPEGKSCTPKPPPSLPRTPSGW KRALQKGDTCPCGPSTAST
2449	7946	A	2654	597	785	NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQEF EAS LGNIVRPCLYI
2450	7947	A	2655	237	656	RGQGWVGDSSQGRGGAKEGLLP SH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS VLPPP GDRVMEGGPPTLLQHRSPH P GGERHGF S*SKFPPPPGSRPQKERR KGQRGM CVRVGQIN
2451	7948	A	2656	109	290	NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY
2452	7949	A	2657	122	359	
2453	7950	C	2658	133	315	MQWLYIATLIPFFWTQRKGTFS GK SQLILDFLQ GALAILSPDPHPGILHR SLWAHLPA*
2454	7951	A	2659	1399	1644	CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPSPGCLGPFT LDGCGLSPPL YLPVFFPGGLLKSSR PLSCLN
2455	7952	A	2660	592	943	RTGCGQTLTVSHPDQARHWP GPGF ALILLYPAQGFHLLPEAGPEGRG SLLTEEGSREANSRSLISAAQLPPA APPQGLGV*MQESSRWGKGGRSKG SLPINLGLNSK LKKTTPP
2456	7953	A	2661	181	401	
2457	7954	A	2662	1163	1457	HPRICWHHSDLHTITKTSHT*SESEQ NPHSESPGPRGCEPPGPRGSEPPSLL *LSLPPPLPFAFCSSCGLMAGFPPK QALSITGPFSPSVALWLGHC
2458	7955	C	2663	275	327	MPFRLSQDCHHSAGAQQ*
2459	7956	A	2664	70	191	DLLQKPQV*DPSRTECVSM*CFLSP *AETTSILPCFPRI
2460	7957	A	2665	40	142	THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQHPKVLQLQAGSTVNQPA HRC
2461	7958	A	2666	479	722	YCIIFLG GFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC
2462	7959	A	2667	265	518	VKTVFLSGLDPLSLNENNMVLIMTS IVIFSHPLHFRFETLIGEWPFNLILG QV*WLTPLIPGLWEAKVGGSLEPRS

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						LRTAWET
2463	7960	A	2668	626	695	GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTLPVLRREAEAGGSLEPRGSIPG WATRVPRPLYIEKKKKK
2464	7961	A	2669	66	610	TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLEDLILGELQVLA FGALSGSISIFPSIPPHSAIHKNSHLR KIPPVPPRQPFRRVWTSGPPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPSPRSQPE *TPCKKNFLMEKISYDFHSQRSSD
2465	7962	A	2670	1077	1598	YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEVVRVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIPAGRDPGPGRPGL LAERYRRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVSPWIPGGCRGPITTVGVT
2466	7963	C	2671	40	180	MSFEAEIVLSPDRRTALHPGLQIETL SHIIIIILSTISFHQLH*
2467	7964	A	2672	1818	2154	PTPVFVPSLFPCHKLPQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRDL VSKIIFKKEQK
2468	7965	A	2673	137	1610	EENIKSYKEYKCHNLYVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL
2469	7966	A	2674	1	490	GNSRRARRLASSPGSAAAAYRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRLAEQPQGHPTDPL STGDQYCGDYELLSWRLWKQNNNA AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF
2470	7967	A	2677	2	215	
2471	7968	B	2678	63	203	SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG*
2472	7969	A	2679	433	895	VFHLPSEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTKAR\DNAC\ND\MGKMLQF\ VLP\VATPRSQQEVIA\YGFQLPTG EGVP*SFAPIWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLPTPWGLLVG GSVAAS
2473	7970	A	2680	235	442	RPTFFYIPFKISKIKPSKIST*RPSSL VG*KSKEKASTQKCLTKIPVPSANL KDFLPKHDEKREL RH
2474	7971	A	2681	199	1061	RRSEPKGWNRAFFPPKVGCGCVW EKTGMGDQNPETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TSTTRAPCENQRGGKQ RSGWLRATKPHTAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSKG**VMER*WSGKHSVKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSTFPPSPRGSSSRKPEARVARKY GPSPQLKPRR WRERKHGKPREMGR SEKSESLEWDRSLPVLRMVDGFSPG KQNRNGQGRGAQSMW
2475	7972	A	2682	415	575	ISGWGVGGSCLSQHFGRTREQEDHL NLGVRDQPGQHSENKVSIIKKKKRN VISI
2476	7973	A	2683	457	549	VSTGNKVVPQGQKVKACI**KVLK MQIAFTFCPGTTLTPVDT*NKVTHL NECNILASLWWLKHDLVFQLLATW LHFNLRSSISENASAPSYCPTGCVAT LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLPSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*ADVSSFQNILQ FIVNHKIKLPT
2477	7974	A	2684	291	364	RLKL*SPHLRSYFEKSKEQLASRTP TGQS
2478	7975	A	2685	2	361	TETLARPPSPLVTNMKLLAETVLLL TICSLEGALVRRQAKEPCVESLSVQ YFQTVTDYGKDLMEKVKSPQLQAE AKSYFEKSKEQLTPLIQEGLGTGT WFFNFELFSVGTGTTAWPPS
2479	7976	A	2686	425	678	LLGAISWELWGTQCPHPVEGVPGPF GLSNPQAGAFREQPTGPVP*SSSFEK SKEQLTPLIKKAGTELVNFLSYFVEL GTQPATQ
2480	7977	A	2687	64	287	RQMA LLKANKDLISAGLKEFSVLL NQQVFNDPLVSEEDMATVVEHSMN *YMSYYSLQATGEPQDLRCCSCAL L
2481	7978	A	2688	983	1386	QEVRYRKVETLRCLLFSSCLVPVCA ASPVSRPGCRFLRSSLHWPTGRLVF RQRGETFLVPEKTVLRGVASAPAQ KAAGRTPVGRPRDARLRADARS*S C*RAARPRRGASGAVGARGCGRPG FPFLRSGGIFV
2482	7979	A	2689	473	706	NLTASKISLKYCKQYLWILFRKRL WPGVVAHVCNPRTLGGRGGQTT*T QEFETILGNMVKPISTKYQKKKKKK RAAA
2483	7980	A	2690	1400	1600	VGGGSGRSSKFPLP*CPPPSCCSLPI SSPPCLSTPGPSLLHVSKGTRRISRL LDKRISKRFTNH
2484	7981	A	2691	6133	7646	YMLFLFLSTKGWTVIONRQDGSVD FGRKWDPYKQGFNVATNTDGKN YCGLPGNEQACKIKSFYKWDFF*L KNIHCWKPVLS*EEFPDKNVEAK DKGRKAVFSFPKFYFW*EILFCFSFR VEYWLGNDKISQLTRMGPTLLIEM EDWKGDVKKAHYGGFTVQNEANK YQISVN\KYRGTAAGNALMDGAS\H LMG\ENRDHDPFHNGHGSFQPPYD\ RD\NDGWYVWHSLLLL*KSH*YHY SESLTIFLIATTSWALTVSHCPKLFM HHSKAFQL*GRHSYSHFTDEI*RDY VICPM SHNYPEIKLEFEHSYFLNNEH LDKYL\LYILKCV*KLSFSFPFGSDT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KGCKSYSSIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPKGG TTVHTSVA VFY*SAKRNLTTVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTDDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ
2485	7982	A	2692	711	865	VTMKTFSLRHKACGQVKNTELT*Q PNSSIQPTSHYYPHCQPNTGMLIRK G
2486	7983	A	2693	26	351	ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLC SQYFQTVT DYGKDLMEKDMSPQLQAEAKSYFE NSKEQLTPLITKAVT*LG NFLSYFV* LGIQPASQ
2487	7984	C	2694	10	123	MSTD RHQGGRRWLGRPPHCYQHE AARSNCATPHHLQP*
2488	7985	A	2695	6	409	FCPALSSSTALFFLRGLWFRGKRLG STDLTLHKPFNLTPQQLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVFPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG
2489	7986	A	2696	736	927	SVAHSSCVSHTMHMTLLGRRATINC LFRNGRGQVQWLTSAPALRKADV GG*LEPRSSRPAT
2490	7987	A	2697	2	251	FFLKPCQLTVATSGGCNFWPQAIFL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV
2491	7988	A	2698	1278	1515	SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY
2492	7989	A	2699	139	260	
2493	7990	A	2700	268	388	
2494	7991	A	2701	233	400	HFLRAKVSVTQARVQWLDNGSLQP PTSMK*SSYLSLSKCDYRHVPM APRHFNK
2495	7992	A	2702	602	758	IICLSVI*NPRTYLTGVAHTCNPSTFG G*GTWNS*GQKFETSLTNMAKLCF Y
2496	7993	A	2703	379	1160	LVDMLQWPPVFHENKCCLGPPPT TH*RPAPAVPTQAGPGTQGLATAS SVSMLCSDKLFSSDQPRV*PGDAE LSVLGVGRSSRKESPDQAPPLPVIC ELSFARVGGAPGEPLQRPVVL*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRPGPENS SVTAQGQPL PGRP*NRTHLFFVPHPGQAASQS SSSPP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGDLPPFPQPV LLAALVHI
2497	7994	A	2704	178	412	LLHSSLGHVARLPTLQNMKTLARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGPVCS FKR

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2498	7995	A	2705	67	398	ISLTLGRHHGKINVYFLYLKMQG*Y FCCTFVSVVNCSDCLSGHSRRKTEG DKVRKEKQEA*AWCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD
2499	7996	A	2706	264	612	KHFSYNFFSFSFFLEGGRVLLCP WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRPPKILGFQASA TALGPLTPFCLIV
2500	7997	A	2707	179	472	
2501	7998	A	2708	498	849	GSLLSRAPIPYPLNWVSFFIPEVRTTP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG
2502	7999	A	2709	768	1073	GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR
2503	8000	A	2710	5451	5678	
2504	8001	A	2711	396	687	TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPKAM WDWFSETFRKVKEKLKTD
2505	8002	A	2712	1	93	LPKRWNSCHEPLVPLFSPLLVNAVL GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSP LVNAVLGVLGSK
2506	8003	A	2713	376	469	NQLPGPERWLTPIPTLWEARA*GL FEPRSL
2507	8004	A	2714	715	1050	
2508	8005	A	2715	404	559	VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTS LANMMEPHL Y
2509	8006	A	2716	3	180	FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIIFYFL
2510	8007	A	2717	1825	1958	LWTISVFWKAGVPLPC*QSPRWTKS ECLSFTPMFLNKS NFKKRI
2511	8008	C	2718	23	349	MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISGAGL ASKKNAVFQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE*
2512	8009	A	2719	41	298	ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRPP*ILQRHSRQNE GHRQEWCGHTA
2513	8010	A	2720	277	651	KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRIN EPSNDWDIYYWGHRS*TSPRNIWK MKSWALLERLCLKTKTKRQRLRGP SFWSTSLEKPRWSCAPRPGHGGSV GW

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2514	8011	A	2721	76	185	VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFPQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSDSSR
2515	8012	A	2722	1685	2124	
2516	8013	C	2723	299	577	MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLLTVP YRWHTLSGVALFPGCCGIFCHSG FQCGRLLPYRVHAPQG*
2517	8014	A	2724	14	213	VDMGSHRVSQDGLELMT*P*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLSYFCS
2518	8015	A	2725	1169	1404	SFLYFNGLMNFPRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQQGGQI P*AQVFETSLDHTPRPCIYPPKKKKK K
2519	8016	A	2726	44	417	CGCGLGEICLSHGVAQHNRGSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNLI*WNPGGPGARGFPGL TPPRGGKKGRAQPPENLVF*EKTG FPIVQRGGLKPPPGPPKGGE*RGGPP
2520	8017	A	2727	624	1023	CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFPFGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTINLGFSSSRVPP VTGGGYKPPPRPPKGGEKTGGTPTG HHRAL
2521	8018	A	2728	36	211	KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP
2522	8019	A	2729	640	898	VLLTCLVCLVSSKTKPNITKQHTKI KFPQSSRARWLTPVIPKFWEA*AGG SPEVRSRLPAAGLEFLVSHLGRKC WDYRHKPPCLA
2523	8020	A	2730	707	1164	SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICA*YNG*RFYLCGMK*GL *SWF*CFSLSLFTA*VKFIKCFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSFIKLPSCPNVQ FVSVCVCVCVCVNLIFKSARLPI
2524	8021	C	2731	270	371	MONLQCFRAFELLTHNSASELPLSA PVTYTEDD*
2525	8022	A	2732	2553	2764	GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFQRPYPSYEQSFPP* TPPNPIKTSFPPRNCNSP
2526	8023	C	2733	25	288	MSKVQTWGRQKTSHTRLSLHTWK VAQRPGRGAPHLDPGVAARQRCSS LSTRVCCHHVSPQPNLGWAASVG DHSQLACSHGPLQSPS*
2527	8024	A	2734	1043	1207	NMMTTHTLKKVGTGGRARWAHTC NASTLGG*GWWIT*GQEFETSLAN MVKLHLY
2528	8025	A	2735	74	233	MVTFNCFLNH*TVTKGFTRLIV
2529	8026	A	2736	11	151	ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE
2530	8027	A	2737	214	369	QKDSPD*SCDCVLKENEISNLRCPQI

MISSING AT THE TIME OF PUBLICATION

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2554	8051	A	2767	108	279	
2555	8052	A	2768	3	314	LLALVKEGPVPLFLLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRIPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL
2556	8053	A	2769	1	465	
2557	8054	A	2770	192	400	
2558	8055	A	2771	1414	1597	SGVYKRCKGGGRFVFLECATSGLSL ISS\GLSWG/RLWGHGGCRLAGGWG GGGGSGGGMALL
2559	8056	A	2772	673	988	
2560	8057	A	2773	749	1169	
2561	8058	A	2774	2	290	
2562	8059	A	2775	3	520	HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YSDKYFEEH YEYRFVMLPRELSKQVPKTHLMSE EEWRR\LG VQK/SLGWVHYMIHE PEPHILLFR\RPLPKSSTKMKFISGIV KSCFKFNVYVVYKVVFWNTWRN GYKSFHPYLCMSCILHSNRARVKC NCK
2563	8060	A	2776	1134	1312	
2564	8061	C	2777	49	282	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRDPQTXESQDRLR CAPCTXHQPPLDTHNRTL VHNR L NIPQKL*
2565	8062	A	2778	1	306	
2566	8063	C	2779	54	212	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAPMPVQSDDSGK RQTG*
2567	8064	A	2780	34	308	
2568	8065	A	2781	35	407	
2569	8066	A	2782	41	360	
2570	8067	C	2783	105	302	MXNLKRLQISMKPAHSGVCPVTRX SEGLGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV*
2571	8068	A	2784	3007	3541	KRVDYWGKSSIICTLLPHRSLC KYYFFFLSLSFKDSFWVIFFFCLSQR WKGERAKEKTTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPA WRLRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKVR
2572	8069	A	2785	272	801	
2573	8070	A	2786	659	842	
2574	8071	A	2787	156	203	
2575	8072	A	2788	441	785	
2576	8073	A	2789	2	28	
2577	8074	A	2790	5	1049	LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGRKKKKY RGKAVGPASILKEVEDKESEGEED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EDEDLSKYKLEDEDEDEDADLSKY NLDASEEEDSNKKKSNRRSRKSRS SHSRSSSRSSSPSSSRSRSRSSSS SSQSRSSSRSSRERSRSGSKSRSSRS VTGALLPHEKDLIQVHLLLRGTERE VVLDDLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKF TS
2578	8075	A	2791	971	1106	
2579	8076	C	2792	291	444	MGCFFPNSWVRAGVLIPVPVICSV RLTWGREARQGWVCRCSQNWVI FAP*
2580	8077	A	2793	1	672	
2581	8078	A	2794	1	691	MDFLLSWVHWSLALLLYLHHAKW SQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLV DIFQEYPDEIEYIF KPSCVPLMRCGGCCNDEGLECVPT EESNITMQIMRIKPHQGGHIGEMSFL QHNKCECRPKKDRARQENGSAQAQ KRDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSSRT SASRSREASRPAAWWATTSWARSR AAAARTCC
2582	8079	A	2795	312	394	
2583	8080	A	2796	490	2890	PVALTDRQTDAPSPSYHLLPGRRR TVDAAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLLGCSRFGGAVVR AGEAEPGAARSASSGREEPQPEEG EEEEKEEERGPQWRLGARKPGSW TGEAAVCADSAPAARAPQALARAS GRGGRVARRGAESGPPHSPSRGS ASRAGPGRASETMNFLLSWVHWSL ALLLYLHHAKWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DIFQEYPDEIEYIFKPSCVPLMRCGG CCNDEGLEC/VVPTEESNIPMQIMRI KPHQGGHIGEMSFLQPNKCECRPK KDRARQEKKSVRGKGKGQKRKRK KSRYKSWVPCGPCSERRKHLFVQ DPQTCCKSCKNTDSRCKARQLELN ERTCRCDGSALAQRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLFTVTRSKSA GLVVGDNIVGKIKGRGGKNLLMS HMDTVYLKGILAKAPRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKGSFGSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRMTNIDDKAKN LRFQWTIAKAGQVSNII PASATLNA DVR YARNEDFDAAMKTLEERAQQ KKLPEADV KIVIVTRGRPAFNAGEG GKKLVDAVAYYKEAGGTLGVEE RTGGGTDAAY AALSGKPVIESLGLP GFGYHSDKA EYVDISAIPRLYMAA RLIMDLGAGKEFH HHHHHAS
2584	8081	A	2797	326	1280	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2585	8082	A	2798	356	518	
2586	8083	A	2799	27	225	
2587	8084	A	2800	470	754	
2588	8085	A	2801	707	907	
2589	8086	A	2802	2	502	VLSPEEDKATITSLWAKVNVE\NAG RKKPLGKAPLVVLPWPTRGFLWN SFGKTL\ASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDA\IKAPLDDSP RATFCPSLSEL\HCDKL\HVDPENFK A/LLGNVLVTVLAIHFGKEFTPEV\Q ASWQKMVTGVA\SALA\SRYH
2590	8087	A	2803	921	1146	
2591	8088	A	2804	1170	1482	
2592	8089	A	2805	1492	1853	
2593	8090	A	2806	909	1180	
2594	8091	A	2807	105	248	CTCSRVSHPNAPRNSLVSMVFRMH PPPLDTFRQ/PQPSFNL*YP*PNYP
2595	8092	A	2808	662	843	
2596	8093	A	2809	263	408	
2597	8094	A	2810	701	950	
2598	8095	A	2812	1426	1525	
2599	8096	A	2813	1	1416	
2600	8097	A	2814	108	520	
2601	8098	A	2815	3	201	GRGLRSPDTVTOQRRRGRSPSAAER *PTRPGVLRALPAPA*GKHCPW\PRP GARRRPPSSPAARPCP
2602	8099	A	2816	318	428	
2603	8100	A	2817	448	647	
2604	8101	A	2818	42	191	
2605	8102	A	2819	3	452	
2606	8103	A	2820	25	519	EFHRLRENPPMVAVSCPTKTNVKA\ AWG\KVGGAHVSRMCAEALERMF LSFPTTKTYFPHFDLASHGFAQV*G ATGKKVADALTNAVAHVDDMPN\ ALSALSDLHAHKL\VDPVNFKLLS H\CLLG*PWAHLPRPSSTPGGCTPS LGTNFLGFL\KHRCNLNPNL
2607	8104	A	2821	270	453	
2608	8105	A	2822	115	427	
2609	8106	A	2823	1	1656	
2610	8107	A	2824	1	1188	
2611	8108	A	2825	1091	1764	SIAYQPKRVQDQTDSPILPELISNF SKVSGYKIN\AKKSQAF\LYTNNRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN APIKLPMPFFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYQNSMVLVVK QRYRSMEQNRALRNNAAYLQLSDL
2612	8109	A	2826	1	1449	
2613	8110	A	2827	2	1675	
2614	8111	A	2828	301	453	
2615	8112	A	2829	1	2139	
2616	8113	A	2830	83	1257	WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAILSKLTQEQTCKHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNYLIFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKTLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDKWDLIK LKCFC TAKETTIRVNRQPTK
2617	8114	A	2831	1	1383	
2618	8115	A	2832	2	153	
2619	8116	A	2833	1	2436	
2620	8117	A	2834	1569	1835	
2621	8118	A	2835	933	2812	
2622	8119	A	2836	56	1692	KSKSKQHSKASRRQEITKIRAELEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDITT NPTEIQTIREYYKHYANKLENRE EMDKFLDTYTLPRLNEEEEVESLNT ITGSEIVAIINSLPTKKSPGPDGFTAE LYQRYKEELVPFLKLFQSIEKEGIL PNSFYEASIIIPKGRDITTKENFRP ISLMNIDAKILNKILAKGIQQHIKKLI HHDQVGFIPGMQGRFNIRKSINVIQ HINRTKDKNHMIISIDA EKAFDKIQQ PFMLKTLNKL GIDGTYFKIIRAIYDK PTASHLNGQKLEAFRLKTGTRQGCP LSPLLFNIVFEILARAIQEKEIKGIQ LGKEEVKLS\LFADDMIVYVENPLP SQPNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIHLTRDVKDL\F KETYKPLLNEIKEDTNKWKNIPCS WVGRINIVK\MAILPKVNIYRFNAIPI KLPMTVFTELEKNYFKVHMEPKKE PALPSQS
2623	8120	A	2837	2	433	
2624	8121	A	2838	371	452	
2625	8122	A	2839	307	497	
2626	8123	A	2840	95	314	
2627	8124	A	2842	2	311	
2628	8125	A	2843	1	602	
2629	8126	A	2845	571	690	CQQGFSFLQAYGPAQHAIS\MRKFK AKYPDYEVTWANDGY
2630	8127	A	2846	130	943	
2631	8128	A	2847	45	405	GIPGRRNMAVADLDLIPDV\IDSD GVFKYVLIPSLGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST
2632	8129	A	2848	1340	1504	
2633	8130	A	2849	3	200	GSCACAGSCKCKCKCTSCCKSEC GAISRNGLWL\R\CCSCCPLGCAKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AQGCICKGASEKCSCCA
2634	8131	B	2850	1	384	MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFWLFSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCAKC AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT*
2635	8132	A	2851	1	2880	
2636	8133	A	2852	584	1253	
2637	8134	A	2853	1	2736	QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLQKLETE RELKQRLLEEQAQLQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALEKEKARCAELEELQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCRDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGGQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGAVGASELANTAKADVPIYLK MESHPTHTCWPGRITLYLLAPSPFDK QRWVTALESVVAGGRVSREKAEA DAKLLGNSLLKLEGDDRLDMNCTL PFSDQVVLVGTEEGLYALNVLKNS LTHVPGIGAVFQIYIHKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQPDISPNIIEAVKGCHLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSCIHFTNYSILIGTNKF YEIDMKQYTLEEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNRYLG PAISSGAIYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRGP PTYNEHITKRVASSAPPEGPSHPRE PSHPTATARGGPSCAGTSPWPPPG AREVPRPDAQHAERAVPREAV
2638	8135	A	2864	426	539	
2639	8136	A	2865	1	1134	
2640	8137	A	2866	766	1115	SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHGWRYAPDR*RSVR RCDGDPLHPDVRRRS
2641	8138	A	2867	61	390	
2642	8139	A	2868	627	1324	
2643	8140	A	2869	343	452	
2644	8141	A	2870	589	672	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2645	8142	A	2871	1	3000	
2646	8143	A	2872	2	191	
2647	8144	A	2873	251	505	GSSSRLGQRTD*ATASRRHFKNKV PGEAKNCSPEDDEIPLYLKGGVAD ALLYRATHMILTVG\GTSICPYVEL AVASFPPKAGS
2648	8145	A	2874	1780	1914	
2649	8146	A	2875	1154	1256	
2650	8147	A	2876	1	2629	
2651	8148	A	2877	334	468	YEEEEEDYD*EEEESEPPLDENDL EEDVVFQPPQIEGEAVYDA
2652	8149	A	2878	2	416	
2653	8150	A	2879	1	4116	
2654	8151	A	2880	3	3080	EEEELEASKSFGPGNEEEKEEKEYE EEEEEDYDEEEEESEAGNQLRQV MHAADPLEIQADVHWTHIREREEE ERMAPASESSASGAPLDENDLEEDV DSEPAIEGEEAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EAELELRVSEDEEKLPAKPKHQRG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPERLFPEPLL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSPLAVDEALRRSDLVEEFWMKS AEIRRLGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLTPRSPSD RELRSAQEERRELSSSGLGLHGSSS NMKTLGSQSFNTSDSAMLTPPSSPP PPPPGEEPATLRRKLREAEPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLPALEGTLPQKRGPLVLS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQGKERRPDSPTRTLGRS EEPTLKHEATSEEVLSPPSDGGPDG SFTSSEGSSGKSKKRSLFSPRRNKK EKKSKEGRPPPEKPSSNLLEEAAK PKSLWKSVMFSGYKKDKKKKADDK SCPSTPFGATVDSGKHRVLPVVR AELQLRRQLSFSESDLSDDVLEK SSQKSRRPRTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYEELMIFARELELEDQRS RLQQELRERMAVEDHLKTEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAMLSKGFSLNWS
2655	8152	A	2881	1	4132	
2656	8153	A	2885	1898	2056	
2657	8154	A	2886	1	233	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2658	8155	A	2887	1092	1339	
2659	8156	A	2888	363	512	EPLEGLLCLEGKGVEIVTILQAETPG EPLPP*KPHS*PGLCLRYRGHTL
2660	8157	A	2889	1	136	
2661	8158	C	2890	12	236	MTPGGFLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSKGIT *
2662	8159	A	2891	1548	1849	
2663	8160	A	2893	1	1441	
2664	8161	A	2894	954	1194	
2665	8162	A	2895	2039	2207	
2666	8163	A	2896	680	757	
2667	8164	A	2897	361	476	
2668	8165	A	2898	226	293	
2669	8166	A	2905	265	396	
2670	8167	A	2906	250	447	
2671	8168	A	2907	632	1038	
2672	8169	A	2908	3	363	VKDDPNDHEQGKRGHKPFLRELPR ATIFFLINL*VIAEVEVQDSCIDQAE EMLLRSGAPDPGVPL*GCFFALVIT HTHSSRAAMAFPVTKKASCYSQE PS*WQNSPNDTQDHSNDLSE
2673	8170	A	2909	57	448	
2674	8171	A	2910	62	371	
2675	8172	A	2911	398	789	VTGAPLMLPVLPKPGMPLAALVTG LSGLLWPCCAELVGTEFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSCTCAGSCKCKECKCTCKK SECCSCCPVGCCKCAQGCVCCKG ASEKCSCCD
2676	8173	A	2912	577	896	
2677	8174	A	2913	2	184	
2678	8175	A	2914	1	459	SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPPNPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRALWIDSDLRCAPLGLS TGGGKSRRIKGLGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLQLLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV
2679	8176	A	2915	440	620	
2680	8177	A	2916	2	987	FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTVWSPPGAE IRMFRFMRDVEPEDPMFLMDPFAI HRQHMSRMFSGGFWILAPFLSITD WQHCQGRTPASRRMQQAGSCSPL FG/MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRSAPGG IRETRRTVRSDSGLEQMSIGHHIRD RAHILQRSRNRHTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQRP LEFRRLSSGAGGRRAGEPRLAIQ GPEDSPSRQSRKYDW
2681	8178	A	2917	121	329	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2682	8179	A	2918	323	457	
2683	8180	A	2919	1	243	
2684	8181	A	2920	147	321	
2685	8182	A	2921	1	2310	
2686	8183	A	2922	319	773	
2687	8184	A	2923	85	369	
2688	8185	A	2924	1	681	
2689	8186	A	2925	1556	1953	HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWWRWQHPRGPGGPVSR RRPPHGGTPTGTVRRGGGGDPAAPG SGCPSPAVVPPRCPGAPLRRATLPP ACCGSLACSPLTL*PAPS/TPPL*ADD SCSVGLPT
2690	8187	A	2926	322	376	
2691	8188	A	2927	365	666	
2692	8189	A	2928	310	448	
2693	8190	A	2929	908	1189	
2694	8191	A	2930	761	913	
2695	8192	A	2931	1188	1373	EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK
2696	8193	A	2932	240	475	
2697	8194	A	2933	1212	1424	
2698	8195	A	2934	403	539	
2699	8196	A	2935	436	594	
2700	8197	A	2936	1	570	
2701	8198	A	2937	1086	1359	
2702	8199	A	2939	40	361	
2703	8200	A	2940	12	337	
2704	8201	A	2941	232	339	
2705	8202	A	2942	951	1069	
2706	8203	A	2943	286	621	
2707	8204	A	2944	299	513	HKCYFTLAHVHLIISFCAATLE*A*P SWGTCNSTPNFVNTTPTLAYYLGL WRSLRPFSDSVSFSFCSGIL
2708	8205	A	2945	97	258	
2709	8206	A	2946	5	464	
2710	8207	A	2947	1	522	
2711	8208	A	2948	76	488	
2712	8209	A	2949	619	746	
2713	8210	A	2950	125	279	
2714	8211	A	2951	1300	1410	
2715	8212	A	2952	1867	1947	
2716	8213	A	2953	2	52	
2717	8214	A	2954	352	538	
2718	8215	A	2955	3	313	QEFGRICPAACFPLESGTPGFSLAS KWTPNCSCSPVGSICACAGSICK\CN RVANRTVLTQTSCCSC\CPVGCABA LPRGCICKGTSDKCRSRCLDARDSC ALQM
2719	8216	A	2956	1172	1914	HFSAPWASPCS/SLLLGLLEGQGIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCQPLVSSAVD RRAPAGRRTFLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQILH RVSLNILPPGAVEDDVQAGRWRVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SRDDVACGSEEEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNPTALAKSKEELSMPKS YQY
2720	8217	A	2957	3	632	
2721	8218	A	2958	3	728	
2722	8219	A	2959	194	451	
2723	8220	A	2960	2	484	NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENSM KGNSIYF*GPGHDP LLNMNIVY*KS LTINNHHMKIT*ESLTEVLFSQGIFS VTNPHPEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA
2724	8221	B	2961	65	391	MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTQIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY*
2725	8222	A	2962	1	2148	
2726	8223	A	2963	816	1014	
2727	8224	A	2964	2	358	
2728	8225	A	2965	84	176	
2729	8226	A	2966	137	426	QACIMREYK\LVVLGSGGVGKSALT VQFVQGIFVEKYD\PTIEDS\YRKQV EVDAQQCMLLEILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI
2730	8227	A	2967	449	602	
2731	8228	A	2968	203	535	
2732	8229	A	2969	2	446	
2733	8230	A	2970	3	240	
2734	8231	A	2971	914	1291	
2735	8232	A	2972	188	266	
2736	8233	A	2973	191	306	
2737	8234	A	2978	1	440	
2738	8235	A	2979	3	670	TSRGRVGTQAGEPRDLRPPPCPSSPL RV\AVV\CLEQPERGAWEAHNIPQ NGDSA VRSFG\TGTHVKLP GPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK VELFTQNGILHIAG\RNKRIKP\GPERF QNCKDLFDLIL\CEERVYDRVGWK I*ISR\EQGDLSPVHVVNLDIQDNH EEATLG\ARFLICE\VCQCQHTTEYM HNEIDELLQEFEEKSGRTFLHTVCF Y
2739	8236	A	2987	367	492	
2740	8237	A	2988	49	332	
2741	8238	A	2989	582	923	
2742	8239	A	2990	523	668	
2743	8240	A	2991	942	1513	
2744	8241	A	2992	176	362	
2745	8242	A	2993	4937	5137	
2746	8243	A	2994	651	836	
2747	8244	A	2995	1686	1883	
2748	8245	A	2996	415	635	
2749	8246	A	2997	2	308	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2750	8247	A	2998	57	598	
2751	8248	A	2999	802	923	
2752	8249	A	3002	119	297	
2753	8250	A	3003	950	1314	
2754	8251	A	3004	1	579	
2755	8252	A	3005	27	483	RDAEDAIYGRNGYDYGGCRLRVEF PRTYGGRGGWPRGGRNGPPTRRSD FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLRKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSGRSGRGRDSPYQSRGS PHYFSPFRPY
2756	8253	C	3006	34	171	MPKSFRVIAERSMHSWYVCFLICFIL HISITLHSLVMVFVTWREY*
2757	8254	A	3007	1688	1871	
2758	8255	A	3008	1	688	MSGWADERGGEGDGRIYVGNLPTD VREKDLEDLFYKYGRIREIELKNRH GLVPFAFVRFEDPRDAEDAIYGRNG YDYGGCRLRVEFPRTYGGRGGWPR GGRNGPPTRRSDFRVLVSGPSP/SG SWQDLKDHMRE\AGDVCYADVHK DGVGMVEYLRKEDMEYALRKL *PPKFRSH\EGETSLHRRFIPERSNQL MATSPVSGLSRGRDLSIPKARGSP HYFSSFPGP
2759	8256	A	3009	428	579	
2760	8257	A	3010	1924	2043	
2761	8258	A	3011	131	395	
2762	8259	A	3012	910	1173	
2763	8260	A	3013	1295	1489	
2764	8261	A	3014	1477	1604	
2765	8262	A	3015	443	805	
2766	8263	A	3016	1	2109	
2767	8264	A	3017	1297	1408	
2768	8265	A	3018	3	314	
2769	8266	A	3019	5	340	GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLGTGEPRVYIRNKV ANTGVPGAPGPSIGGVATPATDYCH RIAPILARRRRRRRRRRRRRRRG GGGGVAGGGGGG
2770	8267	A	3020	1	1973	DGGARARGRAARRRRRRRRRRRRR RRRRRRRRRRRRRRRRRLGLERP QPTSRGRAPGASRAEEKMEELVVE VRGSNGAFYKAFVKDVHEDSITVA FENNWQPDRIQPFHDVRFPPVGYN KDINESDEVEVYSRANEKEPCCWW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLSVNPKNPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVLSINEVTS KRAHMLIDMHFRSLR TKLSLIMRNE EASKQLESSQLASRFHEQFIVREDL MGLAIGHGANIQQARKVPGVTAI DLDEDTCTFHIGEDQDAVKKARS FLEFAEDVIQVPRNLVVIGKNGKLI QEIVDKSGVVRVRIEAENEKNVPQE EEIMPPNSLPSNNRSRVGPNAPEKK

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						HLDIKENSTHFSQPNSTKVQRGMVP FVFGTKDSIANATVLLDYHLNLY KEVDQLRLERLQIDEQLRQIGASSR PPNRTDKEKSYVTDDGQGMGRGS RPYRNRGHGRRGPGYTSGTNSEAS NASETESDHRDELSWLSAPTEEER ESFLRRGDGRRRGGGGKG\QGGRG RGGGFKGNDDHSRTDNRPRNPREA KGRTTDGSLQNTSSEGSRLRTGKDR NQKKEKPDSDVGQQPLVNGVP
2771	8268	A	3021	1	2116	
2772	8269	A	3022	656	883	
2773	8270	A	3023	303	589	
2774	8271	A	3024	2	478	MAGKQAVSASGKWLGMGIRKWYY NAAEFNKLGLMRDDTIYEDVDVKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCSSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLK\EVIRE RKEREWEWAKK
2775	8272	A	3025	323	400	
2776	8273	A	3026	2	396	RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYY\NAARIQNKL LMRDDTIYEDVDVSRP*EDFPEN LYNDRMFRIH*EGHWTLNLKHQILP KEQWTFNFEENFY\LEPYLKE/VLF RERKEREWEWAKK
2777	8274	C	3027	144	341	MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNFLSFQGXQHKKNK TGQHFTSKCTEPFLQD*
2778	8275	A	3028	1070	1335	
2779	8276	A	3029	2	303	
2780	8277	A	3030	149	244	
2781	8278	A	3031	1642	1797	
2782	8279	A	3032	1115	1320	
2783	8280	A	3033	1240	1408	
2784	8281	A	3034	539	669	
2785	8282	A	3035	1155	1579	
2786	8283	A	3036	437	666	
2787	8284	A	3037	51	279	IKGRWEPPPLASFFLTSQGHCS DGP*GWGEAVSPRGRNTLSSSSW HWVPYSELRGRGVACRKEVYKIVQ NTQH
2788	8285	A	3038	3	300	
2789	8286	A	3039	451	760	
2790	8287	A	3040	183	410	
2791	8288	A	3041	602	1145	
2792	8289	A	3042	2	496	
2793	8290	A	3043	710	896	
2794	8291	A	3044	143	601	
2795	8292	A	3046	120	280	
2796	8293	A	3047	2	424	
2797	8294	A	3048	3	452	
2798	8295	B	3049	240	420	XLKGHGQRKVAERADPKPLPQRGR TCPKRRCPPLSDPARCTSFVRDPVN FQASLSHCLAW*
2799	8296	A	3050	310	401	

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2800	8297	A	3051	544	700	
2801	8298	A	3052	1	568	
2802	8299	A	3053	686	787	
2803	8300	A	3054	8	182	
2804	8301	A	3055	227	547	
2805	8302	A	3056	1	523	ESLRKQLGQEPFFDMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIKPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHVLRTQFPSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCSRSCS RNRSP
2806	8303	A	3057	919	1100	
2807	8304	A	3059	429	780	
2808	8305	A	3061	567	682	
2809	8306	A	3062	148	372	
2810	8307	A	3063	113	303	
2811	8308	A	3064	367	449	
2812	8309	A	3065	48	369	
2813	8310	A	3066	979	1254	
2814	8311	A	3067	173	776	
2815	8312	A	3068	1	111	
2816	8313	A	3069	33	494	
2817	8314	B	3070	100	154	MVHLTPVERVCRYCPVGQX*
2818	8315	A	3071	559	775	
2819	8316	A	3072	744	940	
2820	8317	A	3073	1	255	
2821	8318	A	3074	1	1206	
2822	8319	A	3075	905	1823	
2823	8320	A	3076	36	689	
2824	8321	C	3077	215	325	MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLT*
2825	8322	A	3078	1	831	
2826	8323	A	3079	97	236	
2827	8324	A	3080	409	602	
2828	8325	A	3081	818	1095	
2829	8326	A	3082	528	714	
2830	8327	A	3084	91	242	
2831	8328	A	3085	75	430	VSPGLPAARLFQVAYLDSHLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFFL CGPFKVVIICTELQNVSRSPQTTLAT VYCNKITSYICKKKK
2832	8329	A	3086	1000	1145	
2833	8330	A	3087	225	324	
2834	8331	A	3088	3	54	IIHYSLLIIV*CWVQF
2835	8332	A	3089	461	658	
2836	8333	A	3090	337	408	GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCPDPPGRYPLRDSGQSVTLH AGSSATTIQEPRGA
2837	8334	C	3091	155	453	MLGALGAEELSLDSLPEGLLNFSKP GSERGGRLGLVPAAGEGPCPDPPGR YPLRDSGQSVTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E*

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2838	8335	C	3092	121	393	MALPGRLPHRKLGGTLEAPWPGIP SGAVRRHQPPPTTLXXWLGKVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI*
2839	8336	A	3093	270	573	
2840	8337	A	3094	15	297	
2841	8338	A	3095	970	1098	
2842	8339	A	3096	127	296	
2843	8340	A	3097	875	1075	
2844	8341	A	3098	171	404	
2845	8342	A	3099	186	392	
2846	8343	A	3100	2	202	
2847	8344	A	3101	2	242	ARGNMAAATLTSKLDLSLLFRRTSTF ALTIIIVGVMMFF\ERAFDQADAYFT DH\NEGVRPCAIPDLGTRLRGDSGV EKL F
2848	8345	A	3102	79	1137	
2849	8346	A	3103	374	519	LDSRRK**C*LESRPHE*TS/DLSSGS LLI*GIWSILFYPMAP*KFQKEN
2850	8347	A	3104	1	1214	
2851	8348	A	3105	105	379	
2852	8349	A	3106	260	421	LLYGDCTWTSFHLQRLQLHCQVSQ PCREL P*LVSSVLCFPFISEELHCVTG HF
2853	8350	A	3107	420	848	
2854	8351	A	3108	664	1059	
2855	8352	A	3109	73	269	
2856	8353	A	3110	307	566	
2857	8354	A	3112	316	410	
2858	8355	A	3113	200	403	
2859	8356	A	3114	258	377	
2860	8357	A	3115	1767	1893	
2861	8358	A	3116	1	389	
2862	8359	A	3117	3	569	RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTWQKFSSPTEIVERCVES L\IAVF\QKYAGK\DGYNYNLSLRPE F/L*AFMNTL\AAFTKNQEGPWVSL DRMMEETGTPNSDGSARISSGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPLGPGGFQTPPFSSFGLS VLHLPQAHP SLEAH
2863	8360	A	3118	362	712	
2864	8361	A	3119	2	152	
2865	8362	A	3120	134	760	
2866	8363	A	3121	670	891	
2867	8364	A	3122	44	63	SPSNRNTEEGTLTNIIHNLGMYVFL HAVKGTFETP*PG*KARAP*PPLGN NWDYGD RFTSFTGSFFTISPILYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQQEH
2868	8365	A	3123	88	207	
2869	8366	A	3124	2	191	
2870	8367	A	3125	145	865	
2871	8368	A	3126	69	118	
2872	8369	A	3127	1148	1323	
2873	8370	A	3128	197	327	PLGKKFSCSKSLRLLGPFLQL*SLRF

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						RKTTY
2874	8371	A	3129	154	303	
2875	8372	A	3130	3	158	
2876	8373	B	3131	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2877	8374	A	3132	383	529	
2878	8375	A	3133	1981	2132	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFAFLCASINKKWKRI
2879	8376	B	3134	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2880	8377	A	3135	383	529	
2881	8378	A	3136	1979	2131	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFAFLCASINKKWKRI
2882	8379	A	3137	296	592	
2883	8380	A	3139	224	700	VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEFPQIHLKLTFMFKNTT NFIFTAELCDQCQGL*NLHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLEFKSTMGKDQRQI DNNIMN
2884	8381	A	3140	761	963	
2885	8382	A	3141	475	715	
2886	8383	A	3142	381	698	
2887	8384	A	3143	2	235	YASLEPPDRPQVGASCPGTYV*GA VPPSPAGVVGREGVAGKGTGGCTCDK PLSPCSLAGRRGSFPRRPSWTSPRL LCW
2888	8385	A	3144	49	353	
2889	8386	A	3145	174	495	
2890	8387	A	3146	73	226	
2891	8388	A	3147	326	421	
2892	8389	A	3148	1306	1444	
2893	8390	A	3149	53	246	
2894	8391	A	3150	228	271	
2895	8392	A	3151	419	599	
2896	8393	A	3152	1	322	
2897	8394	A	3153	151	375	
2898	8395	A	3154	2017	2191	
2899	8396	A	3155	3	234	LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLLQGLSLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR
2900	8397	A	3156	43	408	
2901	8398	A	3157	3	374	
2902	8399	A	3158	1	823	MAVVAPRTL L L L L LSGALALTQTWA GSHSMRYFSTSVSRPGSGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWMEQEEPEYWDRQTEISKNAQI DLESLRIALRYYNQSED/VPPPKTH MTHHPISDHEATLRCWALSFPYPAEI TLTWQRDGEDQTQDTEL VETRPAG DGTGFKWASVVVPSGQEQRYTCHV QHEGLPKPLTLR WEPSSQPTIPIVGIL AGLVLF GAVIAGAVVA VMWRRK SSDRKGGSYSQAASSDSAQGS DVSL TACKV

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2903	8400	A	3159	1	1264	MAVMAPRTL L L L L L S G A L A L T Q T W A G S H S M R Y F F T S V S R P G R G E P R F I A V G Y V D D T Q F V R F D S D A A S Q R M E P R A P W I E Q E G P E Y W D Q E T R N V K A Q S Q T D R E N L R I A L P L T Y N Q S E A G S H T L Q M M Y G L G R G G S D G A L S F R G L P P V T A Y D G K D N I A L N E D L R S W T A A D M A A Q I T Q R K W E T / A A H E A E Q W R A Y L E G R C V E W L R R Y L E N G K E T L Q R T D P P \ K T H M T H P I S D H E A T L R C W A L S F Y P A E I T L T W Q R D G E D Q T Q D T K L V Q T R P A G D G T F H K G A S C V G P L G E E Q R Y T C \ H V Q H E \ G L P K \ P S T M \ R W * P S S Q P T H P P S W G I H C L A L V L L W K L * S L E A V V A A C E C G R R K S S D R K \ G G S Y T Q A A K P V T S A Q G S D V S L T A C K S V R Q L P C V G L R G K S C F L P F P L V D L E E P W T L F P A K G T L H V S V F M
2904	8401	A	3162	1	342	G S R T V P S P S S G L A S P G S P T H R S L G P T T P P M A S A T E D P V L E R Y F K G H K A A I T S L D L S P N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G / S R D L S V R L W I P V ** E Y S * N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G L E T Y P
2905	8402	A	3163	1	583	D M E S R S V T Q P G V Q W C Y L G * L Q P P P P R F * R F S C L S L P G S W D Y R C V P P H P A N F F I F S R D G V S H H V G Q A G L E L L V S S D P P A S A S Q S A G I T G L S H H A R P D / Y T F L L T V F E P F H G T H V R P P V T C G T L A S N W T P T A F I S L A E N T K V L K V A L K E V P F G F D I A I S K A S G T V Q I R A M S F M K T T F L S P S F V R E C H T H D H V T L L Q S
2906	8403	A	3164	1	347	F F I L F F L R Q S H S V A * A G V Q W H N L D S L Q P L P P G F K Q F S / L S L P S S W D Y R R M P P R P A N F * F L V E T G F R H V G Q A G L E L L T S G D P P A S T S Q S A G I T G V S H G A Q S C P L L Y I E F P L S I L A A T
2907	8404	C	3165	13	399	M E K I P V L F R V A N L I S I I P A P N K S R L C G K T R I S R S A K S K A N T R V F L A C R F G L A G D N A I A N V H A P D A D L E A Q S D V E R T M D L K P C I W V P D T L G E A E Q T A P A D R L S M H T Q H F G R P R R A D H E V R R P R P S W L I W *
2908	8405	A	3166	168	414	N P L L L P N T F P A N G N T I L I K E K V L F L F F * D G S P V L S P R P D C G L Q W R N L G \ S L Q S P P P G F T P F S C L S L P S S W D Y R H P P L R P A N F F L Y F L V E T G F H R A S Q G \ G L D L L T S R S / I P P R A S Q S A / R G L Q G V S H P R P A Y M S L R Y N K P A H V P L K I K V K K
2909	8406	A	3168	28	123	
2910	8407	A	3169	2	123	E N R L M A G G E / H M L A A I L L F T A L R C L C K V K H K P G L H A H * G T A P
2911	8408	A	3170	1	402	Q G F S P P \ E S L R Y G \ S W E G K A L T F P Q P D T H K G S V L E D ** K R K A S L Q L R * E E G I C L \ C L S L G M E C L G V K P / V A Y I L F T E I G E S R L M A G G K / H M L A A I L L F T A L R C

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						LGKVKHKSGLRAHRTAPFLKLIY DTESFAHMFSC
2912	8409	A	3171	1	399	SSSLQPPPP\GFK*FSCIGLPTSRDYR CVPPRPANFVFSVETGFHHVQGAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWCKNSLFTGENVI EANQNLLALRFISAMDLSLRIVRN QTFFF
2913	8410	A	3172	1	451	LYGEGWSFALVAQAGVQWCDLRL LQPLLPGFK\YSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCLSLPSS*DYRCTPPGLA*/F FIFLVEMGFSLARLVNS*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR
2914	8411	A	3173	2	346	
2915	8412	A	3174	1	2430	
2916	8413	A	3175	576	983	GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSAFKKVNSNLST*Q FKYKNKGICACQFSLFPLK*PIPL FFAGEHTIRNYPATVHGALLSGLRE AG\RIADQFLGAMYTLRQATPGVP AQQFPKACETDAF
2917	8414	A	3176	1	2930	RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKAAAAAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPGSAAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDLANLSEDEYYS EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGAFAFQSRPHDR MTSQEAACFPDIISGPQQTQKVFLFI RNRTLQLWLDNPKIQLTFEATLQQL EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIHSGVSG LAAARQLQSFGMDVTLLEARDRVG GRVATFRKGNVADLGAMVVTGL GGNPMVAVVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQDFNVLNKPVSLG QALEVVIQLQEKHVKDEQIEHWKKI VKTQEELKELLNKMVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVSKS HRDLTALCKEYDELAETQGKLEEK LQLEANPPSDVYLSSDRQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVN TRSTSQTFIYKCDVLCPLGLV QPPAVQFVPPLEWKTSVAVQRMG FGNLKVVLCFDRVFWDPVNLFG HVGSTTASRGELFLFWNLYKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRS\SAVPQP\KETVVSRRWA DPWG\RG*\SYVAQGS\SGNDYDL MAQPYHSWAPSIPGAPQPIPTLLC GENITIRNYP/TPVHGALAEVGSRE

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						AGKEIARPSFWGAMY/TRLPRQVATP GCFLAQQVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD
2918	8415	A	3177	62	447	GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPNVHSHTHTHTHT HTHTHTHTVSYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ
2919	8416	C	3178	90	233	MRIGYKVKDGTFLDLQMGGPLPGXX XXSRPKRNHQLSKGEREINLGKL*
2920	8417	A	3179	462	929	SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNPHQPIMPLFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FSCLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGQAGLELLAS SDPPASASHVGITGVSHHTWPMPL LLLI
2921	8418	A	3180	160	272	FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLPP CPANFSYFL*RQSLTVLPRLVSNWS TQVSLLTQPSVLGLQA
2922	8419	A	3181	6	270	RDRVLLCHTDWSIAVESQLTASSN SW\VK*SSCLSLQRTDRYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV
2923	8420	A	3182	92	549	VWQGLHPQLHPHFASQNLIQSLALS LKAGV\QWHDLSSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLQCFNSSS RLEHTDGIHFLSEAMSAIHESFPHI
2924	8421	A	3183	16	661	DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLSSWDYRRPPRPANFC IFSRD/MAFTTLARLVSNS*PQ/CDPP TSASQSAEITGVSHRAWPVLSSPQPF FFFDMESHAIQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPR PANFFVFL*\RDGVSPC*PGWSRSPD LVIHPPWSPKSAGITGLSHCAQYPY QFSKHKDLRVSGKA
2925	8422	A	3184	288	489	CGLILELEKLLL VWIQQIQMSLNKA TI*SNDIFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG
2926	8423	A	3185	3	166	WLYSANVAHAPYRGSALWCLRDS RPPAQYWSAFQHYSL*PTQFPLEFT TKSLLS
2927	8424	A	3186	3	725	LALLGRVYDVLSARD/YVELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLQEKQ TFPPCNAEWSSARGSRLWCSQKSPK DADDTSIYMFYQKVGDNISDSWKN AGRVFKDSKFDANDPILKDQTQE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNQGVKPEGTTETTMK
2928	8425	A	3187	1	1988	
2929	8426	A	3188	134	944	MLRCGGRGLLLGLAVAAAAVMAA RLMGWWGPRAGFRLFIPEELSR GRPR\DPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRA TGDCSEAGLVDDVSDLSAAEMLTL HNWLSFYEKNYVCVGRVTGRFYGE DGLPTALTQVEACDSTRGFGGQT NYKLQEKQTFPPCNAAGGGAQPGAA RLWCSQKSGGVSRDW/ALAVPRKL YKPGAKEPRCVCVRTTGPPSGQMP DNPPHRNRGDL\DPNLAEYTGCPP LAITCSFPL
2930	8427	A	3189	1	312	AQPGVQ*RNLHSLQPPPPGSKRLSC LSLPSS*DHRPPPPCPANF/SVFLVE MGFHHVQGAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR
2931	8428	A	3190	2	176	
2932	8429	A	3191	3	67	
2933	8430	B	3192	1	1587	MVKLSIVLTPQFLSHDQGQLTKELO QHVKSVTCPEYLKRVINTLADHH HRGTDGFGSPWLHVIIAFPTSYKVVI TLWIVYLWVSLKTIFWSRNGHDG STDVQQRAWRSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVTILRRH VETKVRKIRKRKVTTKINHDKIN GKRKTARKQLSQHSISHVLAFSDPP FCKKGSLLQAPPSADDNIKIPAERLR IPLPPSADDNLKTPSERQLTPLPPSAP PSADDNIKTPAERLRGPLPPSADDN LKTPSERQLTPLPPSAPPSADDNIKT PAERLRGPLPPSADDNLKTPSERQL TPLPPSAPPSADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPPSAPPS ADDNIKTPAERLRGPLPPSADDNLK TPPLATQEAEEAEKPRKPKRQAAE MEPPPEPKRRRVGDVEPSRKPKRRR AADVEPSSPEPKRRRVGDVEPSRK KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS *
2934	8431	A	3193	792	1024	SHRKMFORAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPRT LH
2935	8432	A	3194	1	1656	
2936	8433	A	3195	112	368	SHRKMFORAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQMDMTFFSLQ LCAQARTGRSD
2937	8434	A	3196	1	1353	
2938	8435	A	3197	1	452	
2939	8436	A	3198	1	510	
2940	8437	A	3199	2159	2958	

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2941	8438	A	3200	350	927	LFLVSPLKTISGSRNG\HDGSRDVQQ RA*SSNRRRQ\KKRVSSFRGNKIVLK DVITLRRHVETKVRKIRKRVTTK INHDKINGKRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQMDMTFFSLQ LCAQALQREMAERKAAYRHHSPIP VGNRVVQKHLHPHPVGPLI
2942	8439	A	3201	1	277	FFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWGYNRLPPCP AFILFYLF/CRDK/SLAMLRLVLNS\ WAQVILPLQPPKVLGLQA
2943	8440	A	3202	1	340	SIHLPAKPPPNHSTGVVWQHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHLSLLSSWDHRCAPPHL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM
2944	8441	A	3203	2	354	ESLTGVQWHEFASLKPL/PCLSLPR GWDYRRAPPRPAYF*FLVETGFHHI GRAGLKLLTSDDPVSASQSAGITG MSHRAWPLLKYFSALQTLNILQKN KNKNLIKTYFISLHVKIF
2945	8442	A	3204	166	373	EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPHHTL H/TALNI*SCPCCLFIFLVC
2946	8443	A	3205	2	775	LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAVPGRSNGSALTPVWV LIAKQSPPIVKILKFGWFPILAMVIS SFGGLILSKTVSKQQYKGM AIFTPVI CGVGGNLVAIQTS\RISTYLHMWSA\ LGVLP LLMKKFCPNPRSTFCASQKL NSMSCSRLLLLLGGSQGH LIFYIY LGGGVQS* T/TPDLCCGSNLLGRA* SRVTNPAVTGA EVELVRLTWHQGL VDPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY
2947	8444	A	3206	2	348	IAFGRYELDTWYHSPWPPEYARLG RL\HMC EF*IKYMNSLTILTMHMVN CAFDPPLGLPKELSLETRMETFFPAL PSFHSIHCPLCVQPELGKAFGCLSVG AWGCRTHLRFTGLH
2948	8445	A	3207	1	1503	
2949	8446	A	3208	1	635	
2950	8447	A	3209	1	665	MQAICAGGWKA EAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDT\SGQKDYDRVT PPYPYPA/QADVFLICFSLVSPASFE NVRKAWYLNVRHHCPN\TPAILVGT KLDLRDDKD/TRIEKLKEKKLT\PIT YPQGLAHG*GRLGAVKYL G/CAPA AHTSEGLKTVFDEAIRA\VLCP PPVK ERGRENCLPVVNVSAPSFLGPVPLE PL
2951	8448	B	3210	1	693	MYGVSAFVVLSP TGRLP SVLQKEN QQQGV P NSPPLHEQM QMDTGLCRL TPGLTLAQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS

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						RESCGERECVQFSQRTARDRWCI RAELEQDILDSAAVTIIQKWHIKGR ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEA AVRCKGPPTRP AV ELPPRLPVLS*
2952	8449	A	3211	1	627	FFFGKSILLFKKINVTFDIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQ\QGETPS LLKNIKKISRAWWQAPVIPATREG*/ E*GESPEPEGKVCRRAEIAATCTP AWGVQSETLSSKKKSFVLNVPHH PRQASVSFHCFFHNQWGSPLWKKA RTFLLLNGWLSCPHLSTQGNLSA PHLAEAQTLSP
2953	8450	A	3212	114	411	EREFRVFPQVELQGPDLG*LNLLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHVNVQVGFELLT*GDP P/AWASQRVKMTGPTHQAHLEGNF F
2954	8451	A	3213	48	1400	HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDS\LLQPLTSAM/PPSAIPT P QRTSTPGLALFPGLPSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTLP VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYTSTSVISLSAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSTPIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSSTAATS TSLPHPSSTA AVLSGAFCFSTSPAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGLQAPS TVAAVTPLPVGPWPQHPQLPVLPGF GSAFSSFHNSRSLWHLKPGFIWDFK AGRQFWFFRAFGPSRVSGLFLRILH NHPCKNYSIMRLHSQHCHYRSIQLR LWESYPAQPDGVS
2955	8452	A	3214	2	694	QLLNYAPGPGGPRYVDCDLF*NGY HL\WYHD\YGHLEFI\RLQLATQFEN WYMKYQSPHIIQTKYGAETVSGFPR DPPSDVPVRCPRKSLLEQ\YHLGLDS KPQKNTCLESPLWNF\ADFMTE\QSP \TKVLGNKKGIFTRAETTQSSAFL LRERY\WKIAQ*NPGIPHSVARSQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLLDCSRQTRTFSGLG FV VIYSSREH
2956	8453	A	3215	2434	2765	GIILFWAQLFPASFFFFFFFF*DG VSLC CPGWSA VVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLVLS*AS*VHPPWPP QSAGDYQA
2957	8454	A	3216	2	481	LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCPPQAPGSSKSDCS

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						PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR
2958	8455	A	3217	126	364	RAWANLS*LKVLPPGLKGFSGTLT PSTGNNGLVPPPRVNFSGFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGIN PFFL
2959	8456	A	3218	132	342	SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLLVLPKRWDYRHEPLRPDLK
2960	8457	A	3219	2	264	QLTATPPPTGFKQFSCLSHPSSWDY RYVPPRAKFCIFS/VRRGFTMLAR MVIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVQGDLN LLTLRSAHLSLPKCWDYRRKPPGLA CFMILNSYLV
2961	8458	B	3220	134	3038	PGMEDGSDDMDTSVEDIGGRSCVT RFVRTLLIMEHGVKPHSKHLETFY AFLYEFAKMGEESQFLLSLQAIST MVHFYMGTKGPENPQVEVLSEEEG EEEEEEEDILSLAEEKYRPAALEKMI ALVALLVEQSRSERHLTSLQTDMA ALTGGKGFPFLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLA VQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAAYLLVS LIPSNFRQMFSTRSLHIPTRDLPLS PDTTVVLHQVYNVLLGLLSRAKLY VDAAVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFPKLPSEP AIATNHNKQALLSFWYNVCADCE NIRLIVQNPVVTKNIAFNILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGAVEELFNLMLFIAQRPD MREEELEDIKQFKKTTISCYLRCLD GRSCWTTLISAFRILLESDEDRLLV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLLTLL NSYSPPELRNACIDVLKELVLLSPH DFLHTLVFPLQHNHCTYHHSNIPMS LGPYFPCRENKILIGGKSNI RPPREL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKFE TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQLDSA TEKLTPRGKKPKERKTKDDEGGNS HLKGRAC*
2962	8459	A	3221	2170	3139	DLRALALLSVHTPKQLNPALIPTL QELLSKCRCTCQQRNSLQEQEAKER KTKALALWTTIITFRVGGGSNTLGV TGLRVVCSAEPKPKYK*QKN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEEHTVDSCISDMKTE

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						TREVLTPSTSDNETRDSSIIDPGTE QDLSPENSSVKEYRMEVPSSFSED MSNIRSQHAEQSNNGRYDDCKEF KDLHVCCKDSTLAEESEFPSTSISA VLSDLADLRSCDGQALPSQDPEVAL SLSCGHSRGLFSHMQQHDILDTLCR TIESTIHVVTRISGKGNQAAS
2963	8460	A	3222	3	344	PESHSAQAQGVQWPDGLSLQLSLP AFKQFSCSLSPSSRDYRRASPRANF *FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLPCLKSPQ
2964	8461	A	3223	1411	1741	GYLQFSFSFFLFFFFFFFFLGGESHV T/RGLECSSVISTHCNLRPLPGSSDSR ASASRVARTRGMHHHTRQIFVFLV QMGFHHVGGAGL/DSS*PSVVHPP RPPKVLGLQA
2965	8462	A	3224	361	462	RHFLSTETCYCNSFF/RHSSSKNYTK LKRYE*VS
2966	8463	A	3225	3	89	
2967	8464	A	3226	1	336	VCQVCGFRSLHTNVNRHLLLNKP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSGIIYLCQYCEYSTGQIEDLKI HLDFKHSADLPKCDCLMRFGNE RELISHLPVHETT
2968	8465	A	3227	951	2075	RTANLNFCKILDKSQALNVNCPAET GL*LRANSRWP/PINCELCEFNISKYF SDLKQHMILKHKRTDSNVCRCVCKE SFSTNMLLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFR\DP HWCEQCDVQFSSSELYLHFQEHSC DEQYLCQFCEHETNDPELA*HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGFSSNNTWKRKRGGQKTFPLLI NLELSTSLTNYRGSPWASELSTSVE VSMAMLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCSPPALIAQPI VGAQE
2969	8466	A	3228	2	415	LDPGSLAGFTSYIQFMYDEFVEEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHCVFSTITES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN
2970	8467	A	3229	607	1317	
2971	8468	A	3230	260	535	
2972	8469	A	3231	246	985	KLRHKMAANKPKGQNSLALHKVI MVGSGGVGKSALTQFMYDEFVED YEPTKADSYRKKVVLGDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR

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						PAPVSRKTAHWAEVFFDLRMREIRARKMEDSKEKNGKKRKS LAKRIRERCCIL
2973	8470	A	3232	1	634	MAANKPKGQNSLALHKVIMVSGSGVGKSALT\QFM YDEFVED*EPTKADSSRKKVVL DGEV\QIGYPLDTAG\QED\YAAIRD\NYFRSGEGFLCVFSITEMESFAATAEFREQILRVKEDENVPFLLVG NKS DLEDKRP GFL*EEAK\NRAEQWNV NYVETS AKTRANVDK VFFDL MREIRARKMEFYYLNGTK NTKRLAERIREGGCIL
2974	8471	A	3233	314	373	
2975	8472	A	3234	1	2129	PSVAGAATLWFHVTLPFCARLCGR RSCTHSGIITEFHFFHL/PFRPIILACGND DCR IHIFAQQNDQFQKVL SLCGHEDWIRGV EWA AFGRDLLASCSQDCLIRIWKLYIKSTSLETQDDDNIRL KENTFTIENESVKIAFAVTLETVL AGHENWVNAVHWQPVFYKDGVLQQP MRLSASMDKTMILWAPDEESGVWLEQVRVGEVGGNTLGFYDCQFNE DGSMIIAHAFHGALHLWKQNTVNP REWTPEIVISGHFDGVQDLVWDPEG EFHITVGT DQTTRLFAPWKRKDQSQVTWHEIARSQIHGYDLKWLAMINR FQFVSGADEKVL RVFSAPRNFVGKFLCHYR\KSLNHVLCNQSDLP EGAT\APALGLSNKAVF/LREDKAPQPPDEEELLTSTGF EYQQVAFQPSILTEPPT EDHLLQNTLWPEVQKLYGHGYEIF CVTCNSSKTLLASACKAAKKEHAAI ILWEITTSWKQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDSNLVIVEKAWIQS/TPEFEPVFSLFAFTNKITSVH SRIIWSCDWSPDSKYFFTGS R/DKKV VVWGECDSTDDCIEHNIGPLPPSVL DRGWGCDQLSASAQCSHPSQRYVV AVGLECGKDLLIYLGKRLIKFQK*M T/ATHCVGNKSKPKVIHWAIQKIYC WEGICSGKT*TRREGRR*VVYTFA SCG*DHTVKIHRVNKCAL
2976	8473	A	3235	451	778	GSGRWKSRVARAGMQISGAHLQL NCKPPPPGLKADPPWLSL\ PSSWDP QMCPTPWLLFVCLVETGFTMLPQ AALQLLS*SDLSA*ASQNAGITGMS HHAGPDTVPLF
2977	8474	A	3236	1	186	FFFEMESRTVTQAGVQWHDLG\SL QPPPPG\SSDSPVSASHVAEITGAHH HTWLIFIFLFL*GVQWHD LGLTAT SSLGSSDSPVSASHVAEITGAHHH TWLIFIFLFL
2978	8475	A	3237	1	353	KIWLFFVFKTDVSILVHPRLECSGAI SAHCNLHLPGLSDSHTSAFRVAGTT GARHQAQLIFTFLVEMGFHHVGHAGLKLPT*EIRPPRPPEVLGLHACAT VPGHKYVNEPIKMVLLK
2979	8476	A	3238	3	453	GQTGTWQGNTGQRVPQLPPHPPPIH

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						LVSRRHGKLRHGFLRPMPEPRGLES GKTGSARGVAACTSP*GRSG\QGGG PRDIAQQGGCRGSACGRRSHEALRP RVWCGEGPQWTW\CAVCPNRSAP GAGLAD\RQHPGESRAWGETRLCE AGGAE
2980	8477	A	3239	232	472	LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQT\VT\TKSR\VK*SSCLS/LP SSWGYRSVPPCPANYFYFL*RQRLT TLPS
2981	8478	A	3240	2	345	MVHVAVAGLNGTHSCPPASSSVLTF GHP\PHEQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDIFPH DPAPPLLLSASWV
2982	8479	A	3241	205	361	DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSGRL\IPHDPAPPLLLSAS WV
2983	8480	A	3242	137	959	IPFPVMLDPAGRQQQRWGRIMGY KVSLGGA*NLGRCKNIHKGSCREGL CLISLRAWEGRVLGEGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARA\WCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGL*TPGLGYEHLKPPF/PSA PAA*PPG\PAKAQAPRKSCAPT\TH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFPSNAPLSPSPHP TTFPEFPCSPTPPPQIPHPQDFPRS
2984	8481	A	3243	23	438	SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\SAQVVVQWHDGSLQPQ TPGPK\YPPATAS*VAGARLIFFK*FL *RWDLTIMPKAGLKL\PATGDPPACL LLSFSLIPTGGFTRFEPTRHSLLLEV GLSPMLVRHWLWA
2985	8482	A	3244	1	1061	ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADVLFKIAPAVV HIELFLRHPLFGRNVPLSSSGGFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKKS\DIATIK IHPKKLPLVLLGHSDRTRCPGEVL WVAIRQIPSP*QNTV\TTGIVSTAQR EGRELGLRDSMDY\QTDAI\NYG NSGGPLVNL\GEVIGINTLKVTAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNS\DFPE VSSGIYVQEVVPNSPSQGGIQQGDI IVKVNGRPLVDSSELQEA\LTESPL LLEVRRGNDLLFSIAPEVVM
2986	8483	A	3245	1	268	QGSPSRDPSPLGGP\NGGIFLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF
2987	8484	A	3246	20	353	KEVGRLTHSVNHSGGREKYVWHP GNAL*Y\GKLPVLP\CP\IFIVNR*VQ*P *PERHVMVTRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL

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2988	8485	A	3247	2	322	KLDNSSKWLENGTFDLSILQDLDNF C*KMGKWSEVPYVQAFF\SIHSLPSL CSQCHL/CPDFPSFSP/YPLLLSPPQT QSPLNPPFPLTPLTSLPRLLLARLN QVPILP
2989	8486	A	3248	141	924	PFSSQTVKLSGGATRNVPSSPKASG GQPSEGWEVALEGDS CAALMRQQ CPGLLKSRK/RAPGNPTASGSAPGA TKRSLGGRARRGLEFVVSRRFFGGGR AQSSLGNAHPHSGTIPKAPHASQQG LGLRLGGLEPSTPPWVHPPARPRAS PDPSRVAGSPRSLPNPPAAGKGGRG SGEEARYFDLS*ILKSLPYPGHERVY QEPQRGVKTSCSCSPF/HLPLLLFQS SPPPSTLVGAGLKIGFLRCPVGGILI GKGFFFNCLHST
2990	8487	A	3249	1	363	QVSLVINWDLPTNR*NYIHR*AYIW NTPLPLHTWPSLGLKLLIFLIPFLEFQ VIGRGGRLDRKGGAINKGTEYDERT LRDIETFYNTSIEEMPFNADHMLM GCPATQPLSGLIIGASDQY
2991	8488	A	3250	1	87	LNETVLLWHSGWMSTVVQTQLLPA ASTWVKQSSHLSLLNSWDHSR/VP PHWANFLIFCR/DRSFAMLPKLVSN PWAQAVLPPLPIVL*LNETVLLWH SGWMSTVVQTQLLPAASTWA
2992	8489	A	3251	3	270	CFNSAWTEPGARSPPRPAHSQPSV TSSPHPRTPAPRPPPLQR/SP*SP*R PRPP/PHVRHNYPSGLKSHH*SAE*P GPLGPIPTVY
2993	8490	A	3252	3	452	
2994	8491	A	3253	1	477	TLLVPQDSERTHPWCLSPADKTNV KA\AWGKVGAHAGEYGAEALERM FLSFP\TTKTYFPHFD\LSHG\SAQG* RAHGK\KVA\DALTKAVAHVDDMP KRRCPP*SDLHGAQAFGWDVPVQLQ SS*SHLPCLGEPWAAHLPRPSFNPW RLQRLPWGQISWGFC
2995	8492	A	3254	3	295	LFLFFFFFF*MESHSVTRLECSGTIW AH*NLHLPSSDSPALASRVAGTTG MCHHIQLIFFVFLVEKGFHHVG*/D MSLSLDLVIHPPWPPKVLGLQA
2996	8493	A	3255	306	519	GTRVERHSRERPSCHLLCEPSQRY SPLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA
2997	8494	A	3256	453	626	HGSCLLHHREQVPIPPGIPNLSDSIL* FPVLRIWMLCLYTSCMWFSQSFWI AVMYFV
2998	8495	A	3257	1537	1909	NVLTVEDHPIPIPSKNRPFHNLPPVN LAFFFFFLNRVSF\CHLGWSA VARS HLTCNLLSPGFKQFSCSLSSWDY QACMHHTRLVFGVFSRDGGFTMLA RLVSNS*PQVILPPLPPKVLGLQA
2999	8496	A	3258	1	342	KTESHSVAQAGVQWCDLGS LQPPP PRFKLFSCLSLSSWDYRGALPRPT DLFA/QFLVEMGFCHVAQAGLELLS SGNLFASASQTARITGVNHHTWPVL

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						*F*VKKIPPSLPGLL
3000	8497	A	3259	1	338	FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFSCSLPNS*DYRCPPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRYLLRRRQ CLRQGLCRASVF
3001	8498	B	3260	188	1504	MRTLLPPALLTCWLLAPVNSIHPEC RFHLEIQEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTV CPKVFSNFYSKAGNISKNCTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVSLMSLATGSILCLF RKLHCTRNYIHLNLFSLRAISVL VKDDVLYSSSGTLHCPDQPSWVG CKLSLVFLQYCI MANFFWLLVEGL YLHTLLVAMPLPRRCFLAYLLIGW GLPTVCIGAWTAARLYLEDTCWD TNDHVPWWVIRIPILISIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLIPLFGVHYMVFAVFPISISSK YQILFELCLGSFQGLVAVLYCFLN SEVQCELRKWRSRCPTPSASRDYR VCGSSFSRNGSEGALQFHRGSRAQS FLQTETSVI*
3002	8499	A	3261	1	1047	MVSISWPRDLPASASQSAGITGLIGA LVLSVGIAEVER/HEI*NP*KCLPGS SHHPHPGRRHVHGLLHWCAGVPP *QPPELLASRLRSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTRGIFETKFLSQIE SDRLALLQVRAILQQLGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTVGVDGTL YKLHPHFSRIMHQTVKELSPKCNVS FLLSEDGSGKGAALITAVGVRLRTE ASS
3003	8500	A	3262	178	568	IFFFFFFFKMESCSVAQAGVQWWDL SSLQPLPPGFMFPCLSLPSSWDYRR PPLL PANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE
3004	8501	B	3263	776	5218	MLGDNSSMSVTAPKTFQWDMMW RRKGLILIALCRPKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDQLDT MLWDSSTNLNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIHIFVPVPQLKSFQKTQVQLRR ILPKPTQKCTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKHLDEAQQNNVEHKVEPFS GVYKKLMGKDVNFEPFQLMPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLRYNVMLENYRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS

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						FQKVLLRKYEKCGHENLQLRGCK SVDECKVHKEGYNKLNQCLTTAQS KVFQCGKYLKVIFYKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKQTQ HKCVYITEKSCKCKECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIIICAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKECGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFNWSSSLT KHKRFHTREKPFKCKECGKGFIIWSS TLTRHKRIHTGEKPYKCEECGKAFFR QSSTLTKHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIIHTGEKS YKCEECGKAFFLWSSTLRHKRIHTG EKPYKCEECGKAFFSHSSALAKHKRI HTGEKPYKCKECGKAFFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFFNR SSNLTIHKFIHTGEKPYKCEECGKAFF NWSSSLTKHKRIHTREKPFKCKECG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFFSRSSSTLTKHKTIHTGEKPY KCKECGKAFFKHSSALAKHKIIHAGE KLYKCEECGKAFFNQSSNLTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFFSQPSHLT THKRMHTGEKPYKCEECGKAFFSQS STLTHKIIHTGEKPYKCEECGKAFFR KSSTLTEHKIIHTGEKPYKCEECGK AFSQSSTLTRHTRMHTGEKPYKCEE CGKAFFNRSSSLTTHKIIHTGEKPYK CEECGKAFFISSSTLNGHKRIHTREKPY KCEECGKAFFSQSSTLTRHKRLHTG EKPYKCGECGKAFFKESALTCHKII HTGEKPYKCEKCKAFFNQSSILTNIH KKIHTITPVIPLLWEAEAGGSRGQE METILANTVKPLLY*
3005	8502	A	3264	1	208	RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLPRLVLN SWPQVTLLPQPPKVLGLQV
3006	8503	A	3265	78	359	RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLSLCLFLMLLTKL PTIIHRTVDAHSLADDDVE
3007	8504	A	3266	48	330	VCGCVWMLRVLCYPGWSAVAQ S*LTAALISL/VNPSSSLSLPSSWDHR RAPPRPANFFNL*RQELPMLRLVL/ NVWAQVILPPWPPKMLELQV
3008	8505	A	3267	200	1033	RSLAPRWHLGHKEKNVTTSVWG WPSGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PLCNGNLPTSMHTLG\HLHGVSNP QPCTYTGESQLTEVLQNLGQR/RNI HNSRLNRLAPRM/LQSFQKEPRPSW VL/CPAWQALYWRV*RPKERRPIEL PSAQLHYGP\PMKDVPLISLANIL PQLPSSGNDVIVATHGQ*SLHHTL L*TPFHLGNVYVAMEEFKALVWY ESTLASLQPEFVPAKNRIQTIQCHLM LKKGRALLP
3009	8506	A	3268	2	2956	LADSSPSNLQIIKELLSMHHPDPA LTKEFDYLPVDSRSSSGFVGLRNG GATCYMNAVQQLYMQPLPESLL SVDDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFFTSIDQMDEYL KKMGRDQIFKNTFQGIYSDQICKD CPHYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCISLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGSRVDQ GGGGSPPKKVALTENYELVGIVIH SGQAHAGHYYSFIKDRRGCGKKG WYKFNDTVIEEFDLNDTLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQRVSDQNSPVLPPKSRVS VVRQEAEDLSLSAPSSPEISQSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMRDENLKFMKNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLQLAIQFLFQTYLRKK KLRVDTEEWIATIEALLSKSFDACQ WLVEYFISSEGRELIKIFLLECNVRE VRVAVATILEKTLDSALFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQGIRAGDLLLRHS ALRHMISFLLGASRQNNQIRRWSSA QA\REFGNLHNTVA\LLVLHSDVSS QRNVAPG\IFKQRPPIAPSSPLLPL HEEVEALLFMSEGKPYLLEVMFAL RELTGSL\ALIEM\VVYCCFCNEHF SFTMLAFHLRNQL\ETAPPHEFKGI RFPTTFMEILVIEDPIAERVVKFVFE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHH\KMSDLYWTPLSNVS NETSTGKTF*RTISDHDTPYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPDDWVSLRSDLDDVDP
3010	8507	A	3269	68	301	NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIPF*IFRRLFVL*KL/ENS ILKYIWTCGPRLVKTTFKNNSES
3011	8508	C	3270	224	518	MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX*
3012	8509	A	3271	342	724	NTYPWAVL/VFFFFFLRWSLTLVAR

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						LECRAGVQWCDLGS LQPLPPQFE* FSCLSLQLALPRPAKFFVILVEMGF TMLAKMVISIS*PCDPPALASQSARIT ILDFMLAPACPLLIIPFTWTLFFRNTI
3013	8510	A	3272	3	367	
3014	8511	A	3273	58	553	VARSAPPDGAVCAGPGSRRTMAE QSDEAV\KY\YTLERFQMHNNHKSST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\ATENFEDVGHSTDA EMSKTFIIG\ELHPVDRPKLNKASGT FKGCV*GNLFTTI*FLVPSWWTNW V\PIAISAVGRRLLGCIRL
3015	8512	A	3274	41	400	KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK/GEPLPSSSSSSSPQK RGFPSSPEK\APGVPPPTPKGSPPGG GVKKKKGRA*KKKPLGLWEKGPNP PGGPGTPTFGGPPGQYPG
3016	8513	A	3275	3	146	WGVITMMVTCSV/A/CTLFWLIAIL AQCNP LYRP*LKDETTWYLKHHWP
3017	8514	A	3276	161	472	
3018	8515	A	3277	3	273	AAAPGNGRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAGCAEYQAPGL
3019	8516	A	3278	124	672	FQRTKLLNGPGDVETGTSITVPQKK WLHVISPFI VQSLTLPFLAKWGDR LQLLQIELAAREVSDI*EETV*NETYL LLCSRKTLDTLKWHSIPSYARLF YI**FCSCLKLAFSQFLPA\DPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFSPDS GF
3020	8517	A	3279	2	991	AAAAPGNGRASAPRLLLLFLVPLL WAPAAVRAGPDEDLSHRNKEPPAP VSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQTNLGIYPMQF VAAIIQLLI\VSEIGVSRTFFIAAIMA MRYNRPGPCWAGAMLCL/AGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLK\MSPDEGQEE LEEVQ\ELKKKDEEFQRTKLLNG\ PGDVETGTSITVP\QKKWLHFISPIF GQALTLTFLAEWGDRS*LTIVLAA REDPYGVA VGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP
3021	8518	A	3280	1	278	QHDLQDQDVAFTEEE*RLAGP\AQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERNQDLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS
3022	8519	A	3281	263	588	DSALPQKEELKMNMFKAVTFKDV AVAFTEEEELG\LLGPAQRKLYRDV MVEN\FRNLLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLS\VK ALLLYDLAQT
3023	8520	A	3282	1	1285	MEDSELPSARSVLPSKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT

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						QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLENLRRKEAEQLRRQK VEEDKRRRLLEEVLKREERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEKAKKKAAAK KMEEVEARRKQEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHAWSQLP*RLA RVLRELQEREKALRLQKEQLQRELE EKKKKKEEQRLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IIHQYYQPPNLELFGTILPLDLEDIF KKSAPRYHKRTSSAVWNSPPLQGA RVPSSLAYSLKKH
3024	8521	A	3283	3	262	FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVSC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE
3025	8522	A	3284	1	269	FFFFPQIGSHPIRLECSDAITFCCSL NLPGSRDPPASAS*VAETGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM
3026	8523	A	3285	3	1191	KSCFNAFFNFEDMQEITQH\FAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTSLKSIIGIGVGAG AYILASRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSGLTTNVV\ EILAHHFGQEELQANLDLIQTYRM HIAQDINQDNLQFLNSYNGRRDLE IERPILGQNDNKSSTLKCSTLLVVG DNSPAVEAVMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVST\SASMTLARSRTHSTSSSLG SGESPFSSVTSNQSDGTQESCESPD VLDRHQTMEISLDDVLLSALLRNN GKSAQQKKISAKPKLEFLCPRPGTC DHGSRKFCYTVLVDPRERSKATAV ALGSFPAGGPAELSLRLGEPLTIVSE
3027	8524	A	3286	3	638	SSKLSGLTTNVVDIILAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQFL LKSYNRRDLEIERPILGQNDNKS TLKG\STLLVVGDNSPAVEAVVECN SRLNPINTTLKLMADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS TSGSMTSVARSR\THSTSSSLGSGES PFSSVTSNQSDGTQES\CESPDVL DRQQTMEVSC
3028	8525	A	3287	1	407	FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCSLLSWDYRAPP/* PG*LFFVFLVETGF/IHVGQPLKLL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFLTELML
3029	8526	C	3288	157	468	MHHIHNASRTFQLIFSSFRGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQPFCTSPAACGQNLPIKHGL

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						PRWSTKGETTADTDSVDLENPILYK YFQL*
3030	8527	A	3289	14	348	EFHSCRPGWSAMTQSRLTLQPPPPG FK*FSCSLSSWDYRHTPPHPASF* LLVDTG/FLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSRL
3031	8528	A	3290	1	2201	MTNLMVERDSEAGTAASRFPNGH AAKGKAQAHYKVRPAEVRCLKL GPEWVTLRYTIKHRPYKLCGKRQH VFFFTSRSDVGFMLTTLKPFGSVSV ESKMNNKAGSFFWNLRQFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIFKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDDELKKVNLNHE VSNEDVLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFPSSNYFTAM WTIAKRLSDDQKRFEKRLMFSHPAF NQLCEHMMREAKIMQYKYLFLSLH AIVKLGIPTILVQTLRLVTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVVDNIHGCPRLRIMINILQ SCKDLQYHNLDLFKGLADYVAATF DIWKFRKVLFILILFENLGRFPVGLM DLFMKRIVEDPESLNMKNILSILHTY SSLNHVYKQCNKEQFVEVMASALT GYLHTISSIENLLDAVYSFCLMNYFP LAPFNQLLQKDIISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL PQLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRM/D TNRNQVLPL/SLDVGTTSATDIQRL LTYISFAGLSELKS
3032	8529	A	3291	3	485	LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSHTNAKGGQRS*AALLGG EGTTPSKDVHLAPHNYHIDFEIQN GTPNRNPSAYPLSDVDTTSCLOIFK E*LCYVFPRSA YCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT
3033	8530	A	3292	1	530	LRKTFIPNRPLILLPPGNSLATHLFF/ ETVSRVAQAGVQWHHLGLLQSPS PGFKRFSCLSLPSNWDYRHAPRLA NFYIFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVSFLLPYTHASSLLQ LLLAPLVTNGQGQEQKPELVREV
3034	8531	A	3293	115	463	VTKQLFNILSFIFFHTSILIFFFLKME SCSVA\RLCSGT\LAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**E/QGFHHVGQAGLRTPGPQGD PARPWAPKVGLQA
3035	8532	A	3294	503	1055	DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP

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						SNKTTWLRPLTQQF*NLPQKKTLLA KK*KDFTHRVLFTA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLKWLLWRTGVS GGSETEIDSEVISGL
3036	8533	A	3295	3	304	FFLVETEFCHAAQAGVQWCDLGLSL QPPPPGLQQSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKPPF
3037	8534	A	3296	324	650	KKEHRVTCFSFWEMESRVA*AEV Q*HDLDLQPLPHGLKRVSCSLPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWSRTPDLVILPALAPQSAGITGG EPPCPATK
3038	8535	A	3297	2	564	FFFFPPQPPSPGFKQFSCLTLPSSWD YRCPPRPANF*FLIETGF/VHVGQA GLELLTSGDLPTPASQNA GITGVRP GTQPASCF*MWQGLIGQNKM TISLL LQSILL
3039	8536	A	3298	352	392	
3040	8537	A	3299	20	200	FTLIQNC FHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGNM VKPHLSLK F
3041	8538	A	3300	971	9082	
3042	8539	A	3301	1	15447	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSRKTSVSQTSLEAKKWLREGIFD GQPERINTADYVGNYLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYND SGYLSKNKLD SGIE PVLKNVEDQKNTSFSKVISNVKDA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPAPRIAS GKIRLCSHETIKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVFVA DIQSEEILQHNQNMMSGLEKVS KISPC DVSLETSDICKCSIGKLHKS VSSANT CGIFSTASGKSVQVSDASLQNAQV FSEIEDSTKQVFSKVLFSKNEHSDQL TREENTAIRTPEHLISQKGFSYNVFN SSAFSGFSTASGKQVSILESSLHKVK GVLEEFDLIRTEHSLHYSPTS RQNV KILPRVDKRNPEHCNVNEMEKTCSK EFKLSNNLNVEGGSSENNHSIKVSP YLSQFQQDKQQLVLGTVSLVENI HVLGKEQASPKNVKMEIGKTETFS DVPVKTNIEVCSTYSKDSENYFETE AVEIAKAFMEDDELTD SKLPSHATH SLFTCPENEEMVLSNSRIGKRRGEPL ILVGESIKRNLLNEFDRIENQE KSL KASKSTPDGTIKDRRLFMHHSLEP ITCVPFRTTKERQEIQNPNTAPGQE FLSKSHLYEHLTLEKSSSNLAVSGH PFYQVSATRNEKMRHLITTGRPTKV FVPPFKTKSHFHRVEQCVRNINLEE NRQKQNIDGHGSDDSKNKINDNEIH QFNKNNSNQAAA VTFTKCEEEPLD LITSLQNARDIQDMRIKKKQRQRF PQPGSLYLAKTSTLPRISLKA AVGG QVPSACSHKQLYTYGVSKHCIKINS KNAESFQFHTEDYFGKESLWTGKGI QLADGGWLIPSNDGKAGKEEFYRA LCDTPGVDPKLISRIWVYNHYRWII WKLAAMECAFPKEFANRCLSPERV LLQLKYRYDTEIDRSRRSAIKKIME RDDTAAKTLVLCVSDIISLSANIS SSNKTSSADTQKVAIIELTDGWYAV KAQLDPLLAVLKNGR LTVGQKIIL HGAELVGSPDACTPLEAPESLMLKI SANSTRPARWYTKLGFFDPRPFPPL PLSSLFSDGGNVGCVDVIIQRAYPIQ RMEKTSSGLYIFRNEREEKEAAKY VEAQQKRLEALFTKIQEEFEEHEEN TTKPYLPSRALTRQQVRA LQDGAE LYEAVKNAADPAYLEGYFSEEQLR ALNNHRQMLNDKKQAQIQLEIRKA MESA EQKEQGLSRDVTTVWKLRIV SYSKKEKDSVILSIWRPSSDLYSLT EGKRYRIYHLATSKSKSKSERANMP AGRTV*K*SKKQKSFYKRRGLGCS MSPSTTFKSGIQ*Y*LSIPEKSF*S*K CQHSYFNSYFQGCSVKPSHDF*RQR IIQNV RQAQR*QL*I*C*INQKYSHG KESRCMCFK*KL*KR*AVAT*KIHE SSITFKKGTINQNTNLRVIQKNQEE TTSISKITVNPDSSELFSDNENNFVF QVANERNNLALGNTKELHETDLTC VNEPIFKNSTMVLYGDTGDKQATQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSIKKDLVYVLAEEKNSVKQHIK MTLGQDLKSDISLNIDKIPEKNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTTSEECRDADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDCKNSASGYLTDENEVGF RGFYSAHGKTLNVSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNNDKTVSEKNNKCQ LILQNNIEMTTGTTFVEEITENYKRNT ENEDNKYTAASRNSHNLEFDGSDSS KNDTVCIHKDETDLLFTDQHNICKL LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDELEACETIEITAAPCKKE MQNSLNNDKNLVSIETVVPKLLSD NLCRQTENLKTSSIFLKVKVHENV EKETA KSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDITYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAIKLSISNSNNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEILQHNQNMGLEKVS KIS PCDVSLETSDICKCSIGKLHKS VSSA NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIRTPEHLISQKGFSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCNVSEME KTCSEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFS DVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTD SKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTKVFPFPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISETSSNKTSSADTQKVAIHELTDG WYAVKAQLDPPLLAVLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFPPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPIQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTKQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPVSPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSE DYLRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3043	8540	A	3302	1	2163	
3044	8541	A	3303	1	5771	
3045	8542	A	3304	1	3395	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLLHSSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFAEPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFFVQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKQPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSFMKIENHNDKT VSEKNKQCQLILQNNIEMTTGTVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLWDF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTFRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC*E KPRALCKLRNGKNLQ*RI*IIK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQSLTC*EHSCFGKRTGFT*KRK NGNW*N*FFF*CSCEKRYSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNGFVKF KNWKKKRRAPYLSGRTLNOQKLIK *I*QDNRSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLCITLSHN*GT SRDTESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFRSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LGGKQTKAKH*WTWL****

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTRFRNYKSSECQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSSRPSSLCVFS*TAVYVWRF*T LHKN*QKCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRIL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKKDNGKG*HSCKNTCSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVVCC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIIAFQ*WRKCWLC*CNYS KSIPYTVDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNTITITCTNKTASSCFARWC RAL*SSECSRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLFK KRKRFSYTEYLASHIRFIFSVNRRKEI QNLSSCNFKI*K*I*K*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRICRFCCCKN RTCPFRLFVRRMLQFTGNKVLDLP* *GHY*ASYVNCCQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQQN EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPI LNWFEELSSEAPPYNSEPAEESCHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTLPYQSPVKELDKFKLD LGRNVPNSRHKSLRTVKTMDQAD DVSCPLLNSCLSESPVVLQCTHVT QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFAEPLTF ANADSGLLHSSVKRSCSQNDSEPT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFR TASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF R
3046	8543	A	3305	1	5771	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPYQSPVKELDKFKL DLGRNVPN SRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPN DTDPLDSNVAHQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKDFLTSEN SLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE

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						NKNSVKQHIKMTLGQDLKSDISLNI DKIEPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWALLMPVHLLKPQN LLC*RFLLTVLGLLAGIPNLDSTLTL DLFLCPYHRFSVMEEMLVVLM*LF KEHTLYSGWRRHHLDTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNMKKTQQNHIYHHVH*QD SKFVLCKMVQSFMKQ*RMQQTQLT LRVISVKSS*EP*IITGKC*MIRNKL SSWKLGRPWNLLNKRNVYQGM QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDLPLSSICQ TNVTIYWQ*SFG*TLMTLLSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTSLCIYCMQMIPSGPPQLKT VLQGRITLLKSFLVQETSF*CLLLIVR YIIKVLVYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNSMKFLFWKVIQ*LTKNLH**IP KLFCLVQQEKNLYLSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQKNIS
3047	8544	B	3306	16	10899	MPNVLEDEVYETVVDTSEEDSFLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGLNGAQME KIPLLHSSCDQNISEKDLLDTENKR KKDFLTSENSLPRISSLPKSEKPLNE ETVVNRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIESP KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDQKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGITLRKCSRNETCSNNTVISQDLDY KEAKCNKEKLQLFITPEADSLSCLQ EGQCENDPKSKKVSDIKEEVLAAA CHPVQHSKVEYSDTDFQSQKSLLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DHENASTLILTPTSKDVLSNLVMISR GKESYKMSDKLKGNNYESDVLT NIPMEKNQDVCALNENYKNVELLP PEKYMVRVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSSEELFSDN ENNFVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLYGDTGD KQATQVSIKKDLVYVLAENKNSV KQHIKMTLGQDLKSDISLNIDKIKEK NNDYMNKWAGLLGPISNHSFGGSF RTASNKEIKLSEHNKSKMFFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPSQEQI TELSTILEDGSGQFEFTQFRKPSYILQ KSTFEVPENQMTILKTTSEECRAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTEN EVGFRGFYSAHGTKLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVSFMFIENHNDKTVSEKN NKCQLILQNNIEMTTGTFVEEITENY KRNTENEDNKYTAASRNSHNLEFD GSDSSKNDTVCIHKDETDLFTDQH NICLKLSGQFMKEGNTQIKEDLSL TFLEVAKAQEACHGNTSNKEQLTA TKTEQNIKDFETSDTFFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISCDQNISEK DLDTENKRKKDFTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAIAGTSPVASSFQGIKK SIFRIRESPKETFNASFGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEET LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSSGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFGRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDELEACETIEITAAPK CKEMQNSLNNDKNLVSIVTVPPKL LSDNLCRQTENLKTSSIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTSCSRKTSVSQTSLLLEAK KWLREGIFDGQPERINTADYVGNY LYENNSNSTIAENDKNHLSEKQDTY LSNSSMSNSYSYHSDEVYNDGGLS KNKLDGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMGLEK VSKISPCDVSLETSIDCKCSIGKLHK SVSSANTCGIFSTASGKSVQSDAS LQNAQVFSEIEDSTKQVFSKVLFK SNEHSDQLTREENTAIRTEHLISQK GFSYNVVNSSAFSGFSTASGKQVSI LESSLHKVKGVL EEFDLIRTEHSLH YSPTSQRNVSKILPRVDKRNPEHCV NSEMEKTCSEFKLSNNLVEGGSS ENNHSIKVSPYLSQFQDQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFSDPVKTNIEVCSTYSKD SENYFETEAVEIAKAFMEDDELTD KLPSHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEPSIKRNLLNEFDR IENQEKSILKASKSTPDGTIKDRRLF VHHVSLEPITCVFRTTKERQEIQNP NFTAPGQEFLSKSHLYEHLTLEKSSS NLAVSGHPFYQVSGNKNGKMRKLI TTGRPTKVFPVPFKTKSHFHRVEQC VRNINLEGNRQKQKQIDGHGSDDSK

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						NKINDNEIHQFNKNNNSNQAAAVTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRVFPQPGSLYLAKTSTLPRJ SLKAAVGGQVPSACSHKQLYTYGV SKHCIKINSKNAESFQFHTEDYFX*
3048	8545	A	3307	1	12500	MPIGSKERPTFFEIFKTRCNKADLGP ISLWNFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNRSHKSLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSNHNDESLLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFKCRCKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAIAGTSPVASSFQGIKK SIFRIRESPKETFNASFGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGSLLAC*KMTVTKV LLVI*QMKMKWGLGAFILLMAQN* MFLCLKCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YKIIILK*LLALL LKKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNYLASL*RRETLRLKKI CQI*LFWKLRLKKHVMVILQIKNS *LLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWTF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPVNM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFLMKKSKVLVKSPVLA NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKKCRILSIMIKTLFLLRLWCH LSS*VIIYVDKLKISKHQKVSF*KLK YMKM*KKKQKQVLQVLTQISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKIISPKNKILI*V TVACLTAPIILMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKSFFVHMKQLKK*KTYLQT VSVK*LRKTTTRINQKFAKRKLWQV VTRHWMIQRIFFITL*IMMNVARIHI RFLLTFRVKKFYNITKICLDWRKFL

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						KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPKYCL KVTNIQTSSQEKILLYVLQNI*YPK KAFHIMW*IHLLSLDLVQQVESKFP F*KVPYTKLREC*RNLI*SELSIVFTI HLRLDKMYQKYFLVLIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNNWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAO*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLICMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRI TELN SVLGILTWKRKTDKSKTLMMDALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPFIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFYIAHDE TSYGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSRN ETCNNNTVISQDL DYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQSLLYDHENASTLILT PTSKDVLSNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYMRVAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAENKNSVKQHIKMTLG QDLKSDISLNIDKIKEKNNDYMDKW AGLLGPISNHSFGGSFRTASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPQSINTVS AHLQSSVVVSDCKNSHITPQMLFSK QDFNSNHNLTPSQAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRDADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KNDCNKSASGYLTDENEVGFRGFY SAHGTKLVNSTEALQKAVKLFS DIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNNKCQLILQ NNIEMTTGTFVEEITENYKRNTENE DNKYTAASRN SHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNICLKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF

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						NKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPCKCE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNIHSASN LSESSRRPSSLCVFS*TAVYVWRF* TLHKN*QKCRVFSVS/TLKIILVRK VYGLEKEYSWLMVDGSPMMER LEKKNFIGLCVTLQVWIQSLFLEFGF IITIDGSYGNWQLWNVPFLRNLLID A*AQKGCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKL VVQIPKKWPLLN LQMGGMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWALLMPVHLL KPQNLLC*RFLTTLVGLLAGIPNLDS FLTDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHHLDYTYFA MKERKKRKQQNMWRPNKRD*KPY SLKFRRLKNMKTQQNHYYHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTLRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNLIKELTYS*QRQKKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQTF SHLVLRWT**DLSFLL*KKQDLPLSS ICQTNVTIYWQ*SFG*TLMRTL LSLI C*LLQATSSGDQNPNAFLLYLLEIF LCFLLVQKRATFKRHSTK*KILLRIL TYFAMKQKTSLCIYCMQMIPSGPPQ LKTVLQGR TLLKSFLVQETSF*CLLL IVRYIHKVLYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFSHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQKEKNLYLSVNPLGL LPPVQKIISD*NDVVLHL*SKNRRVP RPVRKNVRKISRTQLQLKNIS
3049	8546	A	3308	1	9344	
3050	8547	A	3309	1	18345	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEE LSSEAPPYNSEPAEES E H

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						KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRCTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGGKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEETPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGKTLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFFE EITDACRKDSVKMIQKAKKFQI*KK RSWLQHVTVQYNIQKWNTVILTFNP RKVFYIMKMPALLF*LLLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIMYVL*MKIHK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLK NFSQTMRIILSSK*LMKGIILL*EILR

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						<p>NFMKQT*LV*TNPFSRTLPLWFYMET QVINKQPKCQLKKIWFMLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TINGQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IIKRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTH*HLAKRQKLQNFLLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNKLVQLKNGSLLA C*KMTVTKVLLVI*QMCKMKWGLG AFILLMAQN*MFLKLCKKL*NCLV ILRLVVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKIINAN*YYK IILK*LLALLKKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFV IKMKRTCYLLISTTYVLNLYASL*R RETLRLKKICQI*LFWKLRKLKHHV MVILQIKNS*LLKRSKI*KILRLLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWT*V MRKQT*LNTKY*KKVSQLVLEIN** PSRDNPVNMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFLMKKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIYVVDKLKISKHQ KVSF*KLKYMKM*KKKQKVLQL VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQKNGLEKEYLMVNQKE *ILQIM*EIICMKIITVL*LKMTKIIS PKNKILI*VTVACLTAIPTILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTHKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLIVI ILR*GHLHLG*PVVKSFFVHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIRFLLTFRVKKFYNITKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKILLYVL QNI*YPKKAFHIMW*IHLLSLDLKL QEKY*K*R*QIYCCQ*KFS*LRI*WQ *FK*K*YCLYS*R*NGLAIY*SAQHM S*IIWPVYEGGKHSD*RRFVRNF SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETTRIA*LFLKF*ITF* HKKEQNGHSLK*GNRHS*TQNLKE SVPVGTGNQLVTFQGQPERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIEVVPKLLSD NLCRQTENLKTSKSIFLKVKVHENV</p>

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						EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMGLEKVS KIS PCDVSLSDICKCSIGKLHKSVS SA NTCGIFSTASGKSVQVSDASLQNA QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIRTPEHLISQGF SYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTS RQNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSEN NH IKVSPYLSQFQQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTD SKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPsikrNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRITTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFPVPPFKTKSHFHRVEQCVRNI NLEENRQKQNI DGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAAMECAFPKEFANRCL SPERVLLQLKYRSTASGKQVSILESS LHKVKGVL EEFDLIRTEHSLHYSPT SRQNVSKILPRVDKRNPEHCVNSEM EKTCSEFKLSNNLNVEGGSEN NH SIKVSPYLSQFQQDKQQLVLGTVS LVENIHVLGKEQASPKNVKMEIGKT ETFSDVPVKTNIEVCSTYSKDSENY FETEAVEIAKAFMEDDELTD SKLPS HATHSLFTCPENEEMVLSNSRIGKR RGEPLILVGEPsikrNLLNEFDRIEN QEKSLKASKSTPDGTIKDRRLFMHH VSLEPITCVPFRITTKERQEIQNPNTA APQEFLSKSHLYEHLTLEKSSSNL AVSGHPFYQVSATRNEKMRHLITT GRPTKVFPVPPFKTKSHFHRVEQCVR NINLEENRQKQNI DGHGSDDSKNKI NDNEIHQFNKNNSNQAAAVTFTKC EEPLDLITSLQNARDIQDMRIKKK

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						QRQRVFPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDBGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTAAKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAIHETD GWYAVKAQLDPPLLA VLKNGRLT VGQKIIHGAELVGSPDACTPLEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQKRLEALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAQIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVLSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTKYQQLPVSEIL FQIYQPREPLHFSKFLDPDFQPCSE VDLIGFVVSVVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFSVFS ASPKEGHFQETFNKMKNTVENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRRRA LDFLSRLPLPPVSPICTFVSPAQK AFQPPRSCGTYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRTAP TSSEDYLRLLKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI
3051	8548	A	3310	1	7988	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESLH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKNRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESFKETFNASFSGHMTDPNF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAPEAPLTF ANADSGLLHSSVKRSCSQNDSEEP LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPSKDVL SNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIEPKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKND CNKSASG YLTDENEVGFRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSV VSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLDFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNL VSI ETVVPPKLLSDNLCRQTENLKT SKSI FLKVKVHENV EKETAKSPATCYTN QSPYSVIENSALAFYTSCS*KSQNIK KYLFES*ST*KCRKRNSKSKCNLLH KSVPLFSH*KFSLSFLHKL*RKTSVS QTSLEAKKWLRREGIFDGQPERINT ADYVGNYLYENNSNSTIAENDKNH LSEKQDTYLSNSSMSNSYSYHSDEV YND SGYLSKNKLD SGIEPV LKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKNKNAAIKLSI SNSNNFEVGPPAFRIASGKIVCVSHE TIKKVKDIFTDSFSKVIKENNENKSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEILQHN

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						QNMSSGLEKVSISKISPCDVSLETSDIC KCSIGKLHKS SVSSANTCGIFSTASGK SVQVSDASLQNAQVFSEIEDSTKQ VFSKVLFKSNEHSDQLTREENTAIR TPEHLISQKGFSYNVNVSSAFSGFST ASGKQVSILESSLHKVKGVLEEFDLI RTEHSLHYSPTSQRQNVSKILPRVDK RNPEHCVNSEMEKTCSEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLGTVKVSLENHVLGKEQA SPKNVKMEIGKTETFSQVVPVKTNIE VCSTYSKDSSENYFETEAVEIAKAFM EDELTDKSLPSHATHSLFTCPENE EMVLSNSRIGKRRGEPLILVGEPSIK RNLLNEFDRIENQEKS LKASKSTPD GTIKDRRLFVHHVSLEPITCVPRFTT KERQEIQNPNFTAPGQEFLSKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLITGRPTKVFPVPFKTK SHFHRVEQCVRNINLEGNRQKQKID GHGSDDSKNKINDNEIHQFNKNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKKQQRQVFPQPSLYL AKTSTLPRISLKA AVGGQVPSACSH KQLYTYGVSKHC IKINSKNAESFQF HTEDYFGKESLWTGKGIQLADGGW LIPSNDGKAGKEEFYRALCDVKAT
3052	8549	A	3311	1	14305	MPIGSKERPTFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSVPASSFQGIKK SIFRIRES PKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGGKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTFQSQK SLLYDHENASTLILTPTSKDVLNSLV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENNFFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHN TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFGRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLDFEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNL VSI ETVVPKLLSDNLCRQTENLKTSKSI FLKVKVHENVKETA KSPATCYTN QSPYSVIENSALAFYTSCSRKTSVSQ TSLLEAKKWLEGI FDGQPERINTA DYVGNLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLD SGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFDTSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKV FADIQSEILQHNQ NMSGLEKVS KISPCDV SLETS DICKC SIGKLHKS VSSANTCGIFSTASGKSV QVSDASLQNA RQVFSEIEDSTKQVF SKVLFKSNEHSDQLTRENTAIRTP HLISQKGF SYNVVNSSAFSGFSTAS GKQVSILESSLHKVKG VLEEFDLIRT EHS LHYSPTS RQNVSKILPRVDKRN PEHCVNSEMEK TCSKEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQDK QQLVLGTKVSLVENI HVLGKEQASP KNVKMEIGKTET FSDVPVKTNIEVC STYSKDSENYFETEAVEIAKAFMED

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						DELTDSKLP SHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEP SIKRN LLNEFDRIENQE KSLKASKSTPDGT IKDRRLFMHHVSLEPITCVFRTTKE RQEIQNP NFTA PGQEFLSKSHLYEH LTLEKSSSNLAVSGHPFYQVSATRN EKMRHLITTGRPTKVFVPPFKTKSH FHRVEQCVRNINLEENRQKQNDGH GSDDSKNKINDNEIHQFNKNNSNQ AA AVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQRQ RVFPQPGSLYLAK TSTLPRISLKA AVGGQVPSACSHKQ LYTYGVSKHKIKINSKNAESFQFH/T *RLF*WKFM DWKRNTVG*WWM AHTLQ*WKGWKRRIL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETLRLKKICQI*LFW KLRKLKKHVMVILQIKNS*LLKRS KI*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLIRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPVMKRKNLL CWVFIQLAGKKLKLQRNLWTK*KT FLMKKS KVLVKS PVLAINGQRP*ST ERPVKTLN*HVRPLRSQLPQS VKKC RILSIMIKTLFLLRLWCHLSS*VIHYV DKLKISKHQKVSF*KLKYM KM*KK KQKQVLQLV TQISPLIQSLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EHC MKIIQT VL*LKMTKIISPKNKILI*VTVACLT APTILMRYIMIQDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFHMKQLKK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQV VTRHW MIQRIFFITL*IMMNVARIHIFLLTF RVKKFY NITKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEK KILLYVLQNI*YPKAFHIM W*IHLLSLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVLIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSENNHSI KVSPYLSQFQ QDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDEL TDSKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ E KSLKASKSTPDGTIKDRRLFMHHV SLEPITCVFRTTKERQEIQNP NFTA

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						PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQKNIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDBGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAHIELTDG WYAVKAQLDPPLAVLKNGRRLTV GQKIILHGAELVGSPDAPLEAPES LMLKISANSTRPARWYTKLGFFDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEK EAAKYVEAQQRLEALFTKIQEAFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKRRALDF LSRLPLPPVSPICTFVSPAAQKAFQ PPRSCGKTYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3053	8550	A	3312	11089	17637	NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHILKESVPVGT GNQLVTFQGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVKNLDFE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVSIE TVVPPKLLSDNLCRQ TENLKTSKSIFLKVKVHENVEKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLEAKKWREGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDGYLSKNKLDGIE PVLKNVEDQKNTSFSKVISNVKDA

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						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDEILFQIY QPREPLHFSKFLDPDFQPSCEVDLI GFVVSVVKKTVRNEEASETVFPHD TTANVKSYSNHDESLKKNDRFIAS VTDSNTNQREAASHGFGKTSNGNSF KVNCKDHIGKSMNPVLEDEVYET VVDTSSEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVPPLACEWSQ LTLGSLNGAQMEKIPLHHISSCDQNI SEKDLLDTENKRKKDFLTSENSLPRI \SSLPNPEEPLNEETVVNKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEAESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEA PLTFANADSGLLHSSVKRSCSQNDS EEP TSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSLSCLQEGQCENDPKSKKVSD IKEEVLAAACHPVQHSKVEYSDTDF QSQKSLLYDHENASTLILTPTSKDV LSNLVMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYM RVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENN FVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVLYGDTGDKQATQVSIKKDLVY VLAEENKNSVKQHIKMTLGQDLKS DISLNIDKIKEKNNDYMNKWAGLL GPISNHSFGGSFRTASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVS DCKNSHITPQMLFSKQDFNS NHNLTPSQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKTTSEECRDADLHVIMNAPSIGQV DSSKQFEGTVEIKRKFAGLLKNDCN KSASGYLTDENEVGFRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVS MFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEACHGN TSNKEQLTATKTEQNIKDFETSDTFF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLSNSELHSDIRKNKMDILS YEETDIVKHKILKESVPVGTGNQLV TFQGGPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNLDFDEKEQGT SEITSFSHQWAKTLKYREACKDLEL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ACETIEITAAPKCKEMQNSLNNDKN LVSIETVVPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLEAKKWLREGIFDGQPE RINTADYVGNYLYENNSNSTIAEND KNHLSEKQDTYLSNSSMSNSYSYHS DEVYNDSGYLSKNKLDGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAI KLSISNSNNFEVGPPAFRIASGKIVC VSHETIKKVKDIFTDSFSKVIKENNE NKSKICQTKIMAGCYEALDDSEIL HNSLDNDECSTHSHKVFADIQSEEL QHNQNMMSGLEKVKISKISPCDVSLETS DICKCSIGKLHKS SVSSANTCGIFSTA SGKSVQVSDASLQNAQVFSEIEDS TKQVFSKVLFSNEHSDQLTREENT AIRTPEHLISQKGFSYNVVNSSAFSG FSTASGKQVSILESSLHKVKGVLEEF DLIRTEHSLHYSPTSQRQNVSKILPRV DKRNPEHCVNSEMEKTCSEKFKLS NNLNVEGGSSENNHSIKVSPYLSQF QQDKQQLVLGTVSLVENIHVLGK EQASPKNVKMEIGKTETFSQVVPVKT NIEVCSTYSKDSENYFETEAVEIAK AFMEDDELTDKSLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLLNEFDRIENQEKSLKASKS TPDGTIKDRRLFMHHVSLEPITCVPF RTTKERQEIQNPNTAPGQEFLSKS HLYEHLTLEKSSSNLAVSGHPFYQV SATRNEKMRHLITTGRPTKVFPVPPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAAVTFKCEEPLDLITSL QNARDIQDMRIKKKQQRQVFPQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHCIKINSKNAE SFQFHTEDYFGKESLWTGKGIQLAD GGWLIPSNDGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSANISSETSSNKTS SADTQKVAIIELTGQWYAVKAQLD PLAS
3054	8551	A	3313	1	207	CNLCLPDSSDSPASASQVAGKTGLC HHTGVVVFVFLVEMGFHHAGQAGLE LLT*VICVPQPPKALGLQV
3055	8552	A	3314	279	625	SLYVCMHVCMYVFILRRSFALVAQ ARVQWCGLGSLQPPPPGFKRFISCL SLPTS*DYRRAPPHPTNFFVFSAEME FHRVSQDGLYLLTSGDLHPRLASQS AGITGVSHRTRPFL
3056	8553	A	3315	1	418	GSIPPPGVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPO PPGPAPPGARTRTRPESE*SQPGRSP

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						VSRQSLTGADALEGPCLGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG
3057	8554	A	3316	1	354	GFIPPPGVVYCVPYPLKHAPALP* TRQRGSPQSPGALRAK*HVLLETPQ PPGPAPPGARTRTRPESGAWR WVR AGSSPPPPSPHPTPPCFFQVHQGLRS GSANEASLEDPQSRDRA
3058	8555	C	3317	299	365	MSCPECNLTGISSKTNNKLNQ*
3059	8556	A	3318	33	302	PSSWDYRHAPPRLTNF*FLVEMGF HYVG/QAGLELLSSGDPPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHIQNHGPRVQGAKP
3060	8557	A	3319	3	409	SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
3061	8558	A	3320	1	255	
3062	8559	A	3321	1	395	FGYNIPLNHLDPDRVAMYVHAYTLY SAVRPFGCSFMLGYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIVKEVAKIIV VHDEVKDKAFELELSWVGE\ESLKE EDESDDDNM
3063	8560	A	3322	515	560	
3064	8561	A	3323	3	661	KDGVVLGVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\VAGLLADARSLA DIAREEASNFRSNFGYTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GYSVNDGAQLYMIDP\SGVSYGY WG\CAMRQAR\QLAKTELERLQLK KLPSGDIVKEVAKIIVHDEVKDK AFELEL\SW\VGDLTK*RHEILPK\A LRDEAEKYAKESLKEEDESDDDNV
3065	8562	A	3324	3	634	
3066	8563	A	3325	2	487	HIFGKAKEYANSQVVTKDQYAVIC LGGDAVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKCIVKPVHYD RVKKITQRKKEIPVVFLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RLLRFSITDRTQMGR
3067	8564	C	3326	373	727	MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCAPAQPAYLTHDVNS QVSLIKTSLQASSGSGXXXXXXXXXX XXXXXXXXXXGAQAFFFLGGGFF*
3068	8565	A	3327	2	536	VHLVPRQNACAIRLTEPCPPRLK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GWFQTPDLRRSTRLSI PKCWDRREPPHPVKIFLKLSSFSY WVFPVCALNLSLSLFVYTFLSNSLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLSSHTKPCQFS HESA

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3069	8566	A	3328	3	334	FLRQGL/NSVTQAGVQWGDLSLQ PPPPKLKGSSHPSPSSCRHYRHTPP/ RSG*FFVFL*RWGFAMLPRLV*TS G\nPSDMPALASQAGTTSMSTHTWR PYLNFGKFPRKKN
3070	8567	A	3329	1	148	PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWLNLNTHWISEN SGHCMVLMMLTVRSCS
3071	8568	A	3330	3	267	FFFFLDRFSLCGPGWSAV/VQS*LT VNS/TFLGSPNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLP RPVLKSW PQAIFLRHAPKVLGVEV
3072	8569	A	3331	3	269	FETESHSTVRLCSG/TILAHCNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVGQAGLELLT*VIC LPRPPIVLGLQA
3073	8570	A	3332	1	299	FSLIKISMMLLMKMEK*NLQFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLNS NINRHICSQILTKVPGANTKDHP
3074	8571	A	3333	3	261	RQDLSLCHPGWSAVVQS*LIATLS* \VKQSTYLRHPTSWG*RCVPPCPAN FCFFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV
3075	8572	A	3334	3	290	VDFFFFFFSRRSNVLSHRLECSGTISS HGNLCLLGSSDSPASVASQVARITGV HHHTQLIFIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA
3076	8573	A	3335	3	358	
3077	8574	A	3336	76	386	VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPAAAAHPCAPCA PRH*GSR*LESPAPQGPQSRAARMP AWPLPPAPPTDPTAPPAPRSHWPAA PPT
3078	8575	A	3337	66	381	VLPPPSSPALHSPAPPSTCPYLP GAL PPLE/GPPSRPPRTFIGNPGGQGPGE VSPIVLRSPSQPH*PGNQGPCPSSQP PGSPRSEHGC*HRCWALYGQKEK APS
3079	8576	A	3338	1	303	KDRFSFCGPG*SAVTQLNLTADP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSWPQ VILSPLSRARATAPSFPLFSSKDEPI
3080	8577	A	3339	2	212	RFSCLSLPSSWDMHH\SPG*FFIFLVE TGFAHVGQAGLELPASNDPPASTS QSVVITAMSHRRALVPIF
3081	8578	A	3340	2	273	RRSSTQPPRLQCSGTIPAHCNLHPPS PSDYPAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPVKVGPQA
3082	8579	A	3341	135	494	IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIACDCAFSMYDGLFCSNSNS RADWSHCTVSGTYQHTENSIMS

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3083	8580	C	3342	71	217	MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA*
3084	8581	A	3343	1	106	
3085	8582	A	3344	2	1926	MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSSTCRRLRELQSSGKVW KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQQPDDYESYLE GAVYIDQYCNPLSDISLKDIAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELQSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLR RTGIPISMSLLYLTARQLGVPLEPV NFPSSHLLRWCGAEGATLADIFDYI YIDAFGKGKQLTVKECEYLIGQHVT AALYGVVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLAMY PDQVQLLLLQARVYFHLGNLPEKS FCLVLKVL DILQHIQTLDPGQHGA VG\YL\VQHTLEHIL/ERKKEEVGVE VKLARSDEK\HRD\VCY\SFGFIMKA* RGMGY*LC*FYGW\DPWHGSGHE LDSRNMNV\HSLPHGHHQPFYNVL VEDGSCRYAAQEN\LEYNAEPQEI SH\PDVGRVYSQRFT\RTHYIPNAEL VEIRYPEDLEFV\YETVQNIYKCKRK ENIE
3086	8583	A	3345	59	339	
3087	8584	A	3346	1	342	FCSCQPQAGVQRRDLSSLQPLPPG K*FSCLSLPSSWD\YRRPPP/RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLLLN CLLPFLGIPLHSPL
3088	8585	A	3347	1	294	ETESHVTRLECSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGQTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFCLSLPNSWDHRCTPPHLA NFCIFCRDGFPPCWPDSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP
3089	8586	A	3348	2	268	EAESHVA\RLCSDAISAHCNLRLP GLSNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA
3090	8587	A	3349	3	444	FFFEIWSGSVA\RLCCGGTIFAHCNL RLLGSSHPPTSAS*VAGTKGTCHHV QLIAFFVDTGFHHVARLVLS* TQ AICPPRPPKVLGSYASITAPGPTFFL TIILGVQVDKRFYGNLTKDQIKLG NYVWEGLELLSPQKFMKLP
3091	8588	A	3350	1	318	FFFFFLRQSFALAQAGM/QWHDLGS LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL

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3092	8589	A	3351	16	848	VGSGLVSAQQTGCGPGNPSPPGSVS GAMELRVEPAARGQGS LGDPPA\VL LPGALELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPPVSPAPTGWDL VSQ LQPVSSPRGRCPRSGPDLLPLH GQPFHSSSFSSSMQASGEPVQPCPS RSSGS/VKGG LQTVESGPGALKC EALAWLRG*GLLGHS GFAGSVPEV TPGSPHVLNP\GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSPTS*GIP*HRKPWVFSVMHKVG WKV
3093	8590	A	3352	1	293	VLRQGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL/NCIAQAGLE/PP GFK*/CPKHWDRHEPGMPGWVFLI S
3094	8591	C	3353	127	345	MDFELELFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFLLKKL CF*
3095	8592	A	3354	2	215	AHCNLC L PGSSDSPASASRVTGITG VHHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLRT
3096	8593	A	3355	164	311	QRSQGIWVWRFIRRF*II
3097	8594	A	3356	1	381	YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAA\FIIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIK NNE*LIHKTTWKNLKEARA SGV
3098	8595	A	3357	2	764	RTLLHLFAGGCGGTGVAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSFQCTARLVFREESYL PL
3099	8596	A	3358	155	875	DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRGS KQMNTLQCARYVY/HDRKAFGGFY RGLTASYAGISETIICFAIYESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGL\ASCMAYSHTEVH* GRRLAREKGHPSTKSFPCERRALGVP GEEGYPCLFIEGLFAPSFIQIPNTA\ IVLGYLWRLIVYLLGRP
3100	8597	A	3359	1	281	FFFAPETESYSVA\RLCSGTILVHCT LCLPGSSDSPASASQVAGTTGACHH TWLILVILVEIGFHHVQGAGLG/IS*L QVIRPPWAPKVLGIIG
3101	8598	A	3360	135	218	TLQFTSLISYSFCQSWGSKVPLSLPP

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						P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F
3102	8599	A	3361	198	390	
3103	8600	C	3362	5	316	MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXRLI YYRLLFSPCHSF*
3104	8601	C	3363	186	323	MPWLEHTAHFPDKAWITRMALLRN GIVPYDSLWPWITLGRWPNGGT*
3105	8602	A	3364	2	3096	TPRLQSNTRALYQYCPPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDAWKKEVEKKPPM MSIDDAYEVLNLPQGQPHDESKIR KAYFRLAQYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIIL ILKTQSILFNRHKEDLPYKYAGYP MLIRTITMETSDDLFSKESPLLPAA TELAFTVNCNALNAEELRRENGLE VLQEAFSRCVAVLTRSSKPSDMSVQ VCGYISKCYSAQAQFECEKITEM PSIIKDLRCRVLYFGKSIPRVAALGVE CVSSFAVDFWLQTHLFQAGILWYL LGFLFNYYDYLEESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEQHGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQQV/AL* EUVNIVTSNQDCVNIAESMVLSSL LALLHSLPSSRSAFWETLYALDIR VQKLIKEAMAKGALNHLLDMFCNS THPQVRAQTAEFAKMTADKLIGP KVRITLMKFLPSVFMAMDRDNE AAVHIFEGTHENPELIWNDNSRDK VSTTVREMMLEHFKNQDNPEAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLRKPREFLIALLEKL TELLEKNNPHGETLETLTMATVCLF SAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLEIGIGLENLADSPAAT*GS ELVKALQGQ*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHDLFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPVDHEAGDLGYQT
3106	8603	A	3365	1	358	NRLNATPIKIPTAFFAEMDKLNPFL KLNS*NLYRNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRHDQ*NR NQSPEINP*YIGKLFSTVL

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3107	8604	A	3366	2	40	LPRLKQFS\CLSL\PSSWDYKR\PPC PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE* SAS
3108	8605	A	3367	1	223	IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCMKLEN IMLSERSQLQRATYCNDAIYIKNPE
3109	8606	A	3368	307	332	TTYHFFF*TESHSAQAQAHWRDLS SLRPPPPGFKPFSCSSWDYRRTPPH PANFLAFLADTGLHHAGQAGLKLL TSNDPPTPASQSAGTTGVSHRAQPF FSELPTIFFSL
3110	8607	A	3369	3	411	QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPQ* PFQGRFDAFPGYKQQTRPGHT/GQK GLRGPRTQTLSTSQPTACSENSQG SQPSPKRTLS
3111	8608	A	3370	3	166	EESCSVVQGGVQWCDLS*LQTLPP GSSNFCASASRVAGITGAHHHAQL KKKMLF
3112	8609	A	3371	4	312	FLR*SFTLIVQAGVQWRYLGSLQPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPSHRTWLRS FLI
3113	8610	A	3372	3	282	FFFETGSNSVAQAGVQWCNHSSLR PRPSGSSDPPNSSSQVAWTTGVHH TQLLFKFCKDEVSLCFPDWSQTV* RVEHIRDEYETTQHCLYPSN
3114	8611	A	3373	1	164	ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCPA TLLNT
3115	8612	A	3374	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3116	8613	A	3375	363	1246	DTEQIYCIQEPEYGGKKYCTKQSRS YVSWTTHFSSSFIDQSLLSESMA*KS TAPHSSDF*DFLT*KT*NLFFLRSL ALSPQAGVQWRDLGSLQAPPPGFTP FSCVPASPSSWDYRHLPPCPANFFVF FLVETVSIFVFTVLAGMVIS*PQ/CD PPTLASQSAGITRLSHRAR\LCFVF* KKRNAREGGRRLLTIKADFLIFFSFF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRPPPPQLA NFCIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA
3117	8614	A	3376	3	324	DRISLCCPGWSAIV\QSQLTAA\SLPG LKQSFYISLPSS*GHR LAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN
3118	8615	A	3377	3	673	RWSHSVTAQAGVQWRDLSSRQPPPP GSRDSPASAS*VAGTTGTTHHAQFF FFFFFLRRS/LSSV/SQDGVQWHDH SLQPVPPGFKQFSCSLPSSWDYRC AAPRPANFFVF**RRVFSTLARLVSI

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						S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCVHGQAGAVLILCLF LHSKINMFSPLHCTPASTVYSHLPQ RPTKRRLYIRWRWERTWPANAE
3119	8616	A	3378	2	323	RRSFTLVAQAGVRWHILGSLQPLPP GFKRFSCSLSPSGWDYRLMPPCPAN F*FLVEMRFHHVQAGPERLTSGD LPA*ASQSAGITGVATPSQYKLCSL IIMKLN
3120	8617	A	3379	1	311	DFFF*ETASHSVTQAGVQWCDPSSL QPPPPVFKQSSCSLSPSSWDYRHVP PCSVDT/CISILLIPFPLRSGE*SPLLLS WSSCDLGQGTAPLGFWFPMPGKARP V
3121	8618	A	3380	3	404	PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHSVAQAEVQWHDLGSL QPLTPRFKRFSCSLSPSRWDYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR
3122	8619	A	3381	739	1003	NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSLSLSS WDCRHMPNLA/NF/CVLRDRKISPF CPGWSQTPGLKQCIFF
3123	8620	A	3383	1	299	ETESGSLPRLECSGTISAHCNLRLL GSSNSPVSAS*VAGTGACSHAQLIF VFSVESGFRHVQAGLNF*PQVIHP PRPRKVLGLLPVSHHTRPISFFL
3124	8621	A	3384	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSLRTFSSHSNLMELVQD LTASAPMYSSTRDPP/CLGLPKCW DYKREPPRAH
3125	8622	A	3385	2	318	FLSSHLFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLSPSSWDYR RPPRPANFFVFLVKTGFTVLARM VSL*PHDPPASASQSAGITGVSHW CPANN
3126	8623	A	3386	1	325	ASTAQAGVQWPIAAQLQTPPPGFTP FSCLSLPSSWDYRRPPPSANFLYF* *RRGFTMLARMVIS*PCDPPASSSQ SAGITGLSHRAPVIRILRRAGRNT IGGLD
3127	8624	A	3387	3	530	RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLSPSSWDYRRPPRPA /NFFVFLVET/GFTRGSIS*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLTRLCFRKLLTGEEAMP/PF* RQS*CLTSVTLSSAWRSICYDRLVDI QKILFMKTKLPLLFFSQNELYFIIL
3128	8625	A	3388	3732	4979	NFVFLYLRELSSQAKSLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFKHVLY WLFGLVFLNLLLILPVLYNEHRKIL

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						E*GRKVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHGQACSIKMIFLKD VNCA*LIGYI LFCFFFFFFFFLRCGVS\SVAQAGVQ WRNLGSLAQAPPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFFLDF**RPL VFL/SFTVLARMGLIS*PRDLPTSAS QSAGITGVSHHVQLPYFVLNKFTV LGSNSGF
3129	8626	A	3389	1	585	AAAAFLRQGLALV/THAGVQGQDYS SLQPLPGLKAILLPQPECWDYRC MSPCLA/N/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECYDLHILLICSHFYRL
3130	8627	A	3390	3	459	QPGVQWHDLSMQPPPRFKCFSC SLL/SS*DYRC PAPMPQPNFCIFI*RY GFTMLASLVLDL*L*VIRPPWVSQS AGITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQL*GS/WDP ET*HNGHFHFWIKQSEPPIFKGRR*N P
3131	8628	A	3391	1	258	FFFKTDSCSVARLEYS GAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLTLWIH CPPKMLGLQA
3132	8629	A	3392	3	316	VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPALASQS AGITGVHPHPAPNSSCLHTDKRVHT WHKPS
3133	8630	B	3393	49	279	SSSDSDDEEKKHEKLKKALNAEEA RLLHVKETMQIDERKRPYNSMYET REPTTEEMEAYRMKRQRPDDPMAS FLGQ*
3134	8631	A	3394	2	357	
3135	8632	A	3395	1	1765	MSATVVDAVNAAPLSGSKEMSLEE PKKMTREDWRKKKELEEQRKLG NAPA EVDEEGKDNPHIPQYISSVPW YIDPSKRPTLKHQRQPQEKQKQFSSS GEWYKRGVKENSIITKYRKACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGKRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANS PKH QWGEEEPNSQTEKDHNSEDEDEDK YADDIDMPGQNFDSKRRTVRNLRI REDIAKYLRNLDPN SAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGD TISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFVKVKE DFKEQQKESILEKYGGQEHL DAPPA ELLLAQTEDYVEYSRHGTVIKQGER AVACSKYEEDVKIHNHTHIWGSYW KEGRRGMKCCHSFSKYSYCTGEAG

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						KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEEKKRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E A\RLHVKET\MQ\DERKRPYNSMY *TSRP\IEEEMEA\YRMKRQRPDDPM ASFLGQ
3136	8633	C	3396	106	426	MFLKEPVXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXRLXXXXG*
3137	8634	A	3397	25	435	TKYWLLFFLILPFFFWRRSRSVT QAGGQWHDLSLQPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVNSRSQ/CDPLASAS QSAGISGKSQHTRPVLLKTYTNS H/SF*VKGLGWEFIL
3138	8635	A	3398	3	320	KTESHVSTQAGAQWQDLSSVQSPP PGFKRFSCSLPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAGITGVSHCARPIVIFL YLITSR
3139	8636	B	3399	70	199	XMQVTGFRGQNHNVQGSTPTDAS PRRRDVCTAQTQDSKLVNS*
3140	8637	A	3400	198	397	TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PIACPAGTHIPCGPYPC CHVGGGWPAQPLAALG
3141	8638	C	3401	164	313	MTLHFQELKSLKFYLNXXXXXXXXX XGGRFKGSLGGPKFTRACNVKAFL L*
3142	8639	C	3402	165	361	MVKFCANNQGKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGHLPGRV*
3143	8640	C	3403	146	389	MTPISLKGRCRQLGDGKRCSLEDLA LIEGCPHAGRPPPRKSTLEPAFGSPR CQDPVSAMCMTRSPANLDSAERQ APGLGR*
3144	8641	C	3404	157	404	MLSLTSSPLNQKGVVSFVHAILKY QGCKPHFIKKLSRXXXXXXXXXXXXX XXKXXXXXXXXXXXXXXXXXXXXXP PAPSFLWEGE*
3145	8642	C	3405	73	252	MHTPLLAWPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP*
3146	8643	A	3406	2	617	IYIFLKALNFCREVVPISPPPKVRVLF KDSQVTSFPVPAL*KGGQGLGYKT APYKEKTNSLQARVNLGPSRGPLK RPPSSSSPNPNALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAAWDP/ PAGCAQPPTVSPDTTKQVSRTKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPPVPDGNPV LN
3147	8644	C	3407	129	281	MSSHARVNLGPSKDPLKRPPXXXXX XTQRQLFKTFINRCLQVDFFEKIKL *
3148	8645	A	3408	1	303	QAGVHWRNLG\SLQPPPPPTLRRFS

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						CLSLPSSWDYRHPPSHPANFFFFLL LVEARFHHVGGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG
3149	8646	A	3409	3	1039	QQPFVNPALPPGYSYTGLPYYTGMP SAFQYGPTMFVPPASAK*HGVNLT PTPPFQQ\PVGYGQHGYSTGYDDL QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVSVSSSTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCPTIPTH LASPPAAPTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCLRQLSIL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFNVIEWW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H
3150	8647	A	3410	2	344	LRQSVSLLPRTQAGVQWPNLGSLO PPPPRFQRFSCLSLLSSWDYRHAPPC PTKFVFLVETAGFTMLARLVIS*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSIL*SLQ\WPHV*SL AYSIL
3151	8648	A	3411	52	174	
3152	8649	A	3412	2	692	RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSPFRRSPRGP ASPQR*PPRPDPWPPRQASPRCPT D*SRTPAGRITDPQEEAVGGQGPSR GG*APSNSEPPPLYGSGPLDSAFSLG TAFRKTLRIDLTSQSRPPHRSLSLYS GKGLAPGELADALNFLIYPTDFGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSPAKNFFSRY RHHS
3153	8650	A	3413	3	367	MLNYPLDFHPSFFVGGFFFMESRS\ VARLEVPVGVISSHCHLCLPGSSDS PASASQVAGTTGVCH*AQLIFVFLV ETGFHHFDQDGLDLTS*SVHLCPS KCWDYVIHPPQPPKVLGLQA
3154	8651	A	3414	1	595	MGIHHVQGASLELLTSGDLPASASQ GRGVRLYYIEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTPSYFWKPSLQTSPCSGSR SLWASLPSLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL
3155	8652	A	3415	259	941	PVSWSLNSCRFFFFFF*QSLPSVV/Q AGSGQ*RNLDLQPLASRFK*FSSS RL\SSWDYRHMATMARLIFILVE MGFTMLARLVNFLTSSDPPTSAPP KWLGLQGVKPNTRAVGFN**LGY SIILYHSNSPGTDLVFILFIYLYLFL RQEONSAQARVQ*WHNLGSLQSP PPGV\H*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR
3156	8653	A	3416	165	289	ISGLSGLYHIDRLLIVCNCKQKPTYS

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						*NPGLSW*TDFKCLI
3157	8654	A	3417	3	796	PGPRAPPIRCSPLRSAAPRRPST*SAA AWPASAAAGFCPCFYSAAPSTSSR WPAAAGCSLATTAKTSSRVVEMLP RRAAAAGSYEGRAVRA/VMEYAW GAAAA/DHALSVASSILVILFHPLLL RPLCWTPCECLSS*EVIGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY
3158	8655	A	3418	2	603	GFFFFKIVLIQDLFPSTPLPSSVHSGD YGD SGQDP SGTRNTFRRCSPSPFP CQLPRPEAHTHANTRNPPSPHLLSF PHQSSEP*EGVKSLFEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STP/RPSVPSPIQPKTKHVQQHPPAS T*KTG SVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP
3159	8656	B	3419	34	375	MLLGRLTSQLLRAVPWASLPRKGA QLELEEMLVPRKMSVSPLESWLTA RCFLPRLDGTAGTVAPPQSYQC SQIGEGAEQGDEGVADAPQIQCKN VLKIRRRKMNHKKYRKL*
3160	8657	A	3420	2	361	YSTSPAGQVGR LSPSQGGPAGAGG DAG/TPGRCPSAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPSQIGE GPGGTPETQADQVRERPEAHLAEG GAKGSPRRAGRPPRSTCGANESG
3161	8658	A	3421	1	417	RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSI WLGGHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCCKG ARRPGCPALQRRAKAGGR
3162	8659	A	3422	31	756	GRRALRQAGPGSSREGPGARQRDS RGGEPEGAGLPVLGPF GASERDTA RVGGLGASGRELCWKQSPPCGLGW RREKGSEGRGGTRRPSGPATTEG AAA*PE/PGTCVPAPLGP/GPPPTDH APGAPDFPAVEGRSLGRRPPALAQ S/P/GSAGQPGLRSPFTAH/QPAGPGR GLSPSQGGPAGAGGDAGPQEDVRQ PPGELGSRPARFLPQTGLPGPAGTC GLHRNPTQCPSPPDRGKGPKQGG
3163	8660	A	3423	69	258	PRTNRCATNHTPANF*FFVETGLFH VAQAGLELLGSSSPALAPKQLVTG ASHHTRPQ*NFLQ
3164	8661	A	3424	8	292	QSFLFLKTRYLLRHPGWNTVAQ*Q LTVVTSRLN*SFHLSLPSS\WAI MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLPQPPPEMLGLQA
3165	8662	A	3425	123	357	WGKRPGQGGRNPWGPPLPGGK/PP KKGFLGPFTGRFQGSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPKIWE TPLGN

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3166	8663	A	3426	2	311	FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPPHPANFL FLVEMRFHHVLRVLVNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV
3167	8664	A	3427	7	534	TSDFIYKALKLQQEVPAKSHLVQN YRFFFFFFLRLWSLAPVAQTGVQWH DLSSLQPPPPGFKRFFCLSLPSSWDY RCPPPRPANF*FLVETGFHHVDQAG LKHLTSDDPASASPSAGITGVHPRP GQENQDLPGLCVDQLYTENSRRFFSK NYYQTPNFTSRKRDLKISVFFFA
3168	8665	A	3428	368	688	LTVEFLNLLNILSLVCFIHQTN*IICY FNT/SSSHQNA*YI*EPHVPS*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTYYVRESPTDASPSS PKMAA
3169	8666	A	3429	1	90	FFFVLSHQRNLCRRYSRDMAAIHK SKFFLWPGRVAYAYNPSTLGGRGG QIT*AQEFKCS*AAIHKSKFFL
3170	8667	A	3430	259	331	RNE*LLTRFSPLSLSH*VLGVSMF
3171	8668	A	3431	1	639	LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRKNSNHPTETRK\VLGGMRSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQR\RPEDTFMSV/Y YPMQTEHHQTPLDYNRRGTSLLED DEEPIVEDVMMSSSEG\RIEDLNEGM DFDTMDIDLPPSKNR\RETE\LKAD FFDPA\SIMDES\VLG\VSMF
3172	8669	A	3432	1	354	LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTRSGT VDPQELQKALTMTMGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRL TDSFRRRDTAQQ\FIQCVMSV
3173	8670	A	3433	1	788	MAYPGHPGAGGGGYPPGSPSVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESL\YGYFAAVAGQDQID ADELQRCLTQSG\IAG\GYKPFNLAET CRLMVSM\DRDMSGTGMGFSIEF\K ELLGLLEWAGR\QHFIS\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYSTNGKITFDDYIACCVQ T*GVFTDSFSKTGILAQGGCLLNFP WIDFHFNVCVHGVFKSLGSCMNVIN DSNWSSPLLVLFAFG
3174	8671	A	3434	6222	7046	RTVTTFLSKDSHGVIYCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASFC QLRKRKHNLVNCINRNPFMSLKN TSWHSSLVTQRHQQQSKLHFQGS LLH*PSQNIL/SNI*KCINYC*HCSSV LLSYLFIESYSVAQAGVQWHDLG LLQLPLRFKQFSCFSLPSSWDYRS APSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSCVLSNPYHKG RIYLGRMCFLNSTWHLVKSTLFCPL FI

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3175	8672	A	3435	3	287	SRSVAQAGVRWRDLSSLQPPPPRFK QFSCLNFPSSWDYRCAPPRPANF*I LAEMRFRHVGQVGLLELLTSGDPPA SASQSAGITDTSCHCAWPFTF
3176	8673	C	3436	88	303	MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW*
3177	8674	C	3437	354	416	MKESPGGELPQTGKKPVFLF*
3178	8675	A	3438	274	460	TLKNLRSAAASLTGPNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIIYPPPN
3179	8676	A	3439	480	613	LSFRAKMPSPPFQVGIIYPPPN*GPIC LLCFSFLCECVFYRNHLD
3180	8677	A	3440	1	864	YPTTPYQHHPISPPPIPTHNNHQP PTPSHRPQPTQRYTYHHNHTALTPI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPTG*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLRSYGSGLPTFPYLHCSN MPKACSPWRPAADMCTAR\PRFRPF KPDFQGPAPARAHTPPETRRFPRHGPI SRGEP\PGQPCPSQRKENSTPEFPPA SSGIGRVTDGRLAAAPSPPLRIRGS EPDSPFESAEGHRRSPRPRTALAQ SLRNE
3181	8678	A	3441	23	266	EMESHSVTRLECSGAISAHCTLRLP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVVGQAGLKLL/NIVILLRPPKV LGLQA
3182	8679	A	3442	840	887	
3183	8680	A	3443	127	593	DKATKLTFRSYAAVILKIHVLTW VILFRRKIIRDETLKLLDLISLVGKG QCYRVVFFWFFFFFEMKSHSVTR LECSGAISAHCNLCPLGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQGWSRTPDIRVIRPPWPKVLG LQA
3184	8681	A	3444	2	514	FFFFFLRQSL/DSVAHTGGQ/WGGS/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVNSS ASSDLPLGLASHSAGITG\VSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFG DTIQPSTFSFYLT*KIIPILYRVKK
3185	8682	A	3445	2	147	FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN
3186	8683	A	3446	2	328	TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE
3187	8684	A	3447	1	357	GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCPANF FNFYFCRDK/SLPMLPRLVSNWAAQ GIFLSQPPVSVGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTPL
3188	8685	A	3448	2	84	GLTLLPRLVSNWQPQEILLPW/PPKV

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						LKL* <u>AQAGLKLLASGNPPALAPKVL</u> KL
3189	8686	A	3449	1	439	
3190	8687	A	3450	1	552	GNEFSILKSPGVSVFRNGNWPIGGER IPDVAALSMGFSVKEDLSWPGLA\AV GNLFHRPRGYPSWVMVKGSGTKL ALTPQAVVISYPLENRVYVMVGKAN SVFEDLSVTLRQLRNRLFQENSVLS SLPLNSLSRNNEVDLLFLSELQVLH DISSLLSRHKHLAKDHSPDLYSLEL AGLDEIGKRY
3191	8688	A	3451	3	1111	ILKSPGVSVFRNGNWPIPRE\RDPP DVAALSHGLPL*KKDLSWPGLA\VG NLFHRPRATVMVNVNGVNKLDLP P\GSGISYPLENAVPFSLDSVANS\IH SLF\SEETPVVLQLAPSEERVYVM/VK GRANSVFEDLSVTLRHSRNRLFVK KTLFLSFTPPQILLSRNNEVDLLFLS ELQVLHDISSLPSPKHL\ARDHSPD LYFTGSWAGL\DEIG\KALLGEDSEQ FRDASKILVD\ALQKFADHDHVPVFM VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQVPYNLA\YKYN FEYS\VVFNMVLWIM\ALALA\VIIT SYNIWNMDP\GYDSIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC
3192	8689	A	3452	3	371	MLPLARCSSSCLAPLSTYQTQVKTO VHTETCI*MFIAALFIIVRR*KQPKCP SENK/WNKIWHIHTMK*YSATKKN KVLTYATI*MTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD
3193	8690	A	3453	2	318	ETESRSVAQAGVQ*RNLSLQ/PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWD SW
3194	8691	A	3454	33	504	GLHNFLTYKATIISAVVYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWWIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRIKIFCS*KDAINK MKKWPGVVAH
3195	8692	A	3455	16	1011	WPVRAQAGQRPVLHTQVASLFAGV PCVLSHPKKGLLVPPFPSPKKGHLG KPHCLPSAGRGAAGLGPLAQQPVS PAPASPMAPCKPKGLPPLPMGVEPE ILATMPVLTSHPP/SPEPMQSGNMPP S/PPSLCAFVPRWSHPPVPGWARWS CP/ALPAAPPSL*HWTRMQPPFCVPL RVPWVPSSGARGMKESGLDGQGFL GPTPSASPWGPWFDIRLPGCKQGIL AFKVTGPPTGFPDFEGKRFFKENKP PG*LESKAPDTVK*NPPSTNPPPPAPA FLTWDCCAYRGPAGFLLVCQPSLLS LILKNIDDTLKCVERFEKLTASKQP KATVVLARRS
3196	8693	A	3456	1	348	PQQLRCFSFWRKDTKVDWLLLNRG

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						ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPRGPGEAEPL LRSSSGRPAR/HQT*KKSGASPSDPR SASR*ALRREGGNPPRGPGEAEPL LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG
3197	8694	A	3457	2	247	PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA
3198	8695	A	3458	1	515	GLGSLGPPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGVAVP FPPTVAPTRRSRSPQSC*WGLQH QLCPGSMEEHMTPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPVGP/PINLA AQLPPQVPHAPHA WQLPSAPK
3199	8696	A	3459	2	223	IYISPKALKFCREVGPIPPPKKGSF PKIPR*QIFPPRC*KTGKGQGIKRP IRGKVLRCPLNLGPPRVL
3200	8697	A	3460	2362	2696	
3201	8698	A	3461	1586	2325	SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCPWWQISVVP RPSSRP/WLALEAEKDSGEKPGK GASRPEDLQIGRLQTRLKEREDIIK QLTKKKVEDVPSRVVSVPNLASYS KNFLSGDLSSRINAPPITSPSLDPSP SCGRITYKPNQSTDAKTATRTPDGET AQAKEVQKQGSFQEWFTKYFSF
3202	8699	A	3462	125	489	YYLFFFFFFLRLQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGDVRNLEE
3203	8700	A	3463	1503	1511	LFPVPFACPSLNCSPPPIGVHLPIG*I QRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFGHPAKGIHFR KP/RHPG*CVFILTD\CVHLH*KIND FIDTNFAMKSGYPNRIVRISFCLHT
3204	8701	A	3464	54	593	RTALPAQHVA STWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN*\n PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPPSQDGLD LGNRAGWGCSPECLSKAPGGGPA QAHPGPNPHTYRK PQWCWKLSPGH ALAPSPPRREVALNLNLYSFIVPRDSP RPCIISL
3205	8702	A	3465	2	324	FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFSCSLSSWDYRRP PPHLA/NFFVFLVDMGFTVLRMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG
3206	8703	A	3466	142	413	AQEFKTS LGNMAKPCLYKKYKKM SWDYRRSPRPANFSC\FLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG

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						VSHHTRPQIFLLPLSN
3207	8704	A	3467	241	523	NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYASAKR KIR*/PCAATWMNLEDMMLSEVSQS LEDKYSMLPFM*SIYVKYLEQSN
3208	8705	A	3468	137	382	NSAVHQKFISIPNTSLPHSLAILKPQI NSLEEET*PFWCKKSSPVPKMRGER NDDNFHKVLLNVTNVDKPGQLRSP KWFCWG
3209	8706	A	3469	2	363	FFFDTESYSVAQAGVQWHDLCSLQ PPAGFKQFFCLSLPSSQDYRHLP WLANF*FLVETGFHHVGQAGLKL TSSDLPASGSQSAGITGMSQRTLQQ LSLKTTELNRNFRCPYCIINA
3210	8707	A	3470	135	466	GIDTILTLNQ*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFSCSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVIS*P RDLPAEFL
3211	8708	B	3471	27	21189	MKVSAARLAVILIATALCAPASASP YSSDTPCCFAYIARPLPRAHIKEYF YTSGKCSNPVVFVTRKNRQVCAN PEKKWVREYINLEMSMICSGHHV YPNLPTDSFPGLDQFRGNYLHSRDY KNPEAFKGRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNPKPKVIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLPSFISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPSRILCGTSLIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTLFKGIFPPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGGKKLCPYQFRLMGPWKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHPFYNLLKMLSFPLLLAVTLT FY*
3212	8709	A	3472	9	339	ITLSLLSFFNLRPSFALLAQAGVHW RDLDSLQPPPLRFK*FSYLKSPRSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVN CARPPSLFS
3213	8710	A	3473	1	50	
3214	8711	A	3474	1	1256	MAAAAAQGGGGGEPRTTEGVGPG VPGEVEMVKGQPFVGPRTYQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFHQTYCQRTLRENQILLRFRH ENVIGIRDILRASTLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSLAPSSYIHANVHLRS* SPPTWLIQHHLADLKVCFGLAGIC RSWRHDHTGFLTEYVATRWYRAP EIMLNSKGYTKSIDIWSVGICILGE MLSTRAIFPGKHLYDQLNHILGILG SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKALDLDLDRM LTFNPNKRITVEEALAHPLYEQYY

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						DPTDEPVGEGSPSPFGMELADDLPKE RLKELIFQETARFQPGSAGRPPSPR QTSLHPGGWTCPPARPLSRDC
3215	8712	A	3475	877	1463	LPFTAWP*E/QLQQA VHAGLPQQA K ILFDGGSEIGKILPAFQSGNLSCQLH **IGQRAGRGLRIGRQGGFSFHQ* DGQQLIALH/QPGPERVAASGPRWF APAGENPV*WWFRNRQNPLIALRSL PAFQSGNLSCQLH**IGQRAGRGL RIGRQGGFSFHQ*DGQQLIALHRLA LRELQQA VHAGLPQQA KILFDGGSE IGKIPV*GLLRWPPLPRDVQWDSAP LLRARWGL*GER*PREVPAALQGE* PQALLPGGGEPGWQPAEPHPAGGV HRAGPPGGGCWARAGGHQKHL RPAAGVPPDRGCLLQLGQIPH*AGE QVQAGPGTGQPAGEQAQRGLSGNA GPHQVPAEGDTGHLCD
3216	8713	A	3476	29	1076	EQRDPQDIFSQRKSSAFPPSPEIEILS GGKSLSLQLHTPSPG/QQGETPRGG QQSQH/PCQGPGGGVPRYACAGGV PVERTGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSPP GVPGHPEYPE/HGGSEALLHEFLLPP VSRLH/HGPLYPQMSNGTLHHYFVP DGDYEENDDEKCCQL/PLQGE*PQA LLPGGGEPGWKPAEPHPAGGSSPC WAARWEDAGRVLGGHQKHLRLP RRGRELWQVPAAGVPPDRGCLLQL GQIPH*AGEQVQAGPGTGQPAGEQ AQRGLSGNAGPHQGAEGDTGHLCD GAQGLIRAAGPHH
3217	8714	A	3477	3	591	ERNYLFFLRWSLTLSSRLRGQWRN LG*\MQPPPP\GFKA\FSCSLPSSWD YRRMPPCPANFCILVEIGFHCLAKL VLNSRPHDPPTSASQSAGITGVSHR AQT*KGIHLNELCTALAKEGRAWS GR*AGAATPAP/PAPFTL*PGCIPES WSPMPPPHPLTALCKATHAGTK HPLHTKTVSSCGAVLQPTPQRKD
3218	8715	A	3478	1	235	RDHPGQH/GETPSLRKIEILAGHGVR HL*SQLLGRRLRQENCLNSGGRGCSE PRSCHPTLAWAIEQGSVSRKEGHF RLA
3219	8716	A	3479	2	928	RPPRPGTERALPSRLRSRPRVRTETP SPSSSGPPPSRSNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRSVPSGR TPALRGTRAPSDQKGKARPPEP APSRPCPGSRFCRASRSRTSPRPPTP ARESGNPGRSP\DGGEKAAAQGS*K ESAACSNRAWS*WAA\SPPWITVTR QKRRGTLDQPPNQEDKPGARTLKS EPGKQAKVPERGQEPVKQADFVRS KSFLITPVKPAVDRKQGA KLNFKEG LQRGISLSHQNLAAQSALMMEKEL HQLKRASYASTDQPSWMELARKKS QAWSDMPQIIK

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3220	8717	A	3480	1	435	EKINKIRWLPQQNAAHFLLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPILKPMDLMVEA SPRRIFANAHTYHINSISVNSDHETP NIVDIKPANMEELTEVITAAEFHPPH QCNVIFYSSSKGTIRLCDMR
3221	8718	A	3481	204	397	VPILKPMGSYG*EASPRIRIFANAHT YHINSISVNSDHETYLSDDLRLNL WHLEITDRSFNIV
3222	8719	A	3482	1	1462	PLRSWLPRLPDSQADIISTVEFNYS GDLAT/GDKGGRVVIFOREQEVLAQ PRRPAIP*SVSSFLSTSCREVVQGC EFSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLSLEIEEKINKIRW LPQQNAAHFLLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPILKPMDLMVEASPRRIFANA HTYHINSISVNSDHETYLARS*PGGI NLWHLGNHR*EAFNIVDIKPANME ELTEVITAAEFHPPHQC�VIFYSSS KGTIRLCDMR/SSALCDRHS/KSFFE EPEDPK/SSRSFFSIEISSISDVKFISH SGRYMMTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYLRATKLCSL YENDCIFDKFECCWNGSDSAIMT GSYNNFFRMFDRDTRRDVTLAEASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFNKKILHTAWHPVGQCYL PWLATNNLYIFQDKIN
3223	8720	A	3483	603	659	MCGFFVFFFWRRSL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCLSLPSS WDYRRPPPCLANFLFLVEMGF/TTV LARLVNS*PRDLPTSASPSAGITGV S*HASSRL
3224	8721	A	3484	84	202	
3225	8722	A	3485	3	577	ILGFPPFVRWGSHTVAQAGVQWCD HGSLQPRSPGVK*SSHLSSLGSWNH RHATTTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQTVGITGVSHWT WPNTGFSVLTA TNKNLKFHYAISK CLVRAKLSSRLKIEERNKALSAPV VSVSIFDRVLRLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ
3226	8723	A	3486	3	248	SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFCFHKNFSLGFEIV RPGHPLVPKRPDACFMAYTFERESS GEEEE
3227	8724	C	3487	185	340	MDNFCSSSLCDFCHQKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL*
3228	8725	A	3488	1	546	NDRLN*TRELTSHERRRFRPSSRLT DAQIRINWRQVLSAGSLYIEIPGRR AAEGGARNFSFVLLLEFAEGQLRAD HVLICFHKNREGQKPPLLRFTSFSG LEDGEDRGNPLVPKETPDACFHGLT TFERE\SSGEEEEVGARLRGLGQFP RPGAHPLVKPGWGKEPVDSPHLAL GLSPML

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3229	8726	A	3489	1	526	FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSFSSWDYRCPP HPANFCIFSRD/MGFTILARLVNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHS\VAQAGVQWRDLGSLQP LPPEFK*FSCLSLPSSRDHRHPLSLPA KFHIFSRDRVSPCWPGWS*TPDLR
3230	8727	A	3490	276	735	FFFFFLRQSFSLVSQAGVQWHNLG SLQPPPPGFRQFSCLSLPSSWDYRHP PPCPANFCIFNRELIIVYLIKTFG/IHV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQGVIPRIVTHKRETGSQTLYSIV
3231	8728	A	3491	2	344	FIFIF/NFLRWSL/DSVAQAGAQWRD LGSLQGPPPGFTPVSCLSLPSSWDY RCLPPRPANFFAFLVETGFTVLARM VSI*PRDPPASAYQSAGITGVTTAP GLLF*INICLAAFYFV
3232	8729	A	3492	109	559	QFLHRLVHDSGEVWMKLE**NTL LAKMVISISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHHPPGRRHVHGLLHWCA GVPP*QPGKH
3233	8730	A	3493	1	593	ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSL\SWDYRHPPQHSANFL AFLVETGF\TVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRFLLFL FFFETESCSVTQIGVCSGHDLGSL/ QLRPPGITPFSCLSLPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA
3234	8731	A	3494	3	484	RFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCGLPLNSWDYR RGPPRLVNLCIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HCARPDEIFYQC*Y*ETEMVRRST TQDRAGSTTVLKLGLRPEREIVN LALGALVYRNITPN
3235	8732	A	3495	104	288	GEVICGRRRSEVSRNLVDLEPKGP WGHWQGG*GDRRAGGTP*GE/GHL RKKAI*GLQVQGRPRTEGPLGA/PG KGDP*TPTEGPRGDARNCDACPRPR ARPVLVW
3236	8733	A	3496	3	641	RPPFFFFFFFFFFFFRRL/NSVTQAR LQWHYLGLSLQAPPPGFTLFSCSLP SSWDHRRPP/RMPG*LFFAFLVETGF QRVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFSFFSFET GS\FSVAQAGLQWA\NHSSLQAPSP GFTPFSCSLPSSWDCHPPRPANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG
3237	8734	A	3497	1	296	VSRRFKQSIPP*AS*GWDHRCVPPS LANFFFLLEMGFPMPLPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL
3238	8735	A	3498	1	347	KKTGRRKRNMIDYEKKKNKEQEER

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						RKKRKKRKSSSSSSPEEKKEEKVK KREEEENRKKEEEE*DK/KEED RRKHESRRRLRAVGDEVINKVCQE LKRTIPVGRDYRLDPSS
3239	8736	A	3499	2	286	PQPCSLAPNPPRMPPGSF/TPCSPPR SNITL*KQRPPSPPSPEPPRIAQQRV AQNLTSPRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF
3240	8737	A	3500	3	954	RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRRSEVAPSSDRPGRCAPPPL TASGDLRVPRGRSGRGPAGTAPGPG *RAGASPGQRHPPGCSWPQ*TRKG EQVFFSPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAAHRCASPACP S\PRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQHPCKPIAPISP KIPQSPGSGWTGDTLSPH
3241	8738	C	3501	68	199	MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL*
3242	8739	A	3502	11	520	IRVDDFVAHRSRCCVAFSSFTPRSR RRPKRRRRRRRENDPAASSLPPAHL CSVSQSAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWRR EDG/RPSKRSRMAQREAQRTSPQR GNGRPKTSEKCPPEEKAVCRTPG
3243	8740	A	3504	78	595	NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSACYS\GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESGQGILLGLLRKAI GSPGKRSAPVQPNWEGGNG*EAAW ASSSSPSCKVTAPLAPSELPSPKFL RNKKAQRKISHLLEVTVGHLLC
3244	8741	A	3505	2	267	ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQG QYLPS*KHTKV
3245	8742	A	3506	1	323	IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAET FSLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMUSDHNGIQEISNRKIAG KSPNT
3246	8743	A	3507	3	814	SSGLAGTPFPSEGAVCRSQPG*GSG \SPPLPVGPACWYLP CGP*DQRCPPG SLGPSAEPGS*NLSCPRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLPSP TFPAWSVPRFQPGAAPSSADLVHFI AASGPSASLSSSLSTKAPSLPLGACL PAGGV*TFGPSPG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAQAQKEGGAGL GKGLGSFACGRPHLPAYFACGRPH LPPAYFVLDLPFAKVLNRINI

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3247	8744	C	3508	112	252	MFRSMYNXXXXXXXXXXXXXXXXX XXXLGMSEXXXXXXXXXXXXXXLG F*
3248	8745	A	3509	448	715	FFHSIKIIEFFFFETESCSSVTQTRVQ WFDLGS LQPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE
3249	8746	A	3510	55	295	SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/YPPSSSSSSSL*LPKLDKDIIRK EN
3250	8747	A	3511	2	853	DLMCKKMKHLWLFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGWVRQPSGKELEW IGSLYFTGTTHYSPSLKSRVTISADT SENQFSLTLTSVTAADTAVYYCARP RNIVGSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVT\SWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVP\SSSFGHPRT Y\ CNGKSQSPATTKVDKGELSPK\ S\ CDKNSTHAPPGPQHLETPWGGPVS LFFFPKT
3251	8748	A	3512	3	2310	QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSKKAS GYTFTNGLAWVRQAPGGGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNYATGAWFAYWGQGLVT VSSGES*AWYPGIQCISMLEL*ISAF WGRPGLTAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPRIDKNR GASAPWAQLCPTPRSHGTTSLAAS KGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVT\SWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTK TYTCNV D HKPSNTKVDKR/VW*EA STGREGVCWKPGSALLPGRTPAVQ QPRAARHAPS VSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSPP QRPNSPLPQLGHLLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVI LHLFLAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGGTRGV RPGHGRPARPTLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMEALHNHY TQKLSLSLGLK
3252	8749	A	3513	1	1677	AEVQLVESGGGLVQPGGSLRLSCA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAAGTTDYAAPVKGRF

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						TISRDNSKNTLYLQLNSLRAEDTAV YYCAKDEFSSTRKNFLTGQSKTFAA YYGMDVWVGQGLTVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVTWSWNSGALTSGVHTFPAVL QYSGLYSLSSVTVPSSSLGTQ\TYT CNVNHKPSNTKVVDKTVELKTPLGD THTCPPCTP*LLGGPSVFLFPPKP KDTLMISRTPR\VTCVVVDVDPRKT PEGQVPTWY\VDGLAEVHKCQDKSR GKEQYNSY\YRVV\SVLTVV\HQDW \LNGK\EYK\CRVSHKSPQAPIETH LPKPKGSPQNPQVYTLPPSRDELT N\QVSLTCLVKGFYPSDIAVELESN GQPGNNFK\TTPPVLDSDGSFFLYSK LTVD\KSRWQQG\NVF\SCSVME\A LHNPYTQKSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNAKTPWPWAKKKKKKKKKK KGGRSRVSLGPKLRTQTLS
3253	8750	A	3514	1	164	TRVNENQIESKAAAYALFYKRQDVA RRLSPAGS/SGAPASPCSSPPSSEF MDVN
3254	8751	A	3515	1	712	EILIIHLKRFSYTKFSREKLDTLVEFP IRSGARERMAGGRQKGEVYQY*P SPHPQ\DLDFSEFVIQPNESNP KYDLIAVSNHYGGMRDGHCMCQA VGGACPGGSGQGGDQDLPE*LGM *ASGEGSSVVGRK*TRSEIWLSEEA RKGRRG*LSFPFR\TTFACNKDSGQ WHYFDDNSVSPVNENQIESKAAAY LFYQRQDVARRLLSPAGSSGAPASP ACSSPPSSEFMDVN
3255	8752	A	3516	3	3090	IPLLQLLLRRLWRRHGRWTEPREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKHWHYKQWEAYVQG GDQDSSTFPGCINNATLFQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGQPPIERKVIELPNIQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLRTARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEDEDFKGQPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGEIAEAY ADLVKQAWSGHRSIVPHVFNKVK GHFASQFLGYQQHDSQELLSFLDGL LHEDLNRVKKKEYVELCDAAGRPD QEVAQEAQWQNHKRRNDSVIVDTFH GLFKSTLVCPDCGNVSVTFDFPCYL SVPLPISHKRVLVFFIPMDPRRKPE QHRLVVPKKGKISDLCVLSKHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEAIEGSRE DIVVPVYLRERTPARDYNNSYYGL MLFGHPLLVSVPDRDFTWEGLYNV LMYRLSRYVTKPNSDDEDDGDEKE

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						DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGVNTRCPFLDNCLGTSQWP PRRRRKQLVQLQ\TVNSNGHNRLH HSPCTKSNAPVHCYSTWKP\EMK K\RYYYDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPPPFGGK\ EREKPWYCP\SCKQHQLAT\KKLAD LWMLPEILIIHLKTFFPYTQVLPEKK LEHPSWKFPYPGTLD\FS*/EFVIQAH QNEVEIRELYK\YDLIAVS\NH\YGG MRDGTLTQHLACNKDSGQWHLLLI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ\DTLARLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAP KKKKKALSALSLLVSAPLLLFVLGA PARHCRLSRGYCSPVPLNRSPLPGKN RSCLLAVRAPPCVCPSSSDPPF
3256	8753	A	3518	1	271	PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCHVQGAGFELLT SGDPPTSASQSAGITGVSHRSRPVD FLNYLLRKSYPFT
3257	8754	A	3519	3	633	FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCLSLWRSWHYCRH HAQLIFVFLVKTGFTMSVKADLEL LTSGDPTASASQSAGITGVNHQCPA SKQF*FHCKSW\CLF*MQSLSFFLG GGQSRVGGAGVQWHDLDLSLQPLS PGLKQFSSLPLPSSWDYRGVPLRLA NFCIFSRDGVSLCWP\GWS*TPDLKA NPTRLGLPKGWGL
3258	8755	A	3520	2	430	CLKNMVGAGEVDEDLEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLTLN\GRYFGGRIVVKA CFYNLDKFRVLDLAEQV
3259	8756	A	3521	3	1076	HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPD\PDSEDEDYER\ ERRKRSMGGAAIAPPTSLVEKDDEL PRDFPYEEDSRPRSQSSKAAIPPPVY \EEQDRP\RSPT\GP\SNSFLANMGGT VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKT\NKRGGKIIVGDATE KDASKKSDSNP\LTEILKCPTKVLL RNMVGAGEVDED\LEVETREECEK\ YG\KVGKCV\IFEIPGCPLMMEASTG YFLEI*EELNSAIKAVVALN\GRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVV
3260	8757	A	3522	1381	1787	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3261	8758	A	3523	1147	1553	LEYVAHPLHQLLILNNFYSVLNEKY

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						LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3262	8759	A	3524	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3263	8760	A	3525	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3264	8761	A	3526	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3265	8762	A	3527	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSVDSPT LASQSAGITGVNHHAWLFFFCSD/RD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRIYPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYIFYFHRDEGSLCCPGWS* TPELK
3266	8763	A	3528	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3267	8764	A	3529	10304	11097	FAFSPK*HSCLRCPIC*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCWWLEENLWLSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFFLRWSL/DSVA QAGVYWRDLGSLQPPPPGFKRFSCSL SLPSSWDYWHLPCLAKFCIFSRDG/ GFTIWARLVLS*SCDLPASGSQSA GITGVSHHTWLQVTFYFLKEMRSCY FSQVGWPQTPGLKQCCHLKLSSW DYRHMSPHLAISGS
3268	8765	A	3530	87	411	ARLVQNTVAQLKEVQYKLFGLF FE*/QSHSVAQAGYSAVIAHCNLSL

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						LGSSDPFFSAS*VAGTTGMCQHAW LIFDR*WR*GLAMPLRLEM*IFLISH LRLIWSAWS
3269	8766	A	3531	31	403	THLNGLQIRGSPLFFF/FELESSVA\ RLQCSGVISSHCNLRLPGSSNSPASA S*IAGITGAHHNPG*FFVFFSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFTRHGAIPQWGQVPFHRS
3270	8767	A	3532	7	1047	
3271	8768	A	3533	3	53	
3272	8769	A	3534	7	960	
3273	8770	A	3535	1538	2287	WWSSSKLRLIYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCLSLPSSWDYRHPHPLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IPL ESSDFYTTTTFETESHVS/TQAGVQCR NLGSLQPPPRFKQFSCLSLPSSWDY KCTLPRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV
3274	8771	A	3536	3	263	LGVGDRVSLCHPVWSASSL*SQT PG LK*SSHLSPSRWDNRHAPCLA/SL KNFCRDRGLTMLPRLVSNWAQAI LPPQLPEVLGLQV
3275	8772	A	3537	33	295	AGMQWCSLGSLLQPPPPVLRSSHLS LPSSWEYSHTC\NFCIFCRDGFVLP RLLG*SNRPASS*NTGITGVSHRAQ PSLFLSYSFFF
3276	8773	A	3538	3	33	
3277	8774	A	3539	1	375	
3278	8775	A	3540	3	340	HEVVAA*YYG*PSIAQEVAGTLAE LDVTLQILLEDKFLQNKVFLTGP HIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI
3279	8776	A	3541	30	284	YSVSTPLRDSNPNNHLSLGHCPASS QTEPQAPQALGQPATKLLPHQP PP /MPQPSSKP*VSATSLCTSPPLPLCP AGGSSGTT
3280	8777	C	3542	127	435	MAASXNPEVLDITEETLHSRFL EGV RNVASVCLQIGYPTXASVPHSI NGY KRVLALSVDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCC CSP S*
3281	8778	A	3543	3	417	
3282	8779	A	3544	2	881	RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*VRGHLGFCFTREDLT EIRDMLLA\NKVPTAARCWCQLPP CEVTVPA\QNTGLG\PEKTSFFPGL* VSPTKNLPGGTH*KS*SYVQL\IKTG DKMGSQTKAKAAEKMLKNLPPSPF GAGQPKQGVRKNGKHPTNPESA*I STRGKLCHSRFLGGCPANVAKCLS CKIGYP\TVASSTPII\NGYKRVPGP CLWTPDYTFPLAEKVKAFL\ADPSC LCVLLPPVGAATTACFALLLQPPA

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						KVEAKEESESEDEDMGFGGLFD
3283	8780	A	3545	2	311	DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCSLSPGSWDYRHV/PPCLAN FVFLVETGFRHVQGTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF
3284	8781	A	3546	1	290	KTFFFFFF*DRVLFCCPG*SAVAQISW LTAALTSWAQGSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSLRAL
3285	8782	A	3547	229	486	IKIKINQAWVCACLSLPSSWDYRHG PPHPANFVFFLVETGFTMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV
3286	8783	A	3548	2	431	ARGSIYQNDTTI*NMULDNRASECT VRELVKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNANTFT* LIFIKCSAQHQNAHSFPV/PHRTF/S KIDHFLWCKRGLNCKCKMIQIIQNVV CDHTALNKKPMPERSLEK
3287	8784	A	3549	2	194	VDFFFFFFLRWSI/NSVTQAGVQWRN LGSLQALPLGFMFSCSLSPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HLICKRGRQ VP*LFFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMFSCSLSPSSWD YRCPPPAHPANFFLHF
3288	8785	A	3550	2	489	ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMRYAFIGPLE TMHLNAEGML\SYCDRYSEGKIHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHWRDE\CLMR LAQV*RSSSCSPQLNFLC
3289	8786	B	3551	13	441	MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKFAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLAFVIRXR GINGVSPKVRKVLQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG*
3290	8787	A	3552	1	775	RRVPA\VPETLKKKRRNFAELKIKR LRKKFAQQMLRKAR\RKLIYEKAK HYHKEYRQMYRT*NFEWARMGK KKLANFYVPAEPQIWRVFVIRIRGIN GVSPKGSEFFQLRLRQ\FNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRGLWAKSNKK R\IAL\TDNAL\IARSLGKIRHILAW DLIHEIYTV\GKRFK\EANNFLWP\FK LSFSTKVEMKKKTTHFVEGGDAGN R\EDQINRLIRRMN
3291	8788	A	3553	1	356	SHHVQLLEFFVEMGSPCVSQA\VL* LLGSSDPVLAENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGSCSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF

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3292	8789	A	3554	3	352	HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHANP/CFFLTESNWVA QAGVQWRVLS*LQPPA*FKGFSC SILSSLS/WGYRCLPP/HPANFFFF*K GFFWFPSWNAMGKKWFN
3293	8790	C	3555	55	201	MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQAEVAVSQDHATALQP G*
3294	8791	A	3556	3	212	QEFFFFFFEM*SRCVTRLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF
3295	8792	A	3557	2	265	EKESRSVTRLECRGAISAH*NLHLP GSSHPPSASHVAGTTGACTT/AQLI FFVFLVETGIHHVGDGLNHL/NLVI RLPQPPKVLGLQA
3296	8793	A	3558	354	675	HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDLSLQ PPPGFKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS
3297	8794	A	3559	1	1203	
3298	8795	A	3560	2	634	VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQEEYARRAAAAAASAE AGIATTGTEGERDSDALLKMTISQ QE\FGRT\GLPDLASSMTEEEQIAYA MQMSLQGAEFQAESADIDASSA MDTS*\PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI
3299	8796	A	3561	506	930	IRTTQIGLCLSQVYFVFDLHAQYEH KATNITPTLSKIIISIRPRFIFPVT*L LNMFASFSPMPVPSLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSRANCKV NPVIGSISKYVLCSSSFGFNPSIGSET SGLAYRK
3300	8797	A	3563	3	271	FFLET*SCSVG\RLCSGVILAHCKL RFPGSSDSPASASGVVGTGAHHHT RLFCIFSRDGFHHVGDGLDLL/NL VIHPPWPPKVLRLQA
3301	8798	A	3564	1	218	ETGSPSVTRLECSSIQ\SAHCNLDLP GSSDPPVS\APQVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*T\IH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG
3302	8799	A	3565	1	294	ASTFFFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPASAS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA
3303	8800	A	3566	3	292	FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP
3304	8801	A	3567	3	389	
3305	8802	A	3568	1	672	
3306	8803	A	3569	1	2018	MSDNGVRTGAPSTDQRTGMSVRAE

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						WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRPCPALGGLASGPGKAEQF SRSLYLPDHLGEGNGGLLGKSLEPY RSACMSAAGLKITGSKETKRRLLI SIDWSRDLMNLCIYFRVYCQEKQEE RRELPRITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVVTAGLVIW AGTCYYIYKFTKGRAQSVRTLARN GSTVKMETVVGVSQTLAINEAEIK TKPQVEIGAETGARS GPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTD AEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVGAGAD VRACIQPQTVAKKQAEVTSGARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVG DGT DMLSCT QPQLVASVQADTLSDGKIKVRGNV NTMPKEGAGVDMKAQGMASQGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRVCGQP LVVANPQGEALPGAKNKVGNPHT VLKVGAGEGTTDS AQPEAVVSFQG EALLGTKNKVKGPNPVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLP GAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLP GAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLP GAKNKVKGPNP VVS KAGAREDTV GSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKA EAGAGIMGSVQ VQVVASFQGEVLP GAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGNTIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSEEGSGTQACRKTQPNIHDI YWNGIGVEDWIAAERWIKFRFQTM DGDWENSWSWADDENEASIGSWG ASDKAGIIRSWAVACDETSVKSWA GARAENVVIGITWARAGEQASGGL

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						WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGSKPRFEDQASGEGSW AGAGGQASGGMLGPEDQSSGRSW ADTADQASGG SRLGHVDQSSGGA WAGTLDQSGGGSKPRFENQTTEEG SWAGAGGQAGGGSKVGPEDQSSG RSWANS GDQISGGFLVGIVDQANG GSWTGAGHPASVGP KPIFEDQVSGR GSWADAREQVVGDSRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWGGASGDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPGDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGA EAVIGSWCWTEEKADIVSRP DDKDEATTASRGAGEEAMICSRIE AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRSFWA ESENSNTFRSKSGK DASFESGAGDN TSIKDKFEAAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSSRGIYPYM VPGAGMGSWDGAMIWSETKFAHQ SEASFPVEDES RKQTRTGEKTRPWS CRCKHEANMDPRDLEKLCMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNNPYPVSRQKA LNALNNISVAAENHRKV KTYLNQV CEDTVTYPLNSNVQLAGLRLIRHLT ITSEYQHMTNYISEFLRLLTVGSGE TKDHVLG*EQRQSQCHD*SRGQGK LEGQFPG
3307	8804	A	3570	1	611	YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP EYRWDMHRPW RTHRP DEEK RIMEKDWGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP
3308	8805	A	3571	1	379	EMESHVTRLECS/GTILVHCNLC LGSSDSPASAFQVAGITGVHYNA*V IFVFLVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L
3309	8806	A	3572	6	222	DRVSRSA AQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK

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3310	8807	A	3573	1	445	
3311	8808	A	3574	1	3212	DSINNLAELNKFALRKQLEQDVL SYQNLRLKTLLEEQISEIRRRREESFSL YSDQTSYLSICLEENNRFQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQNGFPDRLASTE QTEIMKDLKSGGCKNGYLRHTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLESRPDLLKVVRELLLGQ LFLTEQEVSGEHLDGKTEKTPKQKG ELVHFVQTNSFSKPHDELKLSCEAQ LVKAGEVPKVGKLDASVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQELKEFKTC NKQLHQKLILAEAVMEGRPTPDKT LLNAQPPVGAAYQDSPGEQKGKITT SSVWRDKEMDSDDQRSYEIDSEICP PDDLASLPSCKENPEDVLSPTSVAT YLSSKSQPSAKVSVMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAITVLCGTEGAQDG LSKPKNNGSDGEEMTFSSLHQVRYV KHVKILGPLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPRYDSLVSQARELSL QRQKIDGHGICVISRQHMNTMIKA FEELLQASDVVYCVAEGFQEQLNQ CAELLEKLEKLFLNGKSVGEMNT QNELMERIEEDNLTQHLPEPSEPS ASHALSDYETSEKSFSDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGS FVQGSTSIFASGSELHSSLTSEIHFLR KQNQALNAMLIGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECESEKERHNQQLIQEVRC GQELSRVQEELKLRLQQLSQNDKL LQSLRVELKAYEKLDEEHRRLREAS GEGWKGQDPFRDLHSLLEIQALR LQLERSIETSSTLQSRALKEQLARGA EKAQEGALTLAVQAVSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHLWASKNGRH VLGLIEDYEALLKQISQGQRLLAEM DIQTQEAPSSTSQELGKTPGHPAP LSKFVSSVSTAKLTLEAYR/RGLK LLWRVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKFAKTP*RF LQLSKVRQEKVIFDQ/LVVTHKILRK ARGNLELRPGGAHSRT/CSPSR/PGS ALATRKEHRNQQHSAEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMTVNIPWKVIIHLICLIPPRQ
3312	8809	A	3575	1	1362	SGNIKVLERFLYIDTKFSQNRCCQA LPMASAYQSNLPHNYTMTVHNN

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						QLAQUALRVYSQHAIGAVLYKYSMQ VHEDCYKFWNSNGMQLCEERSLTD QHCVHKFHSPLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQFWEEKCCGKIG SYISISQYLEPSTPGSWLLA*KWNP/ RPAPPDSADKLKEKEPQTQGESTS LSLALSLGQSTDLSLTYPADPQ/DRR R*SRSSWSSRSEN/SRRDQTSIDRH/ LTVEYLPGLHNSNCPKGLLPTFSSW VFVKLGPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSWR*RRLR HKLLACSK*SYSWKEKCGCNGKRK TAR*H\TRAFVGFYEDSRGRRFMC SGALTK**K*WGSGA/IRDSAFKSP*I VDMPLY\RHPLKVEGLKTLITLQL MRLFVVVPDASFA
3313	8810	A	3576	1	673	EGGW MEDYDYVHLQKKEEFEMTH IELLDKGSITRQGMSQL*LEQLKLFV RLEQEVSRPIDHDLAIWTPAQPLAP GRSGGLGPSDRQLLLFYLEQCEAN LTTLTNAVDAFFTA\VIATNQPPKILV GASKVLL\SAHKL\FIGDTLSRQA K\AADVR\SQVTHYSNLL\CDLLAQGI VATTK\AAALQYPIAFPGPKDMV/E KRVKELGHSTQ\QFPPRS*QGLGSP EGW
3314	8811	A	3577	3	531	FFLLQSL/DSAGQARVQWCDLGSLO PLPPRFMRVSCSLSSWDYRHLPP RLAMIFVFLVE/QGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFFETGSGSIAQGGVQ*CNLGSLOP LPPRLKPSSHLSLLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK
3315	8812	A	3578	1	223	GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL
3316	8813	A	3579	3	341	FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCSLSPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLLT RDPPTSASQSAGITGVSHRARPVAI FMFCEYPLFSSH
3317	8814	C	3580	168	347	MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSTIV*
3318	8815	A	3581	852	1216	GFLINGNTDFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCSLSPSS WDYRHLPPQYPS*IFVFLVETGCSSY STIL**RP\HVGQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI
3319	8816	A	3582	2	238	
3320	8817	A	3583	680	891	
3321	8818	A	3584	697	979	IFGVSQGYKILWKMNSLPGVSFES KRSF*KQ*LQILSS*FAKKIFYWHEN NRCKWRPNIPKCIYSITSQKLFYPS LLFFPLPTFLGVGGAR
3322	8819	A	3585	2	518	GRGYQNPRQCTSDRLSEHVSEGES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPDSQEDSFQGRQKSKDKAATPRK DGPKRSVLSKSVPGYKPKVIPNAIC GICKLGRESNKERKG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL
3323	8820	A	3586	1	165	SLEDVLLCHPGTA\YCSLELLGSISP PALTLTSEASLPGRDYREIPGSPCQL FL
3324	8821	A	3587	1	249	LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*D\YRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT
3325	8822	A	3588	3	282	NSWDYRHLPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS
3326	8823	A	3589	1	714	
3327	8824	A	3590	1	726	MAEGETESPGPKKCGPYISSVTSQS VNLMIIRGVVLFFIGVFLALVLNLLQI QRNVTLFPPDVIAIFSSAWVPPC CGTASAVIGLLYPCIDRHLGEPHKF K\REWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLFLATVVTHL*V YNGVYQYTSPDFLY\RSWLP\CIFF AGGITMGNIGR\QLAMYECKVIAEK I/LIRNEEGKK\YLLYRKAR
3328	8825	A	3591	469	537	PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFRINCHGKTYLFKG SQHWRFEDGVLDPDYPRNISDGF GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQPNEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPQFINLDWHGEPWQ ADAAMAGRIYISG
3329	8826	A	3592	193	384	
3330	8827	A	3593	96	1635	ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKKCQRDEL CS\YYQSCCTDYTAECKPQVTRGDV FTMPEDYTVYERLGEEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAEVGAASKPEGIDSRPE TLHPG\RPQPPAEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKL\RDVWGIEPI\DAAFTRI NLFRGRPYLFKG*\QYW\RAFEDGV\ LGPWIYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERVYFQRG KQYW\ESYQFPGTSPVQEECEGSS\ SAV\FEHFAMMQRDSWEDIF\ELLF \WGAERSGWVTRI\QPQFHLAGEWH GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKK\RFRR\RNK\GYRS\Q R\AHSRGR*PETPRRP\SRAMWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFSFGDKYYRVNL RTRRVDTVDPPY\RSIAQYWLGC

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						APGHL
3331	8828	A	3594	44	166	
3332	8829	A	3595	3	1173	SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGGNTAWECKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQKSEYPDLF EWFCVKTLKVCCV\PGTYGPDCLA CQGGSQRP\CSGNGHCS\GDGSRQG DGSCRCHMGYQGPLC\DCMDRLL QLRSRNETHS\CTAVRTGLSDSYPP CCLSLGCWRGVGHAWIRGRNTHQ PGYSSRVWIAAFSPACDESKTCSG LTNRDCGECEVGWV\RTAPCVDV EKCAAQT\PPCSAAQFCKNANGSYT CE\ECDS\CVGCTGEGPGNCKQCIS GYAREHGQ\CADVERVPH*PEKTL EEKTKTCYNTPGSY\VCVCPDGFEE T/RRCLCAAGRRLKPQKGESPTQLP LP
3333	8830	C	3596	1	300	MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPAPGV PLV*
3334	8831	A	3597	359	1229	MPQPPTLGQEMTGPSQPWTGKGGL PGP*QLRAKAQEVDSHLGRKKIKQ QNRSKSC
3335	8832	A	3598	2	311	VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAQPAPVS GPPPTSGLCHFDPAAPWP\PGGLG MLPPHPQDWPAQP*HPPGLGLFFEIF SAS
3336	8833	A	3599	1	426	
3337	8834	A	3600	18	738	
3338	8835	A	3601	65	425	RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNHGLFD/R GAGKQQWQDS*VTEVLLLLQKTFF QAASEEDIFRHLGLEYLPEQRNA
3339	8836	A	3602	3	233	FFFFFKTLQIPLLLSPPPGPCR\VQSL LPNPFPEKGA\PPFQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPEK
3340	8837	A	3603	7	510	THAPAPSPRAQAP*PLFIHCP*APRV TPPPQPVKCVVPAEVI/SPPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD
3341	8838	C	3604	846	989	MKSYNGMREMGDQASRRKLIKNW TDSKFLDMENGEQKKITPRPGVKI*
3342	8839	A	3605	3	232	KSLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHLGPEDTGTAS PYNRCS*RGRDHLGKRSSTRGTTLG PN
3343	8840	A	3606	303	400	
3344	8841	A	3607	3	404	LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSCSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVQAGLKLLISS

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						DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIYVVTNLNCRM YKLKTYHIPYYF
3345	8842	A	3608	2838	3122	FFFFFETKSCSVA\RLCSGTISAHC NLHLPSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA
3346	8843	A	3609	1	325	RLFFFETVSHSVT\RLCT*AILAHC NLCFPRSSNLASASQVAEITGACY YTQLIFVFSVETGFHHVVGQAGLELL T*VIHPPPPKVLGLQVSATVPGLII GTFSL
3347	8844	A	3610	3	398	GSLQPPPPRLK*FSCLSIPSSWDYKR LPPCPANFCIF\TELGFHQVGQAGLE LLTSGDPPASTSQTGVTGISHHAWP PEILSKGTMGKQMVNMLLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV
3348	8845	A	3611	3	311	AQTGMQW\DLCSVKPPPPRFRFSC LSLLSC*DYKRTPTCPANFC/DFVVE TEFHHVGQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IHK
3349	8846	A	3612	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGF\TVSARMVSIS *PRDPPASASQSAGDTGVSQAPV
3350	8847	A	3613	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3351	8848	A	3614	335	477	TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC
3352	8849	A	3615	135	804	GIDTILTLNQN*SLKTRQ*FTLIIF/IFF FFLRWSLALSPRPDCGLQWRDLGSL QAPLPGFTPFSCSLPSSWDYRCPPP RPANFFCNFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAGITGLSHCT RLFFF*WMESPSVTQAGIQWHDLS LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANF/CIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA
3353	8850	A	3616	3	285	HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS*VKRLSCLSLRLIWGCRQ VPPWLSFKLFWRQGLAVLPKLVSN SWPKMTLLPQPLRLGLQE
3354	8851	A	3617	3	575	PSLRHASHEAGWQCPLGQPLPGY TELRTLPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGGEKGPLD*GALLPGPNRS/S GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPAVP*LHRQPD AAGGTAGPSLPHLPPPLGLRVERS KPGGAAEEQGHPHLEHGP
3355	8852	A	3618	3	379	FFETESCSFTQAGVQWHDLTGTL*SP PPGFK*FSLSLLSSWDYRRPPRTA/ NYIYIVFLVETGFPPYVGQAGQKLLT

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						SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFL
3356	8853	A	3622	1	214	ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCSLSPSSWDYRRAPPLPH NF\CIFSRDGVSPCWPGWSQIS
3357	8854	A	3623	2	309	WCVFFETETHSAAQAGVQWCNLS LQPPPPGVKQFSCSLSPSSWDYRCA SPCLASFCIFSRA*GFTMLTCELLT SGNPPTSASQSAGIQGVSHHTWPSI F
3358	8855	A	3624	1	294	FFFFFFLRQGLTSLARLECSGMISAH CSLDLPG\SGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHQPVEQVRATCSKDGQ
3359	8856	A	3625	23	282	ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPILASQSAGI TGLSHRVQPTSS
3360	8857	A	3626	37	289	QWHDLGSLQPLPPGFRRRLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA
3361	8858	A	3627	70	362	KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHGSGMI EAPWALNPYLGLGPVQILETQK
3362	8859	A	3628	60	303	KLKNHHHHHHQQQQQKQQQQQKK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDTLRPTAIPIGL KMKLPL
3363	8860	C	3629	193	285	MLLVSYPRNSNRCQIQYHEAFCPIIF LRVL*
3364	8861	A	3630	159	483	DPTSFHGHYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG
3365	8862	A	3631	6	244	DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRPAN F*FLVETGFLHVCQAGLKLPTSGDP PASA
3366	8863	A	3632	2	262	NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVFLVETGFL/HV CQAGLKLPTSGDPPPSASQSTWITG VNHRARPQIGF
3367	8864	A	3633	1	1149	
3368	8865	A	3634	280	602	TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCSLSPSSWDYR HPPWPANF*FLVETGFHHVGQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF
3369	8866	A	3635	3	679	SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQSPPGTRDGLFPFPHSASTPP PTGASQPLTGTRGPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKPEACSGEQGNCVLAIEIVLGT QDPSAH*GGAGARGGGALWVTEG

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						VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGL\GLPKLCPHFHCSR ASPAPNSPFCFWSPTSGGPNPFPC
3370	8867	A	3636	1	334	EMESRSVAQAGVQWHDLGSLQPLP PGFKRFSCSLPSSWDYMRAP/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKJTR
3371	8868	A	3637	2	309	FFFFETRSRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANFDFLVETGFYHVAQTGLELLSV RDPALASQSAGIAGVSHRARPGCI F
3372	8869	A	3640	19	458	KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFANF*K QYIFQC*LPLTWLEIFSPFSRETGST KRCRLQDPGPSHFWRVVLGCLLWG QDRAPSWAPLQMQCLCHCLYL
3373	8870	A	3641	1	322	FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCSLPSTRDYRHPPRL ANFF/VFFLYL**GFATLAWLVLSH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI
3374	8871	A	3642	333	438	
3375	8872	A	3643	391	492	
3376	8873	A	3644	598	699	
3377	8874	C	3645	176	319	MCSAQPAFSDIIKSRHLGILGFEYK PRILCQKHMLRLLHSFQNFQR*
3378	8875	A	3646	2	50	QLLGTGMHHYA*LIF
3379	8876	A	3647	3147	3308	FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE
3380	8877	A	3648	1554	3041	GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTPCHF LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMG\FAMLPK LVLNSWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE
3381	8878	A	3649	280	444	
3382	8879	C	3650	135	377	MAGSWGAGQVQWLMSVIPILWEA KMGGSLPRSLRPAWVTQGDVSN RLFHSSASVLWLQATLTGTPKSLEYI TLAFRAK*
3383	8880	A	3651	1791	6596	CPKDTQILIFQKNNFSIRRFTHLAD FLKEFCLTFKKKGRSLL*FCCFVYI IF*KKFVCFCSSLHWCVPLPFFFFL Q/RSHSIGQAGVQWCNHSSLQPCPP RLKHPCTASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPHMYTLKTTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT
3384	8881	A	3652	3	332	ETESHSAQDGVQWRHLSSLQPPLL GFK*FSCSLSPSSWDYSCPSPT/P*LI CFFFFFLIEPGFHHFGLAGLELQTS DLPASAFQDAGITGMSH*TRPELLS LDHTPFT
3385	8882	A	3653	3	272	FETESHV/SPRLECSGVIFAHCSFCL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHHVQGAGLELLA*VI HPPQPPKVLGLHV
3386	8883	A	3654	1	272	ETGSRSTRLCSGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD
3387	8884	A	3655	249	906	RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLFPFP*CKSKPN* NDRRRSSVDSQIHLVGRESAHLPLAG LRVCVSLPLLARCFGQVLQGVPG WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH
3388	8885	A	3656	1	514	FFFFSRSL/NSVIQAGAQRDLGSLQ P/LLPPLKQFSCSLSSWDYRCPP PRLANFYIF/M*RRGFTILARLVLS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTQHQHWAQRGSKPM
3389	8886	A	3657	2	307	FFFFFFETESYSVTQAGVQWHDGLL LQPLPPLKQFSSSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVQAGS GTSDLKVICPPGLPKVLGITGCEPRR L
3390	8887	A	3658	79	91	NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL
3391	8888	A	3659	162	493	DGSSPPVAQAGVQWRDLGSLQAPP PGFTPFSCSLSRSWDYRRPPRPA NF/SCIFIVETGFHRVSQDGLDLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ
3392	8889	A	3660	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSCLI LPSSWDYRH
3393	8890	A	3661	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSCLI LPSSWDYRH
3394	8891	A	3662	17	287	KYHRIQCPNSGCEAVYSSVSGLK HLGSCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRL*SCGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DM*ATREVDVPIVMD
3395	8892	A	3663	3	567	DRKLYTRPGLPTFSQEV LHKWKT DIKKYHRIQCPNQGC EAVYSSV SGL KAHLG SCTLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDW FVVN PTTTKSFEKLMKIKQPAARRRKA EA AAQEQKVSKKGGSSLGIELPETEPS LRVGKDQRRNNE DW* CQPPCKEP/ GAGASASTVPESKAPKD
3396	8893	A	3664	1	184	SSRDILLCTDIASRGLDSTGV ELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT
3397	8894	A	3665	2	1748	HEARTKGNMALSAARLRLLPFVN SVCFLAP\RRGL\TVRSPDEPLPVVR IPVASTSGKLEQRQ\SRRLNLEPGRC LVRPGPLLVSARRPELN\PARLTLG RWERAPLASQGWKSRRARRDHFSV ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQEVA APEVVQ\PTTVQ SSTIPSLLRGRHVVC AETGSGKTL S YLLPLLQRLLGQPSLDSLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSRLLISLEQLS FLVLDEADTLLDESFL ELVDYILEK KDLAVFLYHLRLEAEVEVV EMLGP HGQPCPQHNSDISA YTYERTLMME QRSQMLRQMRLTKTERERE AQLVK DRHSALRLESLSDEEDES AVGAD KIQMTWTRDKYMTETW DPSHAPD NFRELVHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNC PAVRTEKNA QTRQTIIAETKTQKKDTEPRIEADL AVQYDNHYTNTKYCLCQMLREQL ESPQGRLLHAAQSSREIW
3398	8895	A	3666	1	1704	MALTRPVRLFSLVTRLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRLNLRPVLRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGL EPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVC AAE TGSGKTL SYLLPLLQRLLG\HPSLDS LPIAPRGLVLVPSREFF\QHLRAVA QPLGRSLG LLVRDL EGGHGMRRIR LQLSRQPSADVLVATPG\ALWKAL KSRLISLAEELSFLVLDEG\DTLLG*K ASWELVDYILAEKSHIAEGPADLED PFNPKAQLVLVGATFPE\GVGQLLN KVASPD AVTTITSSKLHCIMPHVKQ TFLRLKGADKVAEL\VHIL\KHR\SR AEKGLGPSGTGFVFCNSSSTVNW L GYILDDHKIQHLRLQGGQMPALMRV GIF\QSFQKSSRDILLCTDIASRGLD STGV\ELVVNY\DFPPTLARLTFHRA GESGPVWGAEGPG\TVISFVTHPW DVNPWFKKD*SLAARPKEEVL PGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; v=possible nucleotide insertion)
						AIPR*KKPFAPQSNPDFEQNLIK M
3399	8896	A	3667	2	222	RWSLTLFQAGMQWPNLSSLQPPPP RFKQF*CLSLPSSWDY WYTPPRLAN FCIFSRDGVSPCWSGWSRTPDLR
3400	8897	A	3668	1	29	
3401	8898	A	3669	2	206	VTQAGVQWLALSSLQPLPPG/LK*F YCLSLPSSWEYRHTPPHPTKFCIFFL VEGVSPYWP GWSQTPGLR
3402	8899	A	3670	3	139	TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAPCTPAWATK
3403	8900	A	3671	86	384	
3404	8901	A	3672	3	746	RQEEGLPPVDAIDDA SVEEDLAVA VAGGRLEEVSFLQYPARRRRALLR ASGVRRIDREEKRELQALRQSRDC GCHCDRICDPETCSCSLAGIKCQMD HTAFPCGCCREGCENPMGRVEFNQ ARVQTHFIHTLTRLQLEQEAESF/QG AGGPCPGQPTQPW*GGPGPYFPTGQ APHEQ*AGRQQLQQRHDVYSSTASS SASGTSEAPDCPTHPLPGPGFQPG VDDDSLARILSFSDSDFGEEEEED
3405	8902	A	3673	72	332	LPALET PRAQSKCSPQPSWVSRDY RCVPTHALANF*IFGEMGS/LLCCPR LISNS\WPQGILPPPPKVLGLQGSYS AKITTGFFLK
3406	8903	A	3674	33	396	RVWYLHRVTGRPASCLREVGP GDS LETASLREI WRSRRCRAT/ECSQQRL NHRLARQREHEARLRQQREQNSRY FTDV*HLRSKQAEWSSKTY YQRSM HAYHREKMKEEKRRSLWARLEKL M
3407	8904	A	3675	217	935	QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQRSMHAYQ REKMKEEKRRSLEARREKLRLQMQ EEQDLLARELEELR/REHELAKKN PGAAREAEISQRRAEETDC*TTFVR TLEKEQPETSRDGAGPSPEACRKL GNAE/MKKKKQQAESAEQGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQMEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP
3408	8905	A	3676	1	382	EMEPCFVS*TGV*WHDLSSLQPLP KFKRFSCSKIPE\SWDYRRTP/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMGDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRKWQF EHLNPA
3409	8906	A	3677	1	2456	MPTYPKLEKTDQSTSYTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNCVKTQCKTTQEC SLKWI FTMNETSDREDGLPKGHHVTDSEN DEPLNLNASDSESEELHRQKDS DSE SEERAEPASDSENEVDNQHGSDSE SEETRKLPGSDSENEELLNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEP RHQASD SENEEPPKPRMSDSESEELPKPQVSD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SESEPPRHQASDSENEELPKPRISD SESEDPPRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDSDRENKGEDTEMQNDSF HSDSHMDRKKFHSSDSEEEHKKQ KMDSDEDEKEGEEEEKVAKRKA V LSDSEDEEKASAKKSRVVS DADDS DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLT KIWEEEEKGETQVKEAEDSDDDNIK RGKHMDFLSDFEMMLQRKKSMSG KRRNRDGGTFISDADDVVSAMIV KMNEAAEDLKETFIDSGVMSAIKE WLSPLPDRSLPALKIREGVVLKILQE LPSVSQETLKHSGIGRAVMYLYKH PKESRSNKDMAGKLINEWSRPIFGL TSNYKGMTREEREQRDLEQMPQRR RMNS/DLVVRHPERDLEKVLTGEEK ALRPGDPGFVPRARVPMPSNKDYV VRPKW\NVEMESSRPGILKKGLSRLE KHKRRFAEQRLSKVHRAVKFSIEG NRMPL
3410	8907	A	3678	1	564	TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRRN\ DST GGQTPRRDLEKVL TGKEKALRPGD SLNLV/PRARVPMPSNKDYGVRPK MKCGNGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHAVENP AIEGNKMPIGDPCPGMCPPILL
3411	8908	A	3679	63	361	
3412	8909	A	3680	151	384	
3413	8910	B	3681	385	479	MAGAFRRRFASEVRAQGLESLLH GLRCAGSLRGGQSLPTTMWSPVKV GFE*
3414	8911	A	3682	3	698	VFFFFFFSGCTRGPLFESDFHRAPHRC GQGLAAP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGQAA\PPALVP GEGPSWSDPRGHRCSQATLPRVL AGPLQP*LS*LSL*DPPELRSL*PPL* LRLL**SLEPP*PLLDSNRFPP*PRSP PPLENPRPRPRPRKKPRPPAEP PTESVSDDLPAWSTRISVHLQTS WPSWASLASSMFFKVTKPNSRELW SS
3415	8912	A	3683	138	550	FCCCFTSSEHSLLAYGSCSPRRTEVL CAQQNPSETQAAPLAS\YMWK*PC NSRLKGPGLGEGWPES\RM TSGV TVPGGTSPGTRAGGS\PCPGGLS PEALRQ*GAGSGPRVSPGA/PGCGAPAA YGAASPCPQRCGAL
3416	8913	A	3684	2	555	FFFFFFLGAHVALYSNPTFTGLHIVV GKDWWPP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALRPPFPRVL GPGPFQ\AKAKQRYRPPQGSQ

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						APP/GPPRKQPQPLRKVSG*SGGCDL RLRHRPACPGRVCTLAQLEPATRM GWSYVVGQCGL
3417	8914	B	3685	95	371	MASDEGKLFVGGLSFDTNEQSLEQ VFSKYGQISEVVVVKDRETQSRSGF GFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPW*
3418	8915	A	3686	314	1055	SKCFHLHQVWKQKGEEYRVGTGYG GWSWISKTHVYRFVPKLHGNTNVN YRKSLEGTKNNMDENMDESDDRK CSRSPKKIKIEPDSEKDEVKGSAA KGADQNEMDISKITEKKDQDVKEL LDSDDKPCKERTNGSRR*HENRVT CKLSGEFSSRCGQC**GFSSKD*LQK ENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKD\STNSSKN LSESPVITKAKEGCQSDSDETRTEPK CK
3419	8916	A	3687	11	345	DSLTVASGVQWHNLISLQPLPPGV K*LFCLSLPSS*DYRRAPHPANFSF LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLNQ QTEKSLMVSG
3420	8917	A	3688	1	521	NPTKSCMLEG*NPHVHCK\REGAQA ITGMPI*KATKYLKYFLQKLCVPF QS/YESGVGRCTQDRHWGWHHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V/NKAPIMYHLTYRTHGQ MNP/YHKLPCHIQMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK
3421	8918	A	3689	1	281	ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSLLSSWDYRHAP/PRPG LFL*RWGFHQVQGVQDLELLNSSDP ASTSQSAGITSASHRAWPN
3422	8919	A	3690	3	314	HAEHEITELTATFTKFDNRDGNRILDE KEQEKMRQDLEERL\TRRVLQLET VLERVVAQIDALSSKLEMLEKKGV SLSLFTSFNIRAFKSLFSHYSSVTPI YL
3423	8920	A	3691	61	400	LVTGIWSATCLWVLLLLFEKGCPS VQRLQCS\NVITACCSNL\RGSDN PPTSASRVPGDHRCCHYTWANFLIF LWEMRSHCVGFRLLGLGTPVLKLQT ILOPQPPKVLGLQA
3424	8921	A	3692	33	436	REQEL/CKGKQKDGTSFGGEYGGWY KACKVDSPTVTTTLKNGALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGEVSGRAS CGKRQQQWPGRHR
3425	8922	A	3693	37	355	NSEYGGWYKACKVDSPTVTTTLK NLGALYRRQKGFEAAETLEEAAMR SRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS
3426	8923	A	3694	229	2000	QRERARPSGARRMYDTMSTMVYIK

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						EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILQSLLETCLKKKDDSN LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQQKLQKSE QSVAQLEEEKKHLEFMNQLKKYDD DISPSEDKDTDSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDEKTSBGHDPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNOG KYEEVEYYYQRFLEIFQTKLGPDDP NVGKTKNNLASCYLKQGKFKQAET LYKEILTRAHEREFGSVDDENKPI WMHAEERECKGQKDGTSFGEY GGWYK\ACTVDSPTVTTLNLGAL YRRQKFEAAETLEEAAMRSRKQG LDNVHKQ\QVAEVLN*PLRTLEKQP EPVESL\N\DVVKYESGPDG\GEEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRHR
3427	8924	A	3695	1	314	KVDSPTVTTLTKNLGALYRRQKGF EAAETLEEAAMRSRKQGLDNFTKQ RLPEVLNDP\ENMEKRRSRESL\NVD VV\KYESGPDGGEEVSMVKNWGM RKMKLGA
3428	8925	A	3696	2	450	VNKAGGLIYQLDSYAP/RAEAEKTF SYPLDLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSIKFRPRLTS NEKLMLASMFHS\IKFVVLADPRQ AGIDSLLRKIYEIYSDFAKNPFYSL EMP
3429	8926	A	3697	2	823	FGTRGKAAMAIFSVYVVKAGGLI YQLDSYAPRAEAEKTFSYPLDLLK LHDERVLVAFGQRDGIKRVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSIKFRPRLTSNEKLMLAS MFHSLFAIG\SQLSPE\QSSG\IGCLE TDPFQFH\CSRTLTGKIFVVLADPR QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP\IRCEPL*PQNPEA*SLEVA EKAG\TFGPRVHRLNPVMGPPQNPE SSLQQEYCLLTLPVEIPAALVSAP
3430	8927	A	3698	165	354	ENFGGKITNFAKLFGYILPYSHYFW CLEKNRNR/SLTLLPRLVSNWAQA FLLWPPKVLRLQA
3431	8928	A	3699	3	166	SETGFCHVAQAGLELLVSRSPASV SQS\TGISHQARPSISYFYDHSAPITH TDH
3432	8929	A	3700	1	421	ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRSLPN\SWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLT SFIQPRKHSEFPVMTCPSSNATESK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VGGRGPHGAIARLM
3433	8930	A	3701	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3434	8931	A	3702	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3435	8932	C	3703	282	445	MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTQDSVSKINKNNKTSIS NPE*
3436	8933	A	3704	170	607	WPSG*FQR*SMRLKYYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIHIII FEMESHVTRLECSGTISAHCNHL PGSSDSPASASPVAGTLIDACHHTW LIFYNF*VEMGFHHVVGQAGLKLLT *VTHPPRPSKVLGLQA
3437	8934	A	3705	3	231	FETESLFPRLCSGTISAHCNLRSLG SSNFWLIFCMLVEMGFHHVVGQTSLE LLTSSHPPTSFAQSARITGVSHRTW
3438	8935	A	3706	4	144	
3439	8936	A	3707	333	416	FTGLPCLFSPQNNVSLQSCIDLKFN NN
3440	8937	A	3708	1	1219	MAAVPELLQQEEDRSKLRSVSVD LNVDPQLQIDIPDALSERDKVKFTV HTKTTLPFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPPAPTKPDFD GPREKMQKLGEGECSMTKEEFAK MKQELEAEYLAVFKKTVSSHEVFL QRLSSHPVLSKDRNFHVFLFYDQDL SVRRKNTKEMFGGFFKSUVKSADE VLFTGVKEVDFFEQEKNFILNYN RIKDSCVKADKMTRSHKNVADDYI HTAACLSLAL EPTVVIKYLKVA ELFEKLRKVEGRVSSDEDLKLT RYYMLNIEAAKDLLYRRTQS/ALI DYENSNAKLDKARLKSVDVLA HQQECCQKFEQLS\ESAKEELNFK RKRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLFE
3441	8938	A	3709	527	724	TMKIGLGFSLVSINIFSPVELINFKR KRVAFRKNLIEMSELEIKHARN VSLQSCIDLKNN
3442	8939	A	3710	1	1220	QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRSGDLPGRPP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGGPDNEDYPLFRELWRYHF ATGVWHQMGTDG\YMPRELASMS LVLHGNNLLVFGDTGIPFGESNGND VHVCNVKYKRWALLSCRGKKPSRI YQQAIAINGSLYVFGGTTGYIYST DLHKLDLNTREWTQLKPNLSCDL PEERYRHEIAHDGQRIYILGDGTSW TAYSLNKIHAYNLETNAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAA\TTA\GCMYI HG\GVVNIH\ENKRTG\SLFKI\WLTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSLLELAWEKLLGAFPNLANLSRTQLLHLGFTQGLIERLK
3443	8940	A	3711	2	266	FLMESRSVTRLECSSTITAHCNLCPLVSSDSAVSASQVAGTTGMRHHAQLIFVFLVETGFHHVQGDLHLL/NIVHLPRPPKVLGLQA
3444	8941	A	3712	1	453	FKRAMDLVQEEFLQRLDFSQHSWLPARALVEEALAQRQVDPSGEIVELAKGACPWKEHLYHLESGLSPPVAIFVVIYTDQ/RWTVANIAGCPLPEPWRGLRDEALDQVSGIPGCIFVHASGFIGHRTREGALSMARATLAQRSFLPQIS
3445	8942	A	3713	20	891	RWNSRYDHHQRSFTETMSSLSPGK PWQTKLSSAGLIYLHFGAQVLAQL LGTSEEDSMVGTL YDKMYENFVEE VDAVIDNGISQWAEGEPRYALTTTL SARVARLNPTWNHPDQDTEAGFK RAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQIRPRWNPSGKIVE LAKRCHVPWKEHLLPPGNLGLSPS KWPIFFVIYTD/SRL/EQWRIQCVAQ/ VSPTHSQSRAA\LPEPWRGLRGTRP WT*FSGIPGCIFVHASGFI/SAVNATREGALSMARATLAQRLIPTNLLV
3446	8943	A	3714	176	450	
3447	8944	A	3715	1	472	
3448	8945	A	3716	418	1354	AAARRATCLGCRSCSGATARRASS WRTAPRVHSAVKLDGRRLASGS FDKTASRLLAWRRTFRGQKKTIIGG HGG*C/VTSFCWHPSNPEPICYGVIY GDKTIRIWECEYKNAIPLVNIKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLTNGNGCINILSYPELKA\ VQSINAHP\SMICINQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSDGKMLASASE DHFIDIAEVETGDKLWEVQCESPT\ SQVAWAPQKASAGHLPR
3449	8946	A	3717	1	296	LWDV/EELVCVGAFLRDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLWEVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS
3450	8947	A	3718	2	276	RSTFALVAPAGVQWHDNRSLOPLL PRFKQLSCLSLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ
3451	8948	A	3719	3	613	GLRALRRGQGLPGL*CCSRPQPSPR AQGHPSMGGPMQRTVTPRGMASV GPQSYGGGMRPPPNLAGPGLPAM NMGPVGRGPWASPSGNSIPYSSSSP GSYTGPPGGGGPPGTPIMPSPGDST NSSENMYTIMNPIGQAGRANFPLG PGPEGPMAAMSAMEPHHVNGSLGS GDMDDLKSSPGAVAGLSNAPGTP

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						RDDGEMAA
3452	8949	B	3720	134	471	MYAKGGKGS AVPSDSQAREKLALY VYEYLLHIGA QKSAQTFLSEIRWEK NIMPSPGDSTNSSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG*
3453	8950	B	3721	223	692	MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPPNLAGP GLPAMNMGPVGRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPIMPS PGDSTNSSENMYTIMNPIGQAGRA NFPLGPGPEGPMAAMSAMEPHHVN GSLGSGDMDG*
3454	8951	B	3722	228	292	XLARDDHERVMGRQPRASLRA*
3455	8952	A	3723	1	1753	MYAKGGKGS AVPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLSEIRWEKNITLGEPPGFL HSWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPTTPVCSLTNASSLSHGAGHL QRGGGTPQSA AAPSPVMGSMAPG DTMAAGSMAAGFFQGPPGSQPSPH NPNAPMMGPHGQPFMSRFPGGPR PTLRD\GSQPPAGPPWVSPSSPGA MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPRAYGGGMRPPPNL TRPACLPMNMGPRKFVGPWAQPP VEYSIPYSSSSPGSYTG\PPGGGGPP GTP\IMPSPGDS\TNSSSENMYTIMNPI GQGADRANFPLGPGPEGPMAAY\G \GMEPHHVNGSLGSGDMDG\L\REF PQAPVAGLSNAPG\TPRDDGEMAA AGTFHAPSSQSE\NYSPIGMTMSRV NWAAAPGALCGPRLLPRRCLRAK GLKVTPSGTLDSL ANQGLPMLGGP TRKTLTILLKTQGPRETFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H
3456	8953	A	3725	65	210	ATRAGLIFDDSEHDVWQDASSFRL IFIVDGWHPCLTPQQRRLPAI
3457	8954	A	3726	2548	3800	NSLILLFFFFRQSLTLECSGVISAH HNLHLPSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVGQAGLE LLTSGDPPAPTSQSM*ATTSGLILL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNSESYTSKEKNNLVPN AC*EITM*VATNCDF/SL*RSNY PKLFHNNETTSQKIHLKIKISRPATS GQWILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVDFD QNQQNKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSLLSSWDYRRVPPHP ANFCIFCR/GWGFVSPCCPGSSGTP VLKWRAHLSLPNC

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3458	8955	A	3727	2	217	SSPSPPHPPASPPSSPSPAPASPPPPSLP LPSPDFPPLSPCSSLSPFSSFPSPSPSP SPFSSRGPSPSDNFH
3459	8956	A	3728	25	396	ISGRSTFSLFSRQGLSALSPRLE\CSV AISAHCNLRPLPGSSN\GTTGA*HHTR LILYF/LAEMGFHHVGGAGFEVLTS SNPPASASTSARITGMSNRT\GHLFN FHP*MCYKYRCGSLAGRGGSRW
3460	8957	A	3729	80	460	YISLNVTTLHIFFFFLRQGL\CSVTQ AGV\QWCNLGSLQPLPPRFKNWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG
3461	8958	A	3730	1	316	FFFFFETESHISIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVGGAGLELL TPGDPPSSASQSAGMTGVTHCAWP RCLMF
3462	8959	A	3731	3	1717	RPQTLKGHQEKIRQRQSILPPPQGPA PIPSSTAAGIPRRPRIAWARR/WPLS EPGFRRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEAF KQLNQKKGKKKGKKKAPAEVLT LRARPP\PEGEFI\DCFQIKLAINLL AKLQKHIQNPQRR\DVVHFLFGPLD LIVNTCSGPDIA\RSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTQPQ DPQATPKLPGGT\IDELMQHMDENV DELIRKI\TT\TSRAQPQRHFRVERSOP VSQPLTYESG\PEDEVRA\FLEAKAFS PRIVENLGILGTGPQLFSLNKEELKKV CGEEGFRVYSQ\TMQK\AFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVFLFLYV YVFCIK
3463	8960	A	3732	1	324	
3464	8961	A	3733	1	581	MDKLLETYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIHGLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCQAQGV ALQTMKQEFNLNLVKQKQITEEQL EAVIADFSGLLEKCCQGQINQEVCF AEEGQKLISKTRAALGV
3465	8962	A	3734	39	1935	LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGCLENQLPAFLEELC HEKEILEKYGHSDCCSQSEEGRHNC FLAHKKPTPASIPLFQVPEPVTSCEA

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						YEEDRETFMKNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVLDAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECCKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTENPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSSEL MAITRKMAATAATCCQLSEDKLLA\ CGEGAADIII\GHLCIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSLTLV KAKGPQIPGGNNSEA VIARFPQAWL EK\CCQ/GPQEQEVCFAQEGTKLISK TRAAALGV
3466	8963	A	3735	95	272	RALQPDTTWE*GSQRRPWLPQVTN KPVL*SKTSKS
3467	8964	B	3736	344	1420	MLLKTVLLLGHVAQVLMLDNGLL QTPPMGWLAWERFCNINCEDEPK NCISEQLFMEMADRMADQDWRDM GYTYLNIDDCWIGGRDASGRMLPD PKRFPHGIPFLADYVHSLGLKLGIIY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLQADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDMLLIGNFGLSL EQSRAQMALWTVLAAPLLMSTDLR TISAQNMDILQNPLMIKINQDPLGIQ GRRIHKGSWMPKGSVCVPGCLRDPG TQDSQKGISHRSVHAASVQQG*
3468	8965	B	3737	49	2119	MALWTVLAAPLLMSTDRLTISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTSCLGQLNFTGSVIYEAQ DVLLS*
3469	8966	A	3738	139	536	QSLGFIPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPGFK QSSCLSPPGSWDHWRAAPHQANFA LLVETGSPHAAQASLKLSSSDPSA LASQSTGITGVSHHGQPYISHTLIIFI GKFY
3470	8967	A	3739	1	213	QFCLSLPSSRDYRHEQP/PLIFVFLV ETGFYHVQAGLELLTSGDPPALAS QSAEITGVSPRTRPNLKS
3471	8968	B	3740	75	729	MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQRLGH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLP LSLEEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ

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						PTFRTTYMAYHYFRSKGWVPKVGL KYGTDLLLYRKGPFFYHAX*
3472	8969	A	3741	1	2649	
3473	8970	A	3742	41	656	PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLLRALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVRVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHHKFA\VDRRVLITG SLNWTQTAIQNNRENVLITEDDEYV RLFLEEFERIWEQFNPTKYTFFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT
3474	8971	A	3743	3	267	FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVGQAGLELL/NLVI HPPRPPKVLGLQA
3475	8972	A	3744	2	430	FFFETGGAFVTQAGVQWPNLSSLQP SPPGFKPSSHLSLPSTWDYRYTPPCP ASFCIFVTDGTGFCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIESNVAPVF LFEDSTAIYVYYF
3476	8973	A	3745	2	316	EFLFFETEFCSVTRLECSGAISAHCK LCLLGSRHSPASASRVARTTGTRHH AQRIFVFSVETGFHRVS\RDGLDLL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF
3477	8974	A	3746	1	1053	
3478	8975	A	3747	1	3011	SLQRLPGLMHNLTQTFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETLRLO ALRKMPHIKHVDLRLNVIRKLIAD VDFLQHVLTQLDLRDNKLGDLAMI FNNIEVLHCERNQLVTLDICGYFLK ALYASSNELVQLDVYPVNYLSYM DVSRNRL\ENVPEW\VCESRKLGSF GILGHN\QIC\ELPARLFCN\SSLRKLL GQGHN\QLARLPERLERTSVEVLDV QHNQLELPPNLLMKADSLRFLNAS ANKLESPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEEELEIDLSG NKLKAIPTTIMNCRRMHTVIAHSNC HRGPFPEVM\QLP\EIKCVD\LSCNE\ LSEVTLPAENLPSPNCRLDLTG NPR PCPLITKPLELLNNIRCFKID\QPSTG DG\SGAPAV\W\SHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKNEEYVMVNTFIVMQRKLGT GQKLGGA AVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCHEELKRIKQHKAITEDGKV NGVTESTRILGYTFLHPSVVP RPHV QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNVPDALAAKKLCTLA QSYGCHDSISAVVVQLSVTEDSFCC CELSAGGAVPPSPGIFPPSVNMVIK

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						DRPSDGLGVPSSSSGMASVEISSELST SEMSSEVGSTASDEPPPGV\ALSENSP\ AYPSEQRCMLHPIWLSNSFQRQLSS ATFSSAFSDNGLDSDDEEPIEGVFTN GRRVEVEVDIHCSRATEKEKQQHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEIMKHHQEQQ QQQQPPPPQLQPQLPRHYQLDQLP DYYDTPL
3479	8976	A	3748	1	246	LPTLECSGMISAHCNLR\LPSSSDSP\ ASASQVAGITSAHHYAWLVFVFSV EMGFHHVGQGWRSRLDLVIRPPQPP KMLGLQA
3480	8977	A	3749	153	527	LLVFY\PTPSLKGGRLQ\LDMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEYFPEQNSLH\DRRD RGPPRDLSLPAAPPSPAATGFWSPSR GSWEGCDCWEALPTGHA\VICCFS
3481	8978	A	3750	2	377	IPAASTFFCF\LRQSLTLWPHAGVQW CGLSSLHPPPPGFMLFSCLSLPSSWD YRRPPRPAKFSVFLVETGFHRSVQ DGLDLMTSDPPALASQSAGITGVS HCTRPKEAYFYFLALDPRCKDGVR
3482	8979	A	3751	2	294	LFLHADRLEYSGMTISHLQ\PTPGA QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA\RAGLKLLGSS DPTASPSQSDGITGMSHHSCPSTF
3483	8980	A	3752	80	267	RQGLTILPRLVLNSC/RLKLSSHLSLP KYWDYRQEPCLAIS\IFFKKSLIYY LNLAILYFKCK
3484	8981	A	3753	1	972	
3485	8982	A	3754	1	283	PKPQEIELPEAKNR\PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERSPPK REPGLWRLGTPLCPHDSSG
3486	8983	B	3755	346	472	XRNMNILQYCPSSDMWTLFETCDV HIRKQQMVSVEETIYIVGG*
3487	8984	A	3756	1	1346	MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALSQAAGGP EVQQLRGLSAPGLRLVLD\FINAGGA REGWLLGPRGEKGGGVDEDEEMD EVSLLSELVEAASFLQVTSLLQLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARM\TGTPV LVALGDFLGGPLAPHPYQGEPPSML RYEEMTERWFPLANNLPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNFVAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMNILQYC PSSDMWTLFETCDVHIRKQQMVS EETIYIVGGCLHE\RGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS

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						GLNFDLCAP
3488	8985	A	3757	3	358	TNSMPPMMSMSYRICAMLKGE/DV QALRAHQQRNVKHMRLMDRGL PCHPLPPANINPIRVR/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNYLLS CLTIPFIASFVSLFEKLSAILD
3489	8986	A	3758	1	164	GSTTPAMEFASLFFKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT
3490	8987	A	3759	3	280	FFFETESHSA\RLRYRGITLAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFV\FLVQMGFHHFGQAGLELPN LGIHPTSASPKCWDLPA
3491	8988	A	3760	3	516	AQHQP MNIFYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPPSQVNYIASQ PRWKRNCTKLQIQEKAAQEVK\LA KPFYQNKDITKEEYKEIVRKAVDKV CHSKSGEVNSTKVGN\VKAYVDQ YEYSRKGSQRKLWEGPVSTGKN
3492	8989	A	3761	173	411	
3493	8990	A	3762	438	789	LTWSTPVLPAAPAGKYGNQFQG PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKQLQIEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKAVDKCVLLECSIQKM
3494	8991	A	3763	1097	4669	ILLGTSCGYALAHTQEGEEKKQTS GTSNTRGSRRKPAMTTPTRRSTRNT RAETASQSQRSPISDNNGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLLKKLRSSVAPEKSSS NDSVDEETAESDTSVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSESC AQDLPVLVGEEGEVKKLENTGIEA NVLCLESEISENILEKGGDPLEKQDQ ISGLSQSEVKTDVCTVHLPNDFPTC LTSESKVYQPVSCPLSDSENVESV VNEEKITESSLVEITEHKDFTLKTEE LIESPKLESSEGEIIQTVDRQSVKSPE VQLLGHVETEDVEIATCDTFGNED FNNIQDSENNLLKNNLLNTKLEKSL EEKNESLTEHPRSTELPKTHIEQIQK HFSEDNNEMIPMECDSFCSDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQSPESPKDTI DKTKKPRTRRSRHFSPSTTWSPNKD TPQEKKRQSPSPRETGKESRKSQ SPSPKNESARGRKKRSQSPKKDIA RERRQSQRSPKRDTTRESRRSELS PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDGQRRERERRTRK WSRSRSHSRSPSRCRTSKSSSFGR DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDPEKQENENTRKEKNDIH LDADDPNSADKHRNDCPNWITEKI NSGPDPRTRNPEKLKESHWENRN ENSGNSWNKNFGSGWVSNRGRGR

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						GNRGRGTYRSSFAYKDQENENRWQ NRKPLSGNSNSSGSESKFVEQQSY KRKSEQEFSFDTPADRSWTSASSW AVRKTLPADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPMNVMQQQM NAQHQPMMNIFYPVGVHAPLMNIQ RNPFNHQPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SAVSSKTDKKFAKFQEKAAQVVKI WANPFPYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKAAANLVKA YVDKYKYSRKGSLKKTLEPRVTE KDLG
3495	8992	A	3764	108	253	
3496	8993	A	3765	2	283	RRLFFFETESRSVSRLECSGVISAHC NLH/LPGSSNSPGSASRVAGITGACH HAQLIFVFLVETGFHHVGGAGLEL L/NLMICPPQPPKVLGLQA
3497	8994	A	3766	1	290	RSTFFFFLERVYCSVTRLECSGTIS AHCNLRPLPGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV
3498	8995	A	3767	234	1449	EPGTHDPLFLQGLLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGKLH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPNTLT*PIVHFIFS APTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN KTKHDVKFPLDSTGSELKQKHSIT GIPPDSPRRGGPAGPYQQSQRLEL YQAATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR
3499	8996	A	3768	1	8157	
3500	8997	A	3769	1126	1355	
3501	8998	A	3770	1	1611	MGSRCNLNPPPAHSDDTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRLALQSQPQERRHVGWNSTR GLLPASLPGTASSQSASATASAAALP LKVTGPLARNPTTPWTAALALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN

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						KTKHADVKFPLDSTGSELKQKIHST GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVNTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKGKPEDVMPSVKGAQERL PTVPLSGMYNKSGGKVRLTFKLEQ DQLWIGTKNGTEKLPMSIK\NVVS DPI\EGHEDYHNDGRFQLAPTEA\SY YWVYVWPTQYVDAIK\DTVLGKW QYF
3502	8999	A	3771	482	631	AGGWGPQAPDTPWVGPAQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALL
3503	9000	A	3772	1	1579	
3504	9001	A	3773	3	486	DRYMLTRDYLTVKVWDLNMEARP IETYQVHDYLRSKLCSLYENDCIFD KFECAWNGSDSVIMTGAYNNFFRM FDRNTRDVTLEASRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKIL\HTAWHPAENIHLPAATNN LLHLSRGKVNSDMH
3505	9002	A	3774	72	1317	KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTRGCFHGDRGRACAAL RRWPWRQLRGWGFEVPAPLLRTP AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILED NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPS VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPRSPQAQEA\PNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTLQEPGKPKDEVLR YPDRSLSPEDAESLSVLSVSPDAN QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETS\LDVSSKQ LSPKALAPFQLGN
3506	9003	A	3775	1	350	FGTRKPGAVGAGEFVSPCESGDNT GEPSALEEQRGPLPLNKTFLGYAF LLTMATTSDKLASRSKLPDGPTGSS EEEEEFLE\PPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV
3507	9004	A	3776	3	318	RRGLTLSSRLEYSGIKTHWNHLL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHAWPAV ALLWIN
3508	9005	A	3777	4	378	ARNHHDLCFKKAILFFEMESCSVSQ AGVQWRVFGSLQAPPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLDRMVVIS*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG
3509	9006	A	3778	19	418	VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCSL PSSWDYRRPPRLANFFVFSVETGF

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						HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV
3510	9007	A	3779	3	331	CFIFYFILFYFETESRSVAQAGVQWR HLDSLQAPPPGFTPFSCSLSPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS
3511	9008	A	3780	659	1092	AYNIFQFANRTNTGENLPKTLVIKYYI SSTFRSFFFFFFFLRQSRVAQAGVQ WRNLGSLQPPPGFTPFSCSLSPSSW DYGRPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT
3512	9009	A	3781	8	295	GRVSLRHQAGVQWRSLGSLQAPPP RFTPFSCSLRLRSWDHRRPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY
3513	9010	A	3782	1474	1870	SARGITGVSHCTRPFSSFFFFFFFETE SHSIAQAGVQWRYLGSQPLPPGFK QFACLSLSSWDCHAPRPANFLAF LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFFLLKNIFKFLN FC
3514	9011	A	3783	60	560	SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLSLQPPPGVKRFSC LSLPSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPPASA SQSAGITSVTHRPLPEDSAFYQCRL NLWQSPLECRCSLVLKT
3515	9012	A	3784	3	230	FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH RLIFVFLVETGFHHVGQDGLDLLTL
3516	9013	A	3785	3	4117	
3517	9014	A	3786	1	457	FPVRNLDLSTYICIGQKEEQLPSEYEL YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERP/PK AGHSEHHPDLGPAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT
3518	9015	A	3787	1	298	NNQESCSVTEAGVQWHDLSLQPP PSGFKQFS/CAQLSSQDHRHMPPCP ANFYVFLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK
3519	9016	A	3788	3	286	FFFFLFETQSHSHIRLECSGVISDYC NLCLPSSSDSLVLASGVAGTMGVR HNARLIFVFLVKMRFHVGPRLGP QIPWTGIWIPSHFGPPQSA
3520	9017	A	3789	1	1422	
3521	9018	A	3790	353	470	IPGVSLYSLFSLAQNIPQSTEILKKL MTTNEIQSNIYT
3522	9019	A	3791	1328	1615	VSLFHAGVQWCDLSSLPQPPPGFKR FS/RLNLLSSWDYRRPLPHPSTFCKF VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT
3523	9020	A	3792	2	114	CQPGFVMKGPPAHRVQCQALNKWE

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						TELPSCSR\VCLEPA
3524	9021	A	3794	1940	2062	
3525	9022	A	3795	785	892	
3526	9023	A	3796	1	2745	
3527	9024	A	3797	1	3297	
3528	9025	A	3798	1	2202	
3529	9026	A	3799	1	2868	
3530	9027	A	3800	1	3237	
3531	9028	A	3801	1	2001	
3532	9029	A	3802	1	2982	
3533	9030	A	3803	1169	3269	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPTVSAQNLLK LMSNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNLIFDK PDKNKQWGKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIK KSFCTAKETTIRVNRQPTWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAACK HMKKCSSSLAIREMQIKTTMRYHLT PVRMVIKKSGNNRCWRGCGEIGTL LHCWWDCKLVQPLWKS VWQFLRD LELEIPFDPAIPLLG IYPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTM EYYAAIKKDE FMSFAGTWMKLETIILRKLSQGQK TKHRMYSLIGGNLTMRTFGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGT CIPMQQNCTLCT CTLKLV
3534	9031	A	3804	2821	5793	
3535	9032	A	3805	2	256	KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARHARLFF LYFLVFHRVCLDGLDLL/NLVIHLPR SPK VWGLQA
3536	9033	A	3806	1	2406	
3537	9034	A	3807	139	6503	
3538	9035	A	3808	1	3204	
3539	9036	A	3809	77	277	PHPTPCSCFPW SASSPLT*THQALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC
3540	9037	B	3810	21	219	MMPRSSRTKSCRSSCVAWSSCMKE NKELRAEAERLGHELQQAGLKTK AEQTCRHLTAQVRS LGGT*
3541	9038	A	3811	1	6359	MTLHATRG AALLSWVNSLHVADP VEAVLQLQDCSIFIKIIDRIHGTEEGQ QILKQPVSERLDFVCSFLQKNRKH SSPECLVSAQKVLEGSELELAKMT

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						MLLYHSTMSSKSPRDWEQFEYKI QAELA VILKFVLDHEDGLNLNEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLETEKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMRLHETLKQ CQDLKTEKSQMDRKNINQLSENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSQ LQDNPPQEKGEVLGDVLQLETLKQ EAATLAANNTQLQARVEMLETERG QQEAKLLAERGFEEEEKQLSSLIT DLQSSISNLSQAKEELEQASQAHGA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAQEKQAQLAQTLLQQE QASQGLRHQVEQLSSSLKQKEQQL KEVAEKQEA TRQDHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAEELQLRSEQQKA TEKERV AQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQRCI SELKAETRSLVEQHKRERKELEER AGRKGLEARLQQLGEAHQAETEVL RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKKV AGIESHSELQISRQQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLET LVRKAGEQ QETASRELVKEPARAGDRQPEWLE EQQGRQFCSTQAALQAMEREAEQ MGNELERLRAALMESGQQQEEERG QQEREVARLTQERGRAQADLALEK AARAELEMRLQNALNEQRVEFATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQEQEAD SLERSLEAERASRAERDSALET LQG QLEEK AQELGHSQSALASAQRELA AFRTKVQDHSKAEDEWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRL LQAETASNSARAAERSSALR EEVQSLREEAEKQRVASENLRQELT SQAERAELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSAKH LCQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQLRAEKASYAEQLS MLKKAHGLLAENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAAQSTARELEVMT

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						AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTQKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NQELQEQLRSLEQLQKENKELRAE AERLGHELQQAGLKTKEVAEQTCR HLYLPRLRSLEVAQVAHARPSSFRD LGKFQVATDALKSREPQAKPQLDL SIDLSDLSCIEGTPLSITSLPRTQPD GTSVPGEPASPIQRLLPKVESLES YFTPIPARSQAPLESSLDSLGDVQD SGRKTRSARRRTTQIINITMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPGR NSFYMGTCQDEPEQLDDWNRIAE QQRNRVCPHLKTCYPLESRPSLSL GTITDEEMKTGDPQETLRRASMQPI QIAEGTGITTRQQRKRVSLEPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTSRGTRRSPRIATTTASAA TAAAGATPRAKGKAKH
3542	9039	A	3812	241	6884	LSGITKMTLHATRGAAALLSWVNSL HVADPVEAVLQLQDCSIFIKIHDRIH GTEGQQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAEALAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDLSEFKLREFASHLQQLQDAL NELTEHHSKATQEWLEKQAQLEKE LSAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQAELLAERGHFEEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAQKEQAQLAQ TLQQQEQASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELSRKVEELQ ACVETARQEQHEAQAQVAEELQL RSEQQKATEKERVAKQEKDQLQEQ QALKESLKVTKGSLEEEKRRAADA LEEQQRCISELKAETSLVEQHKRE RKELEEEERAGRGLEARLLQLGEA HQAETEVLRLRELAEMAAQHTAES

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						ECEQLVKEVAAWRDGYEDSQQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQQN KLAELHANLARALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWL EEQQGRQFCSTQAALQ AMEREA EQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGSGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALET LQGQLEEK AQELGHSQSAL ASAQRELA AFRTKVQDHSKAED EW KAQVARGRQEAEKNSLISSLEEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLLQAETASNSARA AERSSALREEVQSLREVEAEKQ RVA SENLRQELTSQAERAEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCCQLQAEQAAAEK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQ LRA EKASYAEQLSMLKKAHGLLAENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAAQS TARELEVMTAKYEGAKVKVLEERQ RFQEERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFQAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQONQELQ EQLRSLEQLQKENKELRAEAERLG HELQQAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\PQLDLSIDSLDLSC EEG\TPL\SITSKLPRTPDGTSPGE PASPI SQR LPPKVESLES LYFTPIPAR SQAP\LESSLDSLGDVFLDSGRKTR SARRRTTQIINI\TMTKK\LDV\AEPD/ SAPNLSFY S\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCQDEPEQLDDWNRIAE LQQRN RVCPPHLKTCYPLESRPSLSLGTITD EEMKTGDPQETLRRASMQPIQIAE GTGITTQQQRKRVSLPHQGGPTPE SKKATS\CFPRPMTPRDRHEGRKQ\ S TTEAQK\KAAPASTKQA\DRRQSM\ AFSILNTPKKLGNSLLRTG*PQRKA LSK\ASPNT RSG\TRRSRPIATTTASA ATAAAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGQCG RSPYLASF FLKAKSLLHHNQI

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3543	9040	A	3813	1	3466	EKEKAAKLEILQQQLQVANEARDS AQTSVTQAQREKAELSRKVEELQA CVETARQEQHEAQAQVAEELQLR SEQQKATEKERV AQEKDQLQEQLQ ALKESLKVTKGSLEEEKRRAADAL EEQQRCSLKAETRSLEQHKRER KELEERAGRKGLARLQQQLGEAH QAETEVLRRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEAAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELA ELHANLARALQQVQEKEVRAQKLA DDLSTLQEKMAATSKEVARLETIV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGGQ QEERGQQEREVARLTQERGRAQAD LALEKAAAELEMRLQNALNEQRV EFATLQEAALAHALTEKEGKDQELA KLRGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQQGLEEKAEQELGHSQSALASAQ RELAAFRTKVQDHTAEDEWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSSQ KLEERLRLQAETASNSARAAERSS ALREEVQSLREEAEKQRVASENLR QELTSQAERAELGQELKAWQEKF FQKEQALSTLQLEHTSTQALVSELL PAKHLCCQLQAEQAAAEKRHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVAEQERTAQLRAEKASYA EQLSMLKKAHGLLAENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREASTARELE VMTAKYEGAKVKVLEERQRFQER QKLTAQVEQLEVFQREQTKQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQEAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAKTHYDAK KQQNQELQEQLRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAET CRHLTAQVRTLEAQVAHADQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGTPLSITRSGGSLPPY VCLWSACCLSGCILVR
3544	9041	A	3814	35	266	
3545	9042	C	3815	383	628	MDPSAGVTIVTCLASLFSGRVLRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI*
3546	9043	A	3816	2	513	DIYGGDYERFGLQGSVASSFGNM MSKEKRDSSISKEDLARATLVITITNI GSTA\WLCALNENIDRVVFGNFLR INMVSMKLLAYAMD FWSKGQLKA LFF/VEHQGYLGAVGALLGTVQND

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						LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPSHLWQMNLLGFC
3547	9044	A	3817	29	175	KSRPGTVAHACNPSTLGSRGGRIPA QEFKTSLGNTVSEPCLYLRKNN
3548	9045	A	3818	171	419	KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENG\HHPKKQSDGMEEYKTFGL GLTNVKKNR
3549	9046	A	3819	2	1209	WPSKETAFNLTTQMPCLOASTWS SYEHNSSEYLLREHVSELDSSFHSV LSLPSDVPLHFHFETLLKKTEIKGNL AENKFVDEYIISPSPVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKL\KEFDFHHTESGSH SNFTAVSNVNVLSRIQNSSRNTARR R\LRSESSYD\DNIVIPMSL\AVAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRNRSAYS KNVEGQDLLLKEYPNFSSSQCA AASPPGLPSENQDLCAYGLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGTSTV PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR
3550	9047	A	3820	7	447	
3551	9048	A	3821	1	373	EQQVLRSTCLGVGAKV/L\VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMILLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCQ TVGMRT
3552	9049	A	3822	1	708	TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLVEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMILLDILPSR GPKAFDTFLDSLQEFPPWVREKLKK AREEAMTRPCLAVDRLTGIPSHILN SSPSDRQINQLAQRLGPEWEPMVLS LGLSQTDIYRCKANHPHNVQSQVV EAFIRWRQRFGKQATFRTL\DNGLAR AVEVDPSLLHMLE
3553	9050	A	3823	791	1090	HFLHGPLAQEDKSERERWQ\HLAD\ LADFALA\MKDTLTNNNQSFNNFM LRIGEHTPAGLPSRRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T
3554	9051	C	3824	172	243	MRPSHGPSEQLCSTLSPPIKPRPT*
3555	9052	A	3825	1	615	
3556	9053	A	3826	1	596	PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEP\AVARC\SHLLV KHSQSRARPSSWRQEKITRTKGGGP GSLINGLHPEDSSSGEEDFVESLASQF SDCK/SSAKARG\DLGAFQKQVRLQ KPFLKTPRFAL\RTGGDERGPCFTD\ T

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						SGIHILPHLSEGGEPRPGLGAGQGG
3557	9054	A	3827	1	295	ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSHLSSLSSWDCRHMPPNL A/NF/CVLRDDKISPCPGWASNPPG LKQCIGILKYPQALTPYELINIWEGI
3558	9055	A	3828	131	771	MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGP/YPLVSSSSKSG RTMPNILDIIASA VENKIPPSKTSKI NVKPELKEEPEESIISAVDENNKLYS DIPHSWICDALQKAFDKEELLKQQ ASNLHEQKKAGVIFEAEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLDNRVPTCEKIEA ILKELEKPAP
3559	9056	A	3829	1	655	MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEMWRPNNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCCLKLAEAGETGRILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFGLYIIRM CIFKKCQSASGSKTRMQGYLE
3560	9057	A	3830	1	515	LTLENQIKEEREQDNSESPNGRTSPL VSQNNEQGSLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDIIASVVENKIPPSKTSKINV KPELKEEPEESIISAVDENNKLYSDIP HSWICEKHILWLRIIIIAVIGSFSKNV GNKDSLQWFLVCIRK
3561	9058	A	3831	6	226	RKGGFFVDLFVR\VSNQVAVNMYK QLGYSVYRTVIEYYASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI
3562	9059	A	3832	37	611	SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHVTALSVAFEFRRLLGLAA KLMELLEISERKGGIFLVDLFVRV SNQVA\VNMYK\QLGYSVYR\TVIE YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIPLPHPGGGLEDH
3563	9060	A	3833	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
3564	9061	A	3834	2	1203	LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGMVGMGQ KDSYVGDEAQSKRGILTLKYPIEHG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPEALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDLYANTVLS GGTTMYPGIADRMQKEITALAPST

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						MKIKIIPPERKYSVWIGGSILASLST FQQMWISKQEYDESGPSI\VHRKCF
3565	9062	A	3835	3	412	SRFPEGLFQPFPG\MKSCGIHETTF HSH\IKFDVAIRKDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSVGSILASL STFQ\QMWISKQEYDESGPLHSSTA KCFLNGLSQIA
3566	9063	A	3837	3	480	SHITVLTNLVNGLNAPVKRHRLAN WIKSQDPPVCFIQETHLTCRDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDFKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH
3567	9064	A	3838	1	834	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP T/KKSPGPDGFTAIFYQ\MLEVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESI M
3568	9065	B	3839	1	543	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP TKK*
3569	9066	A	3840	1	1470	MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPKEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRFIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEIITNCLSDHSA IKLELRIKLTENRSTAYNLNLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPIRSEIEAIINSLPTK KSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASIILIPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRRI SIDAEKAF
3570	9067	A	3841	2807	4148	
3571	9068	A	3842	2	1516	WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ

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						EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRKIKLTQNRSTTWKLNLLND YWVHNEMKAEIKMFFQTENENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAIINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPFLLKTLNKLAIIDGM YLKIHAIYDKPTANVILNGQKLEVF PLKTGTROGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLSNFSKV SGYKINVQKSQAFLYINNROTESQI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNVP CSWIGKINIMKMAILPKETPSHMQR HT
3572	9069	A	3843	3	120	FIIDKKQKQLKSPSIDEWIKWMWYI HKIEYHSAIKGKIF
3573	9070	A	3844	2	244	SRLSFPSSWDYICAPPHLANFCIFLV ERSVAMLPRLVSSSWAQAILPPWP PKAQGFTGMGHHAQSAAGLYIFSG LGSNAI
3574	9071	A	3845	1	2616	
3575	9072	A	3846	1	773	QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTP LLSKVDDIHAICSLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANLAKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV ERLLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQKGPSCGQ NKSTAAFN
3576	9073	A	3847	1	422	CGRVRACGRVREPSSQIHNNMANL FIRKMNPLLYLSRHTVKPRALSTF LFGSIRSAAPRGCGNPGA AVRSL SPGLPA/HHL PACGWGFKKQDCPLR KRCKDCYL VKRRGRWYVYCKTH PRHKQKTRCRTLFPPEST
3577	9074	A	3848	1959	4060	RFFSFFFFFETESHVAQAGVQWCN LGSLQAPPPGSRHSPASASRVAGTT GAHHHARLIFVFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI
3578	9075	A	3849	1	1320	
3579	9076	A	3850	1239	1733	ALFFSFFFFFETESRSVAQAGVQW RDLGSLQAPPPGSRSPASASRVAG TTGARHRIFVFLVEMGFHRDLDFP TS*SAIQLQA*ATAPGPFLFFFFFFF LRRSLTLLPRLECNGAILARCNYL LGSSNSPASASRVAGIAGMHHR LIFCILVEMGFHHL
3580	9077	A	3851	131	436	VTHLHQKKGSVFFFFFFFETESCPV

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						AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIF\CLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP
3581	9078	A	3852	56	192	KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF
3582	9079	A	3853	1	230	FQLHQH\LLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVQFFPLRVRDPG VKSSC
3583	9080	A	3854	3	126	SCCGVGNQFKGPGGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER
3584	9081	A	3855	1	1021	MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWPK KVGKLRSTVVKQLPKTFQAISSTET KDQGPIVPAPVKGEGPIVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGS MVSEPVKNQGLSG\ PGPVKDQDVVVPEH*KGHDSAILV APW*RIKGP\VVPRSPVKNQDPILPV LVKDQGP\TVLQPPKNQGRIVPEPLK NQVPIVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGRLR\PCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPLLQIQHFGPP
3585	9082	A	3856	1	448	SSRKDQGLVVSGPVKDQDVVVPEH QRSRFSCQVVAPVKNQGPVVPESV KNQDPILPVLVKDQGP\TVLQPPKNQ GRIVPEPLKNQVPIVPVPLKDQDPL VPVPAKDQGP\AVPEPLKTQGP/KGT LSLPTVSPLPRV\MIPTAPHTEYIESSP
3586	9083	A	3857	1	573	DPQFISGSPESP\IRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNL\SGHNAINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQ\SESRL\TAEADKP\IKV YREDDTATEETHPVSWKPEI\KRKR FLMNVEFFLSLFFSF
3587	9084	A	3858	1	589	EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLGDTRGFLIDGYPREVVKQGE EFGRRIGDP\QLVIGKE\CSPDT\MTN RL\LQRSRSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIF
3588	9085	A	3859	1	557	KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLLNEAEL LLALAHEFQMKTVTVPWRTTPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM
3589	9086	A	3860	323	656	NEELMPKGRLYPPLANIQEVSINIAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KVTEYLYANKMGFPDTQEPE\DKA KYVK/EKGTWAEWNMDSLLPDVY EWPEICNQAPPVNTIEALPLINTFV CSRGTPFFQTRKR
3590	9087	A	3861	1411	1799	GYLQFSFSFFLFFFFFFFLRWSLTLS PRLECSSVISTHCNLRPGSSDSRAS ASQVAGTTGAHHHARLIVCVLVER VFHHVGQAGLEVLTSGGPPTSASQS ARITGMSHHTRPVICSFQFSDLPEHY F
3591	9088	A	3862	1	1007	MDGGHLFSNLTGKEEVIHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAIASIVSSS ASRLKSVWHIPCPHFLLLRPQLKE AQRKKQLEERCERVEESIGNAVLT WNNEILPNWETMWCSRKVRDLWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAKERWRSSTGGSEVENE GLCVAVCAQQGHVGMFGSDEP SAVSPCEKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFENLPKLFAHFKK NNLTPDIYLID/W*FRLLVGC
3592	9089	A	3863	1	1857	GIPAADR\EASLELIKLDISRTFPNLCI FQGGGPYHMLHSILGAYTCYRPD VGYVQGMFSIAA VLILNLDTADAFI AFSNLLNKPCQMAFFRVDHGLMLT YFAAFEVFFENLPKLFAHFKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLTRLPELPAEE LFGPSIATIQMSRNKKWAQVLTAL QKDSREMREGKSVPTLRLQREFAL GTNQSPMPRPLCCFRLTPGQPRRTD AL
3593	9090	A	3864	1	840	
3594	9091	A	3865	3	288	FFFEMESLYVTRLNCSGTITISVHC NLCFPGSSDSPASASQAGITGTRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL
3595	9092	A	3866	285	489	GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHVSQASLQL/RDLSLPS SWDYRRPPRPANFFVFLVEMGFH HLNKAIKSFACNEIQPLSAVSARA GWGVFEYVSVYFLCSNSDYFSSNPS IANWMREWPLRLSLF
3596	9093	A	3867	3	425	
3597	9094	A	3868	1	156	APHPAN\FAFLVEMEFHDVGGQDL QLLASSDLPASASQSAGITGVSHCN WI
3598	9095	A	3869	1	526	LAESGEGVLVSGGSLRLPCIASRFIF SSYYMSGVRQAPGKLEWVSFIRA TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLGDWPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGLVLM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AEECVSGAVSVGLQDRCTAANRAIFSLEL
3599	9096	A	3870	2	353	
3600	9097	A	3871	136	315	FKYVLSFLFLASGDGESLDEDESEFTLARDFEIGHFFRERIVPRAVLYFTGEAIEDDDNV
3601	9098	A	3872	132	1552	GDKNIQMADHSFSDGVPSDSVEAAKNASNTEKLTQVMQNPRVLAALQERLDNVPHTPSSYIETLPKAVKRRINALKQLQVRCACHIEAKFYEEVHDLE RKYAALYQPLFDKRREFITGDVEPTDAESEWHSNEEEEEKLAGDMKSKVVVTEKAAAATAEPPDPKGIPEFWFTIFRNVDMLSELVQEYDEPILKHLQDIKVKFSDPGQPMFVLEFHFEPNDYFTNSVLTKTYKMKSEPDKADPFSFEGPEIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGGRGTVRTITKQVPNESFFNFFNPLKGKSVASGDGESLDEDESEFTLASDFEIGHFFRERIVPRAVLYFTGEAIEDDDNFEEGEEGEEEEELEGDEEGEDEDDAEFNPKVLIFVLLIHTFSRRDPSQPAECKQQYAEAGAWQTGCRDSRPVGGASVLAQAQSRGQSLHLTRFQVHDFHFHFSFLLILINLYSGN
3602	9099	A	3873	171	324	
3603	9100	A	3874	3	383	
3604	9101	A	3875	2	314	FFFFISALKALFAFLQILLFQVNVLRITAHIVISFINLLSVTPSKAFLLLAFIFCREDYSFTAYATISYLKIGPKANLLNNEAYVITMQVTKSTQNSFRVNGY
3605	9102	A	3876	3	319	TESRSVPQLGVQWRDLGSLQPPPPGFTRFSCSLPSSWDYRHTPPRPANFLVFLVETGFRHVGQTGLELLTSGDPPASASQSAGILCVLCTSTLGNHREHIYRMV
3606	9103	A	3877	118	1341	
3607	9104	A	3878	1	214	GFTSSLACMQMGEMFMGFTCQTHLLALGCALFTAYLGVGMANFMAEGTCERRIVGKKKASITKDHQQRRI
3608	9105	A	3879	1	176	MRTFALLTAMLLLV/HAQAEPLQARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA
3609	9106	A	3880	3	125	AASTFLFPNLKNSLRGSLRTFSSVTNVRKTALTWLN SQDI
3610	9107	A	3881	1169	1512	YTQKNWHLFCFIFLRWSFVLVAQPGVQWCNLSSLQPLPPFR*FSCLSLSSWDYRCAPPRPANF/SVFLVETGFHHVGQADLELLTSGDLPTSASQSAGITGVSHCTWPDILYEI
3611	9108	A	3882	43	347	AGVQ*CDLG*LQLLPLGFK*FSCLSLPSSWDYRRLPPRPANF*FLVETGFHHVGQADLELLTSGDSPASASQSAGITGMSHRAGPI*KSFLKYSTNKLRTT
3612	9109	A	3883	10900	11295	KPWVNETGKLFQDSYSSHHLSGFSFSPFFSETESCSVTQAGVQWHDSL

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						SLKPLPPGFKQFSCSLPSSWDYRR VPTRPANF/SVFLLETEFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF
3613	9110	A	3884	3	227	RFSCSLSSSSWDYRAPPPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLWECC
3614	9111	A	3885	2	296	KWSSALVAYAGVTWHHLGSLRSP PGFKRFCCLSLPSSWDYRHAPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN
3615	9112	A	3886	1	162	LGGLVFPSEVVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA
3616	9113	A	3887	2	474	
3617	9114	A	3888	2	592	STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLELEMNSDLKAQL RELNITAAKEIEVGGGRKAIIFVPVP QLKSFQKIQVRLVRELEKKFQWES MSVFIAQRRILPKPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA
3618	9115	A	3889	1	93	GFTMLP/RLVLNSWVQMICLPWPPK MLSLQA
3619	9116	A	3890	1	252	PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGSEEE
3620	9117	B	3891	18	1121	MASMGTLAFDEYGRPFLLIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVVDKGDVTVTN DGATILSMMDVDHQIAKLMVELSK SQDDEIGDGTGTVVLAGALLEEA EQLLDRGIHPIRIADGYEQAAARVAIE HLDKISDSVLVDIKDTEPLIQTAKTT LGSKVVNSCHROMAEIAVNAVLT ADMERRDVFELIKVEGKVGGRLE DTKLIKGVVDKDFSHQMPKKVED AKIAILTCPFEPKPKTKHKLDVTSV EDYKALQKYKEKFEEMIQQIKETG ANLAICQWGFDDDEANHLLQNNLP AVRWVGGPEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT*
3621	9118	A	3892	1	282	LPSSHTIPGYPNPLHPRFPSSRLPP GIIGGEYDQRPTLPYVGDPPISSLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM
3622	9119	A	3893	3	166	PRFPKSRLLPGIIGGEYDQRPNPILP VGRGGPNDRFPF/RPSRGRPTDGRLS FM
3623	9120	A	3894	101	1926	SPVRGRRRLGRELLGPAAPVPAAS GSRPLGPPAAVMRLRVRLKRTWP LEVPEPETLGHRLRSHLRQSLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNEQPSLATSSNQTSM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QDEQPSDSFQGGAAQSGVWNDDSLGSPSQNFEEAESIQDNAHMAEGTG FYPSEPMCLCESVEGQVPHSLETLY QSADCS DANDALIVLIHLLMLES GYIPQGTEAKALSMPEKWKLSGVYKL QYMHPLCEGSSATLTCVPLGNLIVV NATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQ LVYPLLAFTRQALNLPDVFGLVVL P LELKLRIFRLLDVRVLSLSAVCRDL FTASNDPLLWRFLYLRDFRDNTVR GQD TDWKELYRK RHIQRKESPKGR VFM L LPSSTHTIPFY PNPLHPR\PP SSRL\PPGNGGEYDPKTNTFPMLGD PISSLIPWVLGETPQPSFPPTETHALN PSWPPISRDPNPQSCPGAEGGPPN/R TRFPPLRPQPGGRANLMAGLVISCG LDLLIFISWSLPFVFCFLNYRCQRPW GADLRVLF S
3624	9121	A	3895	2	442	LSQLCGDPQRFDDFLRAYVEKYKF TSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEAL FQL/WTAEPLDQAAASASAI DISKW RTFQTALFLDRLLDGSPLPQEVVMS LSKCYSSLLDSMNAEIRIRWLQIV
3625	9122	A	3896	1	1035	GEFLVIDVIHEVAHSWFGNAV TNAT WEEMWLSEGLATYAQRITTETYG AAFTCLETAFRLDALHRQMKLLGE DSPVSKLQVKLEPGVNP SHLRNLFT YEKG YCFVYYLSQLCGDPQRFDDF L RAYVGE\YKFTSVVAQDLLDSFLS FFPELKEQSVDCRAGLEFERWLNAT GPPLAEPDLSQGSSLTRPVEALFQL WTAEPLDQAAASASAI DISKWRTFQ TALFL\DRLLDGSPLPQEVVMSLSK CYSSLLDSMNAEIRIRWLQIVVRND YYSLT/FHRVRRFPGRARCHACYTIP LYEDLCTGALKSFALEV FYQTQGR L HPNLRRAIQQILSQGLGFOHRARP
3626	9123	A	3897	2	912	CSRSSRTGGWWPAPCSAASRRPTPG PAAAAAATTD/VVTAGCGFGKDFR KGLLKKGACYGDDACFVARHRSA DVLGVADGVGGWRDYGVDPSQFS GTL MRT CERLVKEGRFVPSNPIGILT TSYCELLQNKVPLLGSSTACIVVLD RTSHRLHTANLGDSGFLVVRGGEV VHR SDEQHYFNTPFQLSIAPEAE GVVLS DSPDAADSTSF DVQLGDIILT ATDGLFDNMPDYMILQELKKLKNS NYESIQQTARSIAEQAHELAYDPNY MSPFAQFACDNGLNVRGGKPDDIT VLLSIVA EYTD
3627	9124	A	3898	2	220	YMSKKFSALLQSQERNCLIIINWCSS LCLRVRLYL RQVTVIPRICKVSD\SP CAPEADAMFAFNADGVGDAKG
3628	9125	A	3899	1	346	SANATTKTSETNHTSRPRLKNVDRS TAQQLAVTVGNVTVIITDFK EKT RS SS\TSSSTVTS\SAGS\EQQN\QSSSGV

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						QRAPDKGLPPRSLPTPKGDMSAVN DEIFPEIATWNCEKL
3629	9126	A	3900	76	368	
3630	9127	A	3901	1	1182	MFAKGRGSAVPSDQGAWEKLASY VYEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPPVIRMGNQPPG GVPGITQPLL\NSMDPTRQQGHP\N MGGSQMQRMNPSRPLGPMGPRPHR ITGSGMRPPPNLSLGA\MP\GINMGP GAGRPWPNPNSANSIPYSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DNI\YTM\NPV\PPGGSRSNFQMGPG STGPMDSMGGMEPHHMIGSLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPTSMTMSV
3631	9128	A	3902	2	470	IPTFGLPGSIQSDNGPSFISQITQQVS QSLGIQWRLHIPCWQTSKGVERAN GILKAQLTKLTLEVQKPWDL\LLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLTNRPPSNSQLGGIPSQSSSL MEVIFLWPTRPTRAFFPKPHGGGLPIP K
3632	9129	A	3903	69	523	PLGCASSQISASRNTLCTTASSCCP QVLAHS\KAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS**LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPGLLLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS
3633	9130	A	3904	101	1469	RTHPTFPHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKIILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHQVLAR RKAREIQAKLDQAAKDQALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIQSS PSYLRPYLEAVDIRQIYDKFPEKKG GLKDLFERGPSNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIIT CSTKVCSFGKQVVEKVETERYAYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYYMMNSVLENFTILQVVTNR DTQETLLCIAVFEVSASEHGAQHH IYRLVKE
3634	9131	A	3905	1	1290	
3635	9132	A	3906	2	270	ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKI\VTQPQRHNLQPFHPKLGDVTD DSEED\ENEQVSAV
3636	9133	A	3907	2	288	RWGLALSRLR/AGAQQWFHHGSLQPQ

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						PPMLKSSSRSLSPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSSLT VWASQSAGITGVSHRTHPLLS
3637	9134	A	3908	3	222	FFFETESRSVTARLECSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIFVEMGFHRVSQDGLDLKNL
3638	9135	A	3909	3	175	GTSPKDCEVRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF
3639	9136	A	3910	2	533	RAAEFFFTFNVPALFISMRAVLSLY ATGRTTGVVLDSEGDVTHAVPIYE GFAMPHSIMCIDIADRDVSRFLRL YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINP\QKDETLETEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARSIRKTF
3640	9137	A	3911	1	1213	EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEHRGLLSIRYPMEHG IVKDWNDMERIWQYVYSKD\QLQT FSEEHVPVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQAVLSLYATG R\TTGVVLDSEGDVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYLRLK EGYDFHSSSEFEIVKAIKERACYLF HKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAPELLFGPRI*LEKESE G\HEVPGVRPFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKL\APKDVKIRISAPQERH VYPRGLGGSILASLDTFKKMWVLQ KGDMR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVRPFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCPLPGH HLRRCGCSKKEI
3641	9138	A	3912	2	262	LEKRSHSVTKLGYSGVIIAHCSLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGDLLGSSN VEPPKVLLGL
3642	9139	A	3913	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRSIFTPETN PRAGLEKNYCRNPDGDVGWPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCCVAHPHSW PWQVSLRTRSPRPSSYKVLGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3643	9140	A	3914	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNG\LLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT

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						MLQLSPEEKGKLAAVAQGLQETSIP KKK
3644	9141	A	3915	360	885	NVFVLLLEANQRTSTVTLATVSASGQ MPSTFEGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF
3645	9142	A	3916	1669	4914	
3646	9143	A	3917	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAPHPHSW PWQVSLRTRSPRPSYKVLGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3647	9144	A	3918	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGALLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3648	9145	A	3919	360	885	NVFVLLLEANQRTSTVTLATVSASGQ MPSTFEGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF
3649	9146	A	3920	1669	4914	
3650	9147	A	3921	1	246	FLETEFHSAQAGVQWCHLGSQPP PPPQFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWPGWSQTPDL KQSSGNL
3651	9148	A	3922	10	476	DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCSLSPNSWDYRCVPPCLA NFFVFLVETGFHHVGQAGLELLTSG DPPLPQPPKVLGAGITGMSHHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP
3652	9149	A	3923	2	465	ARARADSARAARAEFEDIMKRNRA ISSPISKAVSGASAGDYSDAIETLLT AIAVIKQSRVAK\DERCVLISSLDK CLHG\IEGQVPTVWGAQLGALSRRK HPFPGERSP\SRRETSRRHRDLLHN EDR\HDDYFQERNREHERHRDRER DRHH
3653	9150	A	3924	3	218	LPPPLSNIHSTLSTPFLPPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTSQPSTPT LPLPTPCSTPSGQALFF
3654	9151	A	3925	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAPHSW PWQVSLRTRSPRSSYKVLGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLSPNYVVA DRTECFITGWGETQEHFYFN
3655	9152	A	3926	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3656	9153	A	3927	360	885	NVFVLLLEANQRTSTVTLATVSASGQ MPSTFEGGLDSSIQLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSAFQTLF
3657	9154	A	3928	1669	4914	
3658	9155	A	3929	1	1542	
3659	9156	A	3930	3	1771	
3660	9157	A	3931	2	1869	RLVVVEAKMAAQAAAAAQAAAA QAAQAEAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPKPPQRIE ARTHLQLGSVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEASLLS ELYCQENSVDAAKPLLRKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGAEYARVVGSEYTRALF LLSKGMLLLMERKLQEVHPLLTLCL GQIVENWQGNPIQKESLRVFLVLQ VTHYLDAGQVKSVPCKLQQLQCCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLKMLDCSPILS SFQVILHEIIMCRLVTGHKATALQE ISQVCQLCQQSPRLFSNHAAQLHTL LGLYCVSVNCDNAEAQFTTALRL TNHQELWAFIVTNLASVYIREGNRH QEVVLYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGQVAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHQNFSSQQLLQD HIEACSLPEHNLITWTDGPPPVQFQ AQNGPNTSLASLL
3661	9158	A	3932	2	614	
3662	9159	A	3933	1	4992	VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTL MEAENMALKRCNFAPLARFRDIS DISFIQSKKVVCFKEPSSTGVSNGDL LHRQPFTEESPSSRCIQKDGTQTNL

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						KCRRGIENWEFISSTTVRSPLQEAES KVSMALLETLRQYQAASVVRSESEP EGCSGTIGNKIIIPMMMTVIKSDSSSD ASDGNGSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEEERVRAHAWNM KFNLAHDCGYSISELNEDDRRKVEE IKAELFGHGRTTDL SKGLQSPRGMG CKPEAVCSHIIIESHEKGCFRTLTS HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNLSQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWLSELVEPAFVPP KEVDFHSSSQMPSPPEPMKKFTTSITF SSHRHSCISNSSVVKVGVTEGSQC TGASVGVFNHSHFTEEQNPPRDLKQK TSSPSSFKMHSNSQDKEVTILAEGR RQSQKL PVD FERSFQEEKPLERSDF TGSHPSTRANCSNFKEIQISDNHT LISMG RPSSTLGVNRSSSRLGVKEK NVTITPDL PSCIFLEQRELFEQSKAP RADDHVRKHHSPSPQH QDYVAPDL PSCIFLEQRELFEQCKAPYVDHQM R ENHSPLPQGQDSIASDLPSPISLEQC QSKAPGVDDQMKNKHHFPLPQGQD CVVEKNNQH KPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLD SGT LDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSK\LLTSKPVAQDQESLGFL GPKSSLD FQV VQPSLPDSNTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKL RKAPVKFAS SSSVQQVTFSRGTDGQPLLLPYKPS GSTKMYYPQLRQIPSPDSKSDTT VESSHSGSND AIAPDFPAQVLGTRD DDLSATVNIKHKEGIYSKRVTKAS LPVGEKPLQENADASVQVLITGDE NLSDKKQ QEIHSTRAVTEAAQAKE KESLQKDTADSSAAAAAEHSAQVG DP EMKNLPDTKAITQKEIHRKKT V PEEA WPNNKESLQINIEESECHSEFE NTTRS VFRSAKFYIHHPVHLPSDQDI CHESLGKSVFMRHSWKDFQHHPD KHREHMCLPLPYQNMDKTKTDYT RIKSL SINVLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTP EQTT QHTVSLNELWNKYRERQRRQRP E LGDRKELSLVDRLDLAKILQNPIT HSLQVSESTHDDSRGERSVKEWSG RQQQRNKLQKKKRFKSLEKSHKNT GELKKS KVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYISNTSSDCRPS EESELLTDTTNNILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA

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						FGHERVCLSPRRIKLYSSITNQQR YLEKRSKH\SKESAGLTGHPLVTSE HTRRRHIQPPTSATACRQPLMTFCF YGFAYS GPFI
3663	9160	A	3938	2	354	NRILVITSKAGEVIKHGDLRCVRDE GMPIYKAPLEKGILIIQFLVIFPEKPL ALSGKSFLQLEALLPPRQKVRITDD MDQVELKEFCPNEQNWRQHREAY EEDGDGPQAGVQFQTA
3664	9161	A	3939	204	374	DHGFLIPLTQGDQKGPPRVHPL*AC YHWNQREKVISSCIGCICMSQIKDP LVKKKKK
3665	9162	A	3940	39	385	AGVQWRDLSSQPPPPGFKRVSCLS LPSSWDYRQPRLANFC/DFLVEMG FCHVDQ\AGLELLTSGDPPASASQS AGITGVSHRTQPCLLFLKTKTWGK WEKDGMFWEMNGAQDQEQ
3666	9163	A	3941	1	200	FETGSYSVTRLVFSVQISAHCNLCL PGSPDPPTSASEVVGTSVCHRTQLI VIYPLQLPKLFRLQV
3667	9164	A	3942	2	458	LFYGVYFLFPLNSCILFVSFTVNHQ IFFFGGGMKSWSVRRLECSGVILAH CNLRLPGSSDSPASASRVAGTTGTC HR\ARLIFVFLVEMGFHHVG/RRDG LGSPDLVIHPPR\TPKGVGGLQGVSH CGPGSPQGFYLIKELGSSQGGEQ FP
3668	9165	A	3943	1	2499	
3669	9166	A	3944	855	2479	PGGSGPGFPTLEGSSKAGRELIGY EPGSSGVGAPLTPHKMKRRELN ALIGLAGDSRRKKPKKGSSHLLR TEPPDSDESSESEEEFGVVGNRSR FAKGDYLRCKICYPLCGFVILAAC VVACVGLVWMQVAKEDLDALKE KFRTMESNQKSSFQEIPLNEELLSK QKQLEKIESGEMGLNKVWINITEM NKQISLLTSAVNHLKANVKSADLI SLPTTVEGLQKSVASIGNTLNSVHL AVEALQKTVDHKKTMELLQSDM NQHFLKETPGSNQIIPSPATSLEDN KTHSENKQDILYLHNSLEEVNSAL VGYQRQNDLKLEGMNETVSNLTQR VNLIESDVVAMSKVEKKANLSFSM MGDRSATLKRQSLDQVTNRDITVK IQSIQKEDSSNSQVSKLRE*LQLISAL TNK\PESNRPPETADEEQVESCTSKP SALPKFSQFLGDPVEKGCPKLRYS P*QGVSKH*KIFQDLFR\KTGQD\VD GKLT\YQEI\WTSLSGAMPEPESLRAF D\SDGDGRYSFLELRVALGI
3670	9167	A	3945	336	519	AALPCEPAFSPLEQVQRGLQDRGQ NQTQRPFLLNVVQA\VSQEG\ACV YAVSELRKEWGRPQ
3671	9168	A	3946	252	2104	LCASSCPFICPPIRPSVCPAAPLLLG CRAMARGYGATVSLVLLGLGLALA VIVLAVVLSRHQAPCGPQAFHAA VAADSKVCSDIGRAILQQQGPVDA

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						TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPASHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEAHRRRHGRLPWAQLFQPTIA LLRGGHVVPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQLTLQDLAKFQPEV VDALEVPLGDYTLYSPPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPFAMV YSPRTGIILNNELLDCERCPWGS GT TPSPVSGDRVGGAPGRCWPPVPGE RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAIMSKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQ\AVS QEGVACVYA\VSDLRKSGEAARS
3672	9169	A	3947	2	97	GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS
3673	9170	A	3948	3	308	PEDSDEKSLSSSVVVHVRPRRRVP RMPRGSRSTRMAPPASRAPQMR AAPRPAPVAQPP/QPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA
3674	9171	C	3949	38	154	MXSNSFWSVPRTVTSSSVRVSMR CCYDFILCELIRIKS*
3675	9172	A	3950	1	192	GSNAEP/ARPDLY/QEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA
3676	9173	A	3951	1	254	LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCEGFNEV LKQCRLANGLA
3677	9174	A	3952	1	142	
3678	9175	A	3953	1	325	FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCGLLSSWDYRRLPP HPANFYFLVDTGFHHVGOAGLELL T/S/GDPPASASQSAGITGTSHRAPPT VNTFNRPPAS
3679	9176	A	3954	3	304	HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVVRMCCCLMLML RWGASFAWYCCFLSFCNWL\SS EDT TGLMITFMLRISALLMRSLQNPEAM TLPW
3680	9177	A	3955	3	961	LLLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCQWSLDNLFLKEGRQ LTYEKNLSSIRAMLNSNDVSEYLYK ISPHGLEARCDASSFESVCC\SFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFMSYQQCFEN

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						FGA\SPFKYPPSMKFSTFNDYAFLTA EEKIIL\PRHRLALLKQVSIRETAGS LCCDEVADTQLKPCGHS DLCMDCA LQLETCP LCRKEIVSRIRQISHIS
3681	9178	A	3956	4	101	RQSLAMLSRLA\LNSWPQVILLPWP PKVLGLQA
3682	9179	A	3957	21	338	HPVLAITLSIFVAFAYAEELDEIQ P/CIMMKTLNKL GIEGMCLNSIKAIY /DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ/PLLFNIVLEVLAKEIRQEEI KV
3683	9180	A	3958	90	360	ALICLV DIESGENSTTRPFASHDQV CIALLRTA\GILCLET FIDSPSHGSRH FLFVLSSPPLTLFPLLHIYLLAVVPI VSPLLSLSDPP
3684	9181	A	3959	1	424	CGRRFSTRSDLTKHRR TDTG\EKPN\ RCELCGRKRTCVSNLNVHRRNHAG HKPHKCEPSKAFSVASKLALHRKT HLGERPAECARVGQVLQPQAPLS QHQRGPHAPPAPLPPLPSSPAVGHC PQSFEGRLEQEKA KGS L
3685	9182	A	3960	153	328	SIASYFTLVCHLLRKCHPRLGTVAH TYPSTLGGGRWIMR\QEFETSLT\ NMVKPCRY
3686	9183	A	3961	1	936	
3687	9184	A	3962	1	1023	
3688	9185	A	3963	15	337	RINNTISWLIYVCKFCLSSFSLIILIIII IIFFETESHVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPPR PANFCIFSRDGVSPCWPGWFRTPDL R
3689	9186	A	3964	3	1105	HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQE KTEEGLG PNIKSIVTMLMLMLLMFAVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTW\ NNSHIALVGKAMSSNETAA YKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFTPQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYLK KTTKRKRGYIKNLVFKKGKKISK KTV
3690	9187	A	3965	1	181	ANVVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHG\CS AEGCGLSSTCY
3691	9188	A	3966	640	961	DGVSASCCPGLGVQWVRFLGSL\QP SASWGFKQFSCLSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASIL
3692	9189	A	3967	2	334	VGLYGRIEASSPMGEGNRW*SGTPA NQG*QE QGIARPKPRGEPGLRNEGG

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						PGAILPGRWAGV*GPTGQEGR*RGS QESCPCPAQSSCSHRVAGLDVGGSH GHSAAFPATP
3693	9190	A	3968	1	361	ARARLRHLRDLRAPAGPVGGGLCAA GTACGWPGPGPLLGERVRAFLRR* RAQHLLHHHRVRAPLPGWREAAG GAPPFLGTYPESQVRLRDAVVPEA GGQDSGSSGSASLRPRSSFSCSCS
3694	9191	C	3969	151	373	MPTAVXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXVLPFLV LEV MQCLCPVLLLYDPNSKTRYV FFKTR*
3695	9192	A	3970	50	441	IPSPPDGFFSNLGRKPPFFPCNFSCQ NILLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVL PFLVLEVMQ CLCPVLLLYDPNSTPRYVFFKTRT FIA
3696	9193	A	3971	3	224	FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVL PFL VLEVMQCLCPVLLLYDPNSFV
3697	9194	A	3972	1	214	PIQFKQRLPFGFLFVVF*EGVLLCH PGWTA VTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV
3698	9195	A	3973	154	341	KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL
3699	9196	A	3974	3	379	FALVAQAGVQWCSFDSLQPPPPGF K*FSCSLPSSWNYRHLPPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTL CFMV FMSFWRNCRKVAKY LK
3700	9197	A	3975	2	35	LKQAPCLCLPSS*DYRHLPPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLR* AQTSPPLPTK
3701	9198	A	3976	1958	2316	IHSSPTKATFFLRQSLALSPRLEYS AISAHNLCFPGSSDSRALAS*AAG TTGACHHIRLIFFLVFLVETGFHH VGQAGLELLVSSDLPIVLSARITG VSHHAQPPPKLLNALL
3702	9199	A	3977	2	80	SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF
3703	9200	A	3978	123	452	KTGSNFAPQLEAQGGNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGQGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF
3704	9201	A	3979	3	250	ATAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPQK
3705	9202	A	3980	2	257	PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPDPAKPPQPNPYKPY PNLGCGL*PQNYCIHCMVSIVYYH MGIETVKSQ
3706	9203	A	3981	2	147	LVEMGFHHVSQAGLKLLDSGNLSA

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						S*RSAGITGISHRAHPPNSTNIYA
3707	9204	A	3982	3	446	QVVRGFGRVSKQMGIP TANFPEQV VDNLPADISTGIYGGASVSGSDVH KMOVSI*WNPYKNTKKSMETHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESISPVGDDTD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK
3708	9205	A	3983	1	162	FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCSFLWSSWDNRRLP HLANK
3709	9206	C	3984	131	442	MNIPLSMSLVVSNMQDVFVXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX*
3710	9207	A	3985	141	429	TGSHFVAQAGMQWCNLWSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF
3711	9208	A	3986	1577	1879	
3712	9209	A	3987	1	219	EM*SCRVTQAGVQWCNLSLQ LPS PGFKQFSCLSVPSGWGYRCMPHP ANFCIFSRDRASPRWPGWSQTPDLR
3713	9210	A	3988	1	414	FF*TGSCFVSQAGTQQQDHSSLQP* TPGLKPSSHLCLSSWDNRHLIFKFF VEMGSRHVAQAGLQLGNNPPTL AS*SARIISWSHRAQPTCTLC SWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT
3714	9211	A	3989	3	666	FFVETGFCHVGQAGLELLGSGNLP AASQSAGITGMSHRVRQHS*YETHR KVFYS
3715	9212	A	3990	1	436	FFFFFLRQNLTLSPRL*CSGTILAH NLQHPGSSDSPASASQVAGITGVRH HIWLIFVFLVEMRFHHVGQASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSFLHL
3716	9213	A	3991	167	563	SESASEFSIFYLFIHHHHHETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APHPANTFNFFLLE IGSHYVAWGSLELLGSSDPPASASQ SVEIIGVSHRGPDSQKSFIHLSPRFP
3717	9214	A	3992	3	456	
3718	9215	A	3993	78	129	
3719	9216	A	3994	96	251	MDQYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSTVFN SQPT HTEE
3720	9217	C	3995	94	351	MKRISTTQYYHCQDYDLRHSKHM CLVSTAFQKVKPLYKYLEILQENLD PQGKDSRWFSVISSPRSQNVK VWR HLQSCLTSHCKH*
3721	9218	B	3996	1	431	MAVASTKSRWETGEVQAQSAKT LSCKDIVAGDMSNKSFWQKGGSK TSSTITAQIAFLQGERKQENLKKD LVRMIRMLEYALKQKRAKYHKLK YGTEL NQGAMKPPSYDSDEAQQQA

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						MRSVHGPLHLSAPPASQKRPTE *
3722	9219	A	3997	772	1391	IANNDALRKLTWNPKFTLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLEFYFK*HA
3723	9220	A	3998	3215	3491	SAKVLRTFFFFFFFFFAIESHCVT QAGVQWCNLASLQSPTEFK*FSCL GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK
3724	9221	A	3999	1	779	MNNGRNRYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTTTRFWAPGVEAPGDDAERRR REASGPATRHSPPLTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAAALRHAKWSSEIRF
3725	9222	A	4000	1	1286	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGGPGLGLLV RPGMPPQPQGPAPLRPDSSDDRYV MTKHATITYPTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPHREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVHIIR ILRDLQCRVPTWSIDFPSWAMELLV EKAISSASISQSPGDALRRVFECIS SGVILKIGSPGLLDPCCKDPFDTLG QQ*PDPASRED/LSTSQCHSLPLETS LAFPPRYHKVLGMDPITRK*AQRF NIHNNRKRRRD\SDGVDGFEEAGK KDKKDYDNF
3726	9223	A	4001	2	379	DLPASATQNAGITGVSHHIWPRIIFL LW*KTFTILTFLSVQYSSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPI VNLHCIFFF*GLTFLLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF
3727	9224	A	4002	229	445	RPGPNFGLLETLTWGLKGTWLWNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG
3728	9225	A	4003	192	529	HEVLNFLTSCVLTTLVFLIADIWLS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI
3729	9226	A	4004	330	754	SDLSQKESSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETMAQVLFSDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE

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3730	9227	A	4005	296	861	VSQDHETMAQVLFSSRNMRNLNVALT FWRKRSISELVAYLLRIEDLGVVVD CLPVLTNCLQEEKQYISLGCCVDLL PLVKSLLKSKFEE*CY*WVLTGLQA VIKRWWSSELSSKTEIINDGNIQLKQ QLSGLWEQENHLTLVPGYTGNIAK DVDA YLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVS
3731	9228	A	4006	2	265	NNFFSFSETESHSVTQAEAQWYDNS SLQP*ILGLKQSFCLSLPSNWDHRC APPHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV
3732	9229	A	4007	3	295	HFNLSHRSAQAKGNRYKEAEALTN AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLTSKYT
3733	9230	A	4008	1	1077	
3734	9231	A	4009	3	285	ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPSCQAN FCILVEMGFHHVGQASLELLTSGDP PASASQSARITGVSHRAQ
3735	9232	A	4010	1	338	VIATYHGGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT
3736	9233	C	4011	269	526	MLARLVNSNLPQVIHHTQPRVGSPT RIPTLSNLPLPLALTSRLWRDHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCVPKP*
3737	9234	A	4012	2	51	
3738	9235	A	4013	83	5229	
3739	9236	A	4014	3	45	EVVHALRCRWWWSWGLKLDLLTPEP EPICGPALLSRSSLRGSHPTAFLLPP QVSQ*RGELGPSTFRAFRAEFPTSRG SKDNKEKNQEQDMAKPATGTGQG G*GADGGAGA
3740	9237	A	4015	3	323	LLWKVESSWRDQKDIMSWEWDKR RRRHHLTDRSQLCSKVKFQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGGEE AVIWHWGTGL
3741	9238	A	4016	2	279	FFFEEAKSHSVTRMLECNGAISAPC NLHLPGSSDSPASASQVVGITGVYH HTQLIFIFSVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA
3742	9239	A	4017	166	939	
3743	9240	A	4018	2	225	KELTGRRCAEPHPRPSPQLLTEEPF TKGRFSGEWRGRNAASMTGPFAE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPIPPV TDRGAIYKRPIWGVVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV
3744	9241	A	4019	142	1336	KARGDCKHPGRCWPEQMAEGERQ PPPDSSEEAPPATQNFIIPKKEIHTVP DMGKWKRSQAYADYIGFILTLNEG

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						VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDEEAENLVATVVPHTLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEV MRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPF AEHSNQLW NISAVP\SW\SKVNQGLIRMYKAEC \EKFVPVIQH/FSKFGSLPIHPVHVGL GGAKPKEPPRGTVSCCLPFPPTPAVA PPSPSPSVSSRLMRGCLLGLGEMG LRGLRA
3745	9242	A	4020	80	283	
3746	9243	A	4021	61	626	DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEEHSQIDEN*** Q*KSYK**QKGIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRIH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKLNLEKEFVASYP PLVEMLK
3747	9244	A	4022	18	161	TSFKNPPPPPGGLKKIPSPPPKKK KFKDVS*PTYFLYNASSVT
3748	9245	A	4023	30	262	NRRQAGFPFAKLGRPSPKGGFPNFF KSSSSKSSF*KNPKGGQWGFPPLIPG FQGPQVGGSLGAPGLKPPWGTQNP PF
3749	9246	C	4024	193	366	MYNYRSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL*
3750	9247	A	4025	3	258	TIDSLKGLPCKQNEPWHTIQCGYL GNSSKWNI*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH
3751	9248	C	4026	164	313	MEGTRIFGKWKLIQSIPNRNSCTTI DLFLKINIHIHTQKAILMKSFDP*
3752	9249	A	4027	9	373	DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNPALSPLSSWDYRRVPPCPS *FFVFLSRRWRFRVGTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK
3753	9250	A	4028	1	336	DRILLHRPCWSTLARS*LTIPS NHLG SVFPPSALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRLVLNAWTQAIQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI
3754	9251	A	4029	514	742	LPKC*DHRHEPPHQAFFNFFVEMG SCHVPQSGQLLLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKS RFCP S
3755	9252	A	4030	1	264	QAQGHKPGSFGPPFAGLKGFPGGLGF PRTGNSGGFPQGGKYKGFLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF
3756	9253	A	4031	7	417	RQDLALSPRLECSDTIIAHCSIKLLG

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						SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ
3757	9254	A	4032	123	376	KTGSNFVPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPrANF GIFKKKGVSPPC*GGLKTPNSGFSPF KPPKGLE
3758	9255	A	4033	3	292	QWHKHGLLQPPPGGLK*SSHLSLPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKHLLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK
3759	9256	A	4034	1	230	FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKQVQNKSVTFPARNLNK MRGASIMLYPIGLSLNDLMQLLSEGF
3760	9257	A	4035	3	189	SWDYRRLPHARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPRCWDYRR EHIAPGHIWY
3761	9258	A	4036	2	148	PGSSNPPTSASQLAGTAGTHHHA*LI FVCLVETGFCHVA*AGV*VKFF
3762	9259	A	4037	348	696	AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG
3763	9260	A	4038	1	295	QNQFFIFIYFKTESGSVTRLEYSGLVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVGGAG LELLTSSDLPASASQSAWGLQV
3764	9261	A	4039	6	151	SQGLALLPRLISNPVWQAILLPWPP KVLGL*AEIAQNKMQK
3765	9262	A	4040	101	318	SNHTLGTS*HFFFETVSCCMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNLH
3766	9263	A	4041	210	306	SWPGTVAHCNPSALGGQGGWIA* GQAFRQA
3767	9264	A	4042	2	147	DFSVKTL*ARREWDRIFTVMKEKNF YPRKVYALKIPFKNEATKKVEV
3768	9265	A	4043	160	525	NTQTRSFGNRLMAPAQSSHKALTK KVMTCNPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCSLCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPPKLLGLQA
3769	9266	A	4044	3	72	KTQVHFQGWQHSVHIITHPCWEKL ALSITPLR*DNRKLQAWNSPRLGPT CLFPRLALMCVLMML*NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS
3770	9267	A	4045	313	358	
3771	9268	A	4046	7	308	AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLDSscyHHSSDFYICHMPMP ISS
3772	9269	A	4047	92	390	ETGSHSVNLAGLQWCDHNSLQP*T

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						PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRSPDP PVWGSQSAGTIGMSHHAQPREIC
3773	9270	A	4048	65	375	SQLTATSTSRVQ*HDLSSPQPPPPGF KRFSCLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP
3774	9271	A	4049	12	292	DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFLPSWWDYRCVPPCPAIF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPHLAATDF
3775	9272	A	4050	40	343	SSSSLILSSSVIYLLNLSDFLVLLLY FLVFRFSVCSFCQFFVKNFNLIFYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL
3776	9273	A	4051	97	282	
3777	9274	A	4052	3	336	FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLLLSSWDHRHVPP RPA NLVYLL*RGGPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG
3778	9275	A	4053	3	294	CCFGDGVSLCRPGWSIECSGNHSSL QAVEPPRLR*SSRLSLGSDWPSHV PLHLANF*TFCTHGVLA MLPLAGLK TPWAQTIPPHLSL PKVLGLQG
3779	9276	A	4054	16	308	MPQPN*SNPPVNCRLPRGPPSQVP PRIHLSPKYSPSEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKPPF* REIKPLPPRLTPSVHSMVL
3780	9277	A	4055	445	448	IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWC SGQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQLKKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK
3781	9278	A	4056	3	284	CLSLSSWDYKCLPRLGYFLYF** RRGFTVLARMVVISRMVVISRMVIS *RRDPASASQNA GITGVSHCARPK EQKLFYPEVSCLYLGLY
3782	9279	A	4057	428	636	DYHIVSLHLF*FLETGSHSVTQAGI QWCDHSSL*PRTPLGKQSSCLSLPE* LGLQE*VTVPGSYSLFF
3783	9280	A	4058	2	113	FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE
3784	9281	A	4060	36	359	RSGVQNGFHQA EVLSVRLCFSTEAL GQNMPFPAPP GATSSPGPRPSCHL HSQKL/TL LHAQTLVTP LPL*GLGLS AWRTL AGGAPGLHPFTTHALSTPET IPGAYRRT
3785	9282	A	4061	17	168	APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH
3786	9283	A	4062	2	375	FFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNMPFP APP GATSSPGPRPSCHLHSQKLPLLH AQTLVTP LPL*WPPWITQGPQPST GHLPTTEILKLK HRRRVPFCHAR

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3787	9284	A	4063	309	620	
3788	9285	A	4064	3	218	LRQSYSVTQAGVQWRNLGSLQPLP PGFKRFSCSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR
3789	9286	A	4065	1	170	NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFKLA*VKPVQSSPAG LHHHTPL
3790	9287	A	4066	29	483	RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RILAEGRKRIYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGQYCGD Y/DASFVEAVEQNTVAGVFPGLGL KFKPCSRVSPCWSDSHHQHSPPAFQP GQ
3791	9288	C	4067	33	236	MRHHAWLIFVLLVETGFHHVGGAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF*
3792	9289	A	4068	1	205	AIGTDKGTRWSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLDEFDF
3793	9290	A	4070	2	44	LSSWDYRHVPPRLANFCIFSRDGGF TMLARLVLS*PQVIHPPQP*VL*L QACATTPG
3794	9291	A	4071	173	369	CSTLI*IRKVWLGAHAHYNPNTLR GRGGRIA*GQVFKTSLGNNVKTCLF LPSPHNQQSLSGFLL
3795	9292	A	4072	1	336	
3796	9293	A	4073	1	200	
3797	9294	A	4074	11	392	
3798	9295	A	4075	1	191	
3799	9296	A	4076	84	264	
3800	9297	A	4077	2	446	DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASAGYQDNIALR EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLLGEESRINLPI QTYSALNFRETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L
3801	9298	A	4080	3	196	SRAGPKNYNFGQGPPTKVKGLA SPFFPLPPFPRPPWFPPPF*NPIFPW W*KGPKKPFLN
3802	9299	A	4081	1	187	SIRLFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARPC SSLIVLHL
3803	9300	A	4082	156	326	KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY
3804	9301	A	4083	3	448	
3805	9302	A	4084	1	4249	AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQQVSSQDLSSCAGRCGEGYS RDATCNCDCYNQHYMECCPDFKR VCTAELSCKGRCFESFERGRECD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPPSGASQTIKSTTKRSP KPPNKKKTKKVIIESEEITEHSVSEN QESSSSSSSSSTIWKIKSSKNSAA NRELQKCLKVKDNKKNRKTKKPTP

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						KPPVVDEAGSGLDNGDFKVTTTDPDT STTQHNKVSTSPKITTAKPINRPSL PPNSDTSKETS LTVNKETT VETKET TTTNKQTSTDGKEKTTS AKETQSIE KTS AKDLAPTSKVLAKPTPKAETTT KGPALTTPKEPTPTTPKEPASTTPKE PTPTTIKSAPTTTPKEPAPTTTKSAPTT PKEPAPTTTPKEPAPTTTPKEPAPTTTK EPAPTTTKSAPTTTPKEPAPTTPKKPA PTTPKEPAPTTTPKEPTPTTPKEPAPT TKEPAPTTTPKEPAPTAPKKPAPTTPK EPAPTTTPKEPAPTTTKEPSPTTPKEP APTTTKSAPTTTKAPAPTTTKSAPTT PKEPSPTTTKEPAPTTTPKEPAPTTPK KPAPTTTPKEPAPTTTPKEPAPTTTKK APTAPKEPAPTTPKETAPTTPKKLTP TTPEKLAPTTPEKAPAPTTPEELAPTT PEEPTPTTPEEPAPTTPKAAAPNTPK EPAPTTTPKEPAPTTTPKEPAPTTPKET APTTPKGTAPTTLKEPAPTTPKKPAP KELAPTTTKEPTSTTS DKPAPTTPKG TAPTTTPKEPAPTTTPKEPAPTTPKGTA PTTLKEPAPTTPKKPAPKELAPTTTK GPTSTTS DKPAPTTPKETAPTTTPKEP APTTPKKPAPTTPETPPPTTSEVSTPT TTKEPTTIHKSPDESTPELSAETPK ALENSPKPEGVPTTKTPAATKPEMT TTAKDKTTERDLRTT PETTTAAPKM TKETATTTTEKTTESKITATTTQVTST TTQDTPPFKITTLKTTTLAPKVTTTK KTITTTTEIMNKPEETAKPKDRATNS KATTPKPQKPTKAPKKPTSTKKPKT MPRV RKPKTTPTPRKMTSTMPELNP TSRIAEAMLQTTTRPNQTPNSKLVE VNPKSEDAGGAEGETPHMLLRPHV FMPEVTPDMDYLPRVPNQGIINPM LSDETNICNGKPDGLTTLRNGTLV AFRGHYFWMLSPFSPPSPARRITEV WGIPSPIDTVFTRCNCEGKTFFFKDS QYWRFTNDIKDAGYPKPIFKGFGGL TGQIVAALSTAKYKNWPESVYFFK RGGSIQQYIYKQEPVQKCPGRRPAL NYPVYGEMTQVRRRRFERAIGPSQT HTIRIQYSPARLAYQDKGVLHNEVK VSILWKIGLPNVVTS AISLPNIRKPD GYDYAFSKDQYYNIDVPSRTARA ITTRSGQTL SKVWYNCP
3806	9303	C	4085	258	362	MFYRNLMKVRAELNCSAIIIEIKA KVLTLFHSN*
3807	9304	A	4086	2	236	QSYNSDSLFFLR SFALVTQAGVQ WRDLGSLQLSPGFK*FCLSLPSS WVYRCPPDPANFLVLVETGFHHV GQGWS
3808	9305	A	4087	224	464	KIFLFFFFFKRQGLT LSCRLDCSVQ *HNHYPLQSRTP ELKQSSCLSHPKY WD*RHEPLCLAPKKEDTLQEQL EIR LLIY
3809	9306	A	4088	129	315	ILKILWIFRIFLLSIKCF*TNMHVCV

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						SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF
3810	9307	A	4089	1	190	FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP
3811	9308	A	4090	1	5229	
3812	9309	A	4091	1	7044	
3813	9310	A	4092	170	422	
3814	9311	A	4093	1	3230	
3815	9312	A	4094	3	151	DTATCCAKWNTEDKVSHVSTGGG AS*ELLEKALPGVDATSTIYYFPAF
3816	9313	A	4095	2	1446	SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTDKLDVKGKRVVMRV DFNVPMKNNQITNNRIKAAVPSIK FCLDNGAKSVVLMShLGRPDGVPM PDKYSLEPVAVELKSLLGKDVLFLK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPK IEAFRASLSKLGDVYVNDAFGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPPERPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAEKNGVKITLPVDFVTADKFD ENAKTGQSTWA\SGITPG\WMGLDC CPRESS\RYAE\AVTRAKQMVWNGP V\GYFE\WEAFA\RGTKALMDEV\VK A\TSRGLSPS*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHLPLGH
3817	9314	A	4096	1	747	MDSSRARQQLRRRFLLLPDAAEQL DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTTYVDFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSQYGLIVFVAGLLLLLAWA VHAAGVSKSDLLCFLTALMLLQL/P VDAVVRGPQLRAPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRRSYLPLRLRGAEFASEPPSAPA HR\ATPPPVEVTPTEAGRFRQAKG ALS
3818	9315	A	4097	1103	1295	EQEGTGLERRRGSPMSKDWP PPHL TPPQGPCGIPVHLSPPSFSIPGPRNS K*ARRSTAPVDCK
3819	9316	A	4098	1	1302	MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGARSPRPPGGCARQPTA GRDAEQPVWADRVRGGAAGAAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTAGAG WLHRLWIPPAFGCRPEYDNGLEEI VFGFEPWIIVNLAMAFSIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGKSSLVNASIP TPPSFPRSPQSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAK

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						K/PPKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAAKLANATYQRS HSASQDRHASEPTSQPSQHSARP AATSQPDRAANQSAVEQARQPSA KHSGKQQADSEAAAGS
3820	9317	A	4099	684	902	
3821	9318	A	4100	143	551	TNEFPFHSRSPPIQTS*AHFPHLITD PDLLSPLSPSHRSRPPEPTSPISPQIQ TC*AHFPHLITDPDLLSPLSPSHRS RPPEPTFPISSPVISWAPISFPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G
3822	9319	A	4101	14	209	ASFVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS
3823	9320	A	4102	126	265	
3824	9321	A	4103	74	196	NLGMLAHAYNSRNLGQVVRTII*G QKFETSHENISRPCLV
3825	9322	A	4104	1	217	NIYMFILCFVLIFNFLNELIT*KHIVIF ICWILSLLLLTLH*FWCHKFHVSW NLEFCIFYFGKIKLDTFT
3826	9323	A	4105	3	268	DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSPSSWDYRHIPPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA
3827	9324	A	4106	3	263	DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM
3828	9325	A	4107	22	208	SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGRCT*GQEFESSLVHMAKP HLYQKIQKICR
3829	9326	A	4108	122	339	EKGFWFCAQGGKNLPGGNSLEPSA SGLKEIFGLNLLNNWE*RGPKTPG NFWIWKKGGV*PLWPGWG*NPGL
3830	9327	A	4109	2	210	KEKIFSPGFKHPPPPF*KTPLK GK RIFSPPRKNWPPQRIFKKAPSSSSS SSSSSSSAQI*SFNSP
3831	9328	A	4110	3	76	ATSESLDVMA SQK*SRSGSPMARR
3832	9329	B	4111	1	2142	MGGAGSPQVILVSHTPQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAPKPSQLERHSRIHTGERPFHCT LCEKAFNQKSALQVHMKKHTGERP YKCA YCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATA CL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPT WALSTSKDPQTEG LRNPQTCVQIRSNPFCAFAQGFSLIS ELRTLNCVGLCDSQSGKQQLGFYS GQPATEAWQKYS LAVCILRSEQEIS ATRLGLKNTNVNKL DGGCGAWN F LGGMSEHNSPPSGRAILLPVVFTEV FPGPWTPEQGSHICRMNLAPTQAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPKTGFPIDPQELLQGPIERTIWP VYTFRSAIVTARAVVWRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPVTASVYGRRLARLRCLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGLLDISIT KSPGRPCFLSVCLHGSDQQKRKGA AATAKRKSKGGGVNVEGRCTWPP EDPPKSWSLAFGLQEKTTLENLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLEDSDPGGLC AV*
3833	9330	A	4112	1	551	
3834	9331	A	4113	3	288	CIGLGVVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTDLTPYISAAFASPVDA DTQLSACTFQLKETPMPSF
3835	9332	A	4114	3	344	VQYYGPAT*VQDGS*GYRTHMYMI NQIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRALDYLLAAEG EVC RKFNLCCLHIDNQGQVFEDI VRDMTKLAHVPMQV
3836	9333	A	4115	6	185	LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHTPVWTKLGPV SKEKKYNQIV
3837	9334	A	4116	1	176	QSIFQICIFFKFTVYMFKTLKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK
3838	9335	A	4117	1	312	GGEKNQDFTFKMESPSDSAVVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLI YKL
3839	9336	A	4118	1	112	GKTFKQKQKQEQKKQK*ELK*KAM GKGPLAAGEIKKS
3840	9337	A	4119	3	355	SQSTKNLPSLARDMDIQIEAQRSP KRSPPRHIIFELTKVKDEKNPKVPV EKHQVIYKGFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP
3841	9338	B	4120	638	3862	MKGTCVIAWLFSSLGLWRLAHPEA QGTTQCQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLQLEDLSLIQAVEWECDE ATKKACYSKGSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLSN LAEIHDQISGMARCPYSPQHNSTAL LTAGGELYAATAMDFGRDPAIYR SLGILPPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFFRENAVEHDCGKTV FSRAARVCKNDIGGRFLLEDTWTF MKARLNCSRPGVFPFYYNELQSTFF LPELDLIYGIFTTNVNSIAASAVCVF NLSAIAQAFSGPFKYQENSRSALWP YPNPNPHFQCGTVDQGLYVNLTER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NLQDAQKFILVHEVVQPVTTPVPSFM EDNSRFSHVAVDVVQGREALVHIY LATDYGTIKKVRVPLNQTSSSCLLE EELFPERRREPIRSLQILHSQSVLFV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSISACPTRNLTVDGHFV WSPWTPCTHTDGSVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVQGNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQARRRICENGPDCAGC NVEYQSCNTNPCPELKKTPWTPW TPVNISDNGDHYEQRFRTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKRV CNNPEPKYGGMPCLGPSLEYQECN TLPCVDGVWSCWSPWTKSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDSNFIPEVSVARSSS VEEKRCGEFNMFMIAVGLSSSILG CLLTLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDKYDSVE AIKAFNKNNLILEERNKYFNPHLTG KTYSNAYFTDLNNYDEY*
3842	9339	A	4121	3	124	NVNRPVSSNEIKIIKSLPVKKSP*LN GFNAEFTKHVKNL
3843	9340	A	4122	1	197	GFKQLS*LSLPNSWDHRHTTTTTPRE MGFHHVGQAGPELPISGDPPAPASQ SAGITGVSHRTRPRI
3844	9341	A	4123	1	268	QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSDDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK
3845	9342	A	4124	3	301	TEEIHGVLSWNLVPDNYPPYYHPPP PSYIYGAQHLLRLFVKLEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI
3846	9343	A	4126	2	214	FFFFKEMGSHYVA*AAVKWLFTGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN
3847	9344	A	4127	2	382	TMVLSPADKTNVCAA/WGMFLSFP TTKTYFFHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLKRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3848	9345	A	4128	2	253	
3849	9346	B	4129	317	683	AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQKLIETDDE KLRTFY*
3850	9347	A	4130	1	82	VDGWVDGWVDG*MDR*VGRWID

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						GWVDG
3851	9348	A	4131	1	240	ASTFFFFSIDRVLLCCPGWTRTPGFI* SSCFGLPKCWDYRSEPPCLATFFFIK KKYKEEHFILILCQIVNMILILYQPT Q
3852	9349	A	4132	3	180	REPPLPAANFVFFVEMRSHHVRQA GPEPPSSDLPASASQSAGITGVHCH AWP*YTYL
3853	9350	A	4133	2	238	SPCAGILEDDRADYQGTRKTSEYSS VTP*EACHT*EGPIAFISWP*KVPIQL TFNERNRARGFQVPYGYDRGLPG TH
3854	9351	A	4134	7	259	IVTAALFTLAPNQK*SKYPSSGKLIN KFWYIYKME*TSISNKQVSTTYSMQ AWVNLKSITLS*RHKGVIYI*SHLYD ILEKTEL
3855	9352	A	4135	141	309	AFDEAIAKLYSVNE*SYKGSTVIMQ LVRVNLAVSATSTGFIVSFVFTYPIIP CYLQ
3856	9353	A	4136	113	205	HNLLMLFDLCLLYWL*LIFLIHELAE NLLN
3857	9354	A	4137	3	215	FETGSCSVTQAGVHWRDHSSLQP*S LGFKQPSNLSLPSSWDYRCTPPHLA NLCIFCKDRVTSYCPGWHPV
3858	9355	A	4138	3	386	
3859	9356	A	4139	1	255	IRLMKEGRMKGQAFIGLPNEKAAA KALKEANGYVLFGKPMVVQFARSA RPKQDPKEG*RKKRTWLFNKVGK WELAPKPMGLDFSL
3860	9357	A	4140	78	153	
3861	9358	A	4141	1	293	LRLPGSSHSPASVS*VAGIAGACHH AWPNFCVFSRDQGFTHVGRAGLGA PDPLDPALPWSPKVMGFTRCEAHP CPSPRMRFLKYVSPVSMVGRPE
3862	9359	A	4142	3	48	PLPRKSVEPGGGTKYKTEQKKRQE RRDRGSK*RKQKAATSEEQQRK* AKTQEDGGTKRSPDGEEDPEKKIHR NREGTRKKGQDPRNGVNNKNREK EQN*RTHTS*SQKVRRTRRGNEV
3863	9360	A	4143	1	276	GTRDSV*GGLKLIPIFLMDFWKEPL GPALAHQLYQGRD*SSDIWIRTA SLHTLPIVGPHLLGDLASFCTLLTPD PCQHVPISRADTVEMG
3864	9361	A	4144	1	154	LVWS*EASKIPGGAEAAHPPTTF
3865	9362	A	4145	2	231	FFFESGSRSVTQAGVQ*HSLGSLQPL PPRFK*FSCLSLPSSWDYTHVPT RPA NFCIFSGDGVSSCWPGWSRTPNLR
3866	9363	A	4146	1	303	GTRGSVKEGAKYTSHRDMGLSTFD RDADQWKENCANVYG*GCRYNNC QAANLNGIYYPGGSYDPRNNSAYE TDNGVWVVSFTGAHYSRAARMKI RPLVTQ
3867	9364	A	4147	3	372	HAGLGAHPLHHPVIQEQEGLPAPRG FGYRSEVD*IRIPAESTGQNSQCQLR K*KDDSYFHCYFCGCVCTCRGRL QSSTSHQCQAAL*LLLVPCLTMLRC ISSLIYT*NLKTVHVSRLNFIYN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3868	9365	A	4148	2	98	RRPFFFFFFFASCI*NLISPNVQLSNFT CILRN
3869	9366	A	4149	1	230	SGRPFLFFFQGKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTTEGPGYPLLGETETKLFR TA
3870	9367	A	4150	1034	2354	DRVLAPVAQTGVQWHDLSLQPPP PGFKRFFCLSLPSSWDYRPP*RPAN FC*FLVETGFRHVQGAGLGLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPPRTFSPSP PHTHTHTHTCSPICPRQSRSFQGPR MPDPDPGDATCGAGPGGSAPARAA GPRSAPRRAKARVQARVQARAQAR WVRALTLLAAHPRLQPVPAIARR AAQSSSSPPPATPAKSPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEVG REEGRGRRGDGLGHGGCVEPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI
3871	9368	A	4151	387	478	
3872	9369	A	4152	757	1477	HKENRNSLELRQNQSSPIWALPLHG LERKGLGRDHSSPHLPLPSERL*K ASASQGPWECCPSRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGPSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN
3873	9370	A	4153	32	255	SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFITNVPTAP
3874	9371	A	4154	1	265	CDTVLLCHPGWSAVAQSQTITTS SQUIRFSLNLPSSQNTRRASHPAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA
3875	9372	A	4155	92	333	FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSLSLSGWDYRC LAQHQAACCIFSRDGISPF*PCWYQT PDLR
3876	9373	A	4156	16	181	ICSLPSTVDVIEFLDYVVKVSLKL*SI IKICDSKHTHIHTYGYVYIFSPGK PV
3877	9374	A	4157	1	355	TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPCLA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQAIGTSHHAWPH LLVLTVCVAHTLFRHFYL
3878	9375	A	4158	1	194	FFFFFTISYIFIYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS

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3879	9376	A	4159	112	270	ILGNSLFKNYK*YLSPAAVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL
3880	9377	A	4160	1	211	RFSCLSLLSS*DYRRVPPRPAIFVFL VETRFHYVGQDGLDFLTSCSARLYL PKCRDYRRELLCPAPASLL
3881	9378	A	4161	2	253	ETDSCSVAQTRVQWYDLGSLQQPP PRFKRFSCLSLPNSWDYKCVPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASAPK
3882	9379	A	4162	198	276	KPFMAQCSF*IYEAIFSCTSSEIRY
3883	9380	A	4163	3	193	HFGRRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVPTT*EA EAGESLEPGGQRLQ
3884	9381	A	4164	2	515	DTEKMSPWDMELIPNNAVPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLNRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNRPAKSGTDLHLH FIKDQTCYNIPLYNSMKKKVLS
3885	9382	A	4165	3	418	HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNAVTRIK EMRNALCTLSLDYAHKLLGDSCTL *LLSHCMLVTLAN*PSSEFTPVAHTL VAKILAFVSTELTSKY
3886	9383	A	4166	1	191	CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSLPSSWDYRHVPEH PTNFVYFFVERKSH
3887	9384	A	4167	3160	3732	
3888	9385	A	4168	2	326	PRSGSESFSCQLSPFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV
3889	9386	A	4169	2	163	LIFVFIVGTGFHHVQGAGLECLTSS DPSASASQSAGITGVNHHTRPPSAF GC*T*GTGFHHVQGAGLECLTSSDP SASASQSAGITGVNHHTRPPSAFGC
3890	9387	A	4170	126	348	HISIFETGSYSVTQAGAQLDGHSL QP*PPGLK*SSCLSLPSSWDYRHMP CPANFYIFCRDGVSPRCGSCNF
3891	9388	A	4171	1659	1970	MLKGGAKIRSRRTGVSHSLHSDL NFFFFWDKSIALSHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR
3892	9389	A	4172	153	278	MRPDTVAHTCNPSTLGGQGGGRIT*T HEFETSLGDMMKPYLYK
3893	9390	A	4173	3	254	LQYLVFISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCCQCIIDLALI AVISSQT
3894	9391	A	4174	3	225	SLTHLTATSILLK*FSCLGLPSSWDH RCPPRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3895	9392	A	4175	1	344	GGALSGGTPGFSPSPGKTAAPGQS GNPPGGF*RVSPSGGSQRGGFPGNT PAPGPLPSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAPVKHLA APTNRYSFHPQK
3896	9393	A	4176	2	201	QPGQYGKHPVLIKNSKIKPFWGDPP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF
3897	9394	A	4177	39	225	KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKSFQ FCQMLLLCMTR
3898	9395	A	4178	322	451	INSTDWAPWLTLVISALWEAEAA/G SRGQEIETILANTVKPRLY
3899	9396	A	4179	234	383	
3900	9397	A	4180	86	216	KQTLGQAWWLTPIIPALWEAEVGR S*DQEIETILPNTVKPHRY
3901	9398	A	4181	1	4123	MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVVPALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRRDLGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPPAGVPGSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFLV HWPQGRTLFLPAALAHPLGHEEFR QLCPQMSPPNFGLSESPRPVRCQCN PGQHRGWLRRWHPLPPAPSLGSG QVLGHLSTTSSHPGAPSPGHWCAA PDPADPAPVTRPPRAQSARGTHLP PCPCRDPTTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTELRAHGGRMAKLRS HRASWASPPDLAAASPHLAPSAA SADGLPATRAQTTPPPPTPSRQAELP PGSPSPGAQGLPGGVDVGIEVPLGR PARAGTVAGGVVGEDVAVEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGTLRQGFWWTLR GTDVETYPFSAPRAASHGVGRHEEL PDPTGPCGGRLLSLTIHGVTIRYHAL LWARGPIMSKSQVLGEWEPVQGGK SSENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVSVLIHFPLISILSYATW GLSLLECIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCVGMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLGPPGLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKY KYEECKDLIKFMLRNERQFKEECLA

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						EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRSLNEHLQALLT PDEPKSQGQDLQEQLAEGLDWH STLSKSSAQKMTKMRMKMFK/CEE DEKVLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRSLNEHL QALLTPDEPKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDVQ VEEDEKVLESSAPREVQKAEESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGPTSSATNVMVSA GPLSSEKAEMNILEINEKLCPQLAEK KQQFRSLKEKCFVTQVACFLAKQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQE RELTLREKLREGRDASRSLNEHLQ ALLTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLS
3902	9399	B	4182	1	799	MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTSIYM FYQKVGDNISDSWKNAGRPFKDS KFDANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHGKQSLTTAQI HFPLISILSYATWGLSLECI PGSPVC TLLVRFSGGPPMDPGSERKGFGRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQ YANRLSPRVGRFINAAGTTX*
3903	9400	A	4183	260	387	REVGRVRWLTTPVIPARWEAEVGRS *GQEIKTILANTVKPRLY
3904	9401	A	4184	1212	1442	
3905	9402	A	4185	3844	4180	KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKKNLLTWLVNKLCP CRAWWLTTPVIPALWEAEAGRSRGQ EITILANTVKPRLY
3906	9403	A	4186	8	385	
3907	9404	A	4187	2	284	
3908	9405	A	4188	1477	1697	
3909	9406	A	4189	17	385	
3910	9407	A	4190	1	837	GKVVLELERFLPQPFTGEIRGMCDF MNLADCLLVNLAYESSVFCTSI AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWWW ENAI AALFRRHIPVSWLIRATLSESE NFEAAVGKLAKSPLIADVNYIAGG TCPREGVVVTRNRDGPDIGPLNPL

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						NGAWLRVETDYYHWKPAPKEDDR RTSAIKALNATGQANLKLEALFQIL TVVPVYNNLTITYTTAMSAGSPYKY MTRIRNPS
3911	9408	A	4191	653	727	
3912	9409	A	4192	26	161	
3913	9410	A	4193	3	186	
3914	9411	A	4194	28	186	
3915	9412	A	4195	356	428	
3916	9413	C	4196	35	430	MKSCRXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKPNFSSNSSEAFIS RSQGHKDAKKEFVPLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXLQSHPLVR*
3917	9414	A	4197	213	394	
3918	9415	A	4198	28	123	
3919	9416	A	4199	1578	1835	SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSAL CNSSWREGAVGCLPMDFPRLHL SPSSLHCRNKP
3920	9417	A	4200	213	305	
3921	9418	A	4201	1715	1850	
3922	9419	A	4202	4016	4315	
3923	9420	A	4203	28	239	
3924	9421	A	4204	7	216	
3925	9422	A	4205	1	576	
3926	9423	A	4206	1	500	
3927	9424	A	4207	1	1266	
3928	9425	A	4208	1	162	
3929	9426	A	4209	1	229	
3930	9427	A	4210	197	416	
3931	9428	A	4211	1	131	
3932	9429	A	4212	76	274	
3933	9430	A	4213	295	2530	RPATMAARPLPVSPARALLALAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDKNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTDVSLARNYTVILGH CY YHGHVIRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKL FPA KKLKSVRGSCGSHHNT PNLAAKNV FPPPSQTWARRH KRETLKATKYVE LVIVADNREF QRQGDLEKVKQRLEIANHVDK FYRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLD WRK MKLLPRKSHDNAQLVSG VYFQGT IGMAPIMSMCTADQ SGGIVMDHSD NPLGAAVTLA HELGHNFGMNHDTL DRGCSCQ MAVEKGGCIMNASTGYP FPMVFSSCSRKDLETSLEKGM GVCL FNLPEVRESFGGQKCG NRFVEEGEE CDCGEPEECM NRCCNATTCTLKPD AVCAH GLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPAN VYLHD GHSCQDVG YCYNGI CQTHEQQCV TLWGP GAKPA PGICFERVNSAGDPY

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						GNCCKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNIPQQ GGRIJLCRGTHVYLGDDMPDGLVL AGTKCADGKICLNQQCQNISVFGV HECAMQCHGRGVCNNRNKNCHCEA HWAPPFCDKFGFGGSTDSGPIRQAG KEARQEAESNRERGQGGQIEPLGSQ EHASTASLTLI
3934	9431	A	4217	2	119	
3935	9432	A	4218	2	147	
3936	9433	A	4219	10	216	
3937	9434	A	4220	245	455	
3938	9435	A	4221	1	2867	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQTGTSRWDG VSKKAPRHLSVPCTRPREARQEA DSTSRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPQEQALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAHVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFLKLPFMVNSVLA GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGGQRMVEQSE KLNQVLEASRLWDNMRKLGECTEE AHQMTDHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTIVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPHFRVESFSE DEWNLLYVAVTRAKKRLIMTKSLE NILTLAGYFLQAEITSNVLKTGV VRACCVGQCNNALSPVDTVLTMK KLAPITY*ATGKIENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPREALLFLVF
3939	9436	A	4222	57	302	
3940	9437	A	4223	1	550	DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPQTSGLSPS RLSKSQGGEEGGLSDKCSRKTLFY LIATLNEFRPDYDFSTARSHFESRE PSLKLVLNAVNCSLFSAVREDFKD LKPQLWNAVGRGDLPLKCDIYSY

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						NPDLSDSPSREDGSLWSFNFFYNKRLKRNRL
3941	9438	A	4224	11	511	GRTRSIAGEETTQRPGPNCGGNCLCLHTLAINMRICYSQTTFFHPLRLKGQRWPF\FSSLELFPVGFPAHLLVQS TLPKPRPERAFTAPSLFPVTLGFCLGRILCQRLLLCPSCLATALSINGYSRTQECQSWKGRDTGLHKGKLLLEALG GTEGFGDRARAKIEDS
3942	9439	A	4225	1	279	
3943	9440	A	4226	1011	1322	
3944	9441	A	4227	3	468	TPLHVYNEVMSVGQKYGIRNAGYYALRSLRIEKFFAFWQDINNLT\TPLECGRESRVKLEKGMDFIGRDALLQ QKQNGVYKRLTMFILDDHDSLDLWPWWGEPIYRNGQYVGKTT\SAYSYSLERHVCLGFVHNFS EDTGEEQ VVTADFINRG
3945	9442	A	4228	1	1236	
3946	9443	B	4229	1	1742	MKRDNSGGCLPAPASAWPARPRQQA EWRALTRGPANHCGIISTLGEPE TPLIGLRTFQCCRLVTDGRVLAGTV SSEPTDGRSPAPGPGRRTSAMVLL KLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGD TGPCGPCSEIHYDRIGGRDAAHLVN QDDPNVLEIWNLVFIQYNRFGNCVE LQASAAFNWNNQRCKTRNRYICQF ADLRRNLNIINDDITGRVHKDRKLL TGDSPFAANALGKLAAQEMMAAY AVSLPKLTALLRVFSTVRSIGERFS PIRVLRLLRHTTPNYIYQRLIPYVCV LPTTELSINLNMLTENDIPLFRALFL NNITDADARVLLQKRPREGWLTTD AFLYWAQQDFSGVKPLVAQHW MTFSADSVSSVHTLTDDLPLESLAD QPGAGNVHLLIPPEGLLYRSLTLPN AKYKLTATLQWLAEETLPDNTQD WHWTVVDKQNESVEDCLIPLFGKP QGKGCLEKSVWAAGRPFYSYAGDK NRQLTRYSDTRWHEDSVNRNWFVSV MVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKG*
3947	9444	A	4230	1	638	
3948	9445	A	4231	1377	1746	
3949	9446	B	4232	1	1716	MSQYYQPQRPEHIELD SHAKFFPH HHLQVADSAHLAASPLRRTHRAL TWAQALPQEEGSGAPSPGAPSPPT KSFGRMTSASAVFILDVKGKMESC YVVQDVLNSWSPAIPLLQPPKVSDD SGGHIEECQCLPVYSFLYKTIEVGI LRILQGAGGGEHPDNFVIVYELLDE LMDFASRRPPTARSCRHHSAEQQA GDGQVTGAPTVTNAVSWRSEGIKS MQRQRPSENRNRYHQAQVFLSGMP ELRLGLNDRVSSSSLAAGQFKKSQ WPTVWRYLCLYPAMRLPQIQDQCG

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						QRQVCAGRNVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPIMKIIKSGYQA LPWVRTSPRVAIPTSYQLEGRRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARRLLRADSAAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAACTGSCWCIPTPSTLRQD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSQVQSMTQ PALDSWTP*
3950	9447	A	4233	1	372	
3951	9448	B	4234	48	1158	MSASAVFILDVKGKPLISRNKGDV AMSKIEHFMPLLVQREEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPPDGDFELMSYRLSTHVKPLI WIESVIEKFHSRVEIMVKAQGQFK KQSVANGVEISVPVPSDADSPRFT SVGQRQVCAGEKRRYFGVLSLGG AREYLMRAHFGLPKCEKERX*
3952	9449	B	4235	153	458	KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEVRKTK NPRPC*
3953	9450	A	4236	3	182	
3954	9451	A	4237	49	607	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASQAFELILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAAEERRQSP*SCSS*RLAE KLRAPRKKCFQKAIEENNFQ*NGQ KRKLTPHKMEAANKETPERPQMAA KLEPFAEEKDKAH*KKCGKNKESK DPADETEAGLI
3955	9452	A	4238	1	356	TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQPPQNTGFPR/SNQPYYN SRGVSRGSRGARGLMNGYRGPAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP
3956	9453	A	4239	1	2206	RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLDYQERMNK GERLNQDQLDAVSKYQEVTTNNLEF AKELQRSFMALSQDIQTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDVVRTDLKQGLNGVPILSEEE LSLLDEFYKLVDPERDMSLRLENEY EHASIHLDLLEGGKEKPVCGTTYK VLKEIVERVFQSNYFDSTHNHQNGL

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						CEEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTHEYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMGGPDNFIQDSML DFENQTLDPAIVSAQPMNPTQNMD MPQLVCPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPE\TLKQ\QNQSQA\SYNQSFSS \QSPS*QQTELQ\EQ\LT\TVVGY HGS\QDQSHQ\VTGNHQ\PPQ\QNT GIST*AIRPYNSRGVSRGGSRGAR GLMNGYRGP\ANGFR\GGYDGLPAP SFLCLKPNSGY\SHSPQFQCLPRDYL WPIQRDG\YIQNFKRGSQSGSPRG APRGRG\GPPRPNRGMPQMNTQQV K
3957	9454	A	4240	1	151	
3958	9455	A	4241	5	120	
3959	9456	A	4242	1	315	EQMVSEDVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV
3960	9457	A	4243	107	4057	PFCCGFPGLCVGVIRSTMSSVAVLTQ ESFAEHRSGLVPPQIKVATLNSEES DPPTYKDAFPPLPEKAACLESAPQEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEQEQA KICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINPPP SVNRTIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQHKYVI GPKGNSLQEILERTGVSVIIPSDSIS ETVILRGEPEKLGQALTEVYAKANS FTVSSVAAPSWLHRFIIKKKGQNL KITQQMPKVHIEFTGEDKITLEGPT EDVNVAQE QIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPDSEKSNLIRIEGDPQGV QQAKRELLELASRMENERTKDLIIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRLS IQKDLANIAEVEVSIPAKLHNSLIGT KGRLIRSIMEECGGVHIHFPVEGSGS DTVVIRGPSSDVEKAKKQLHLAAE KQTKSFTVDIRAKPEYHKFLIGGG GKIRKVRDSTGARVIFPAAEDKDQD

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						LITIIGKEDAVREAQKELEALIQNLD NVVEDSMLVDPKHHRHVFVIRRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIEDLEA QVTLECAIPQKFHRSVMGPKGSRJQ QITRDFSVQIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKSGIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSVTVDPKLHSPGLSGRK GASNSQIRGLKHDVNIQFP\DKD\D ANQHQD\QITFTGYEKNHSSLPDGA LRIVG\ELE\QMVSE\DP\LNHRVSR PASFGARGKSHPPKIMYEFK\VIDRF PNKSGAPKTPNCVNC*RGFP\ENVE ESHSTQHPSILEEE\YLADV\VDSEA LQ\VYMEPP/AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEFP SFWG*RWLPKTL\WGPKTIMIKKE QNPLPAC
3961	9458	A	4244	11	323	
3962	9459	A	4245	3	171	
3963	9460	B	4246	148	405	XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLAFE AAESVGIKPSLELSEMLYTDPRDWQ SVMQYVAQIYKYFET*
3964	9461	A	4247	2	438	AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFSPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCSHNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVVM
3965	9462	A	4248	3	256	
3966	9463	A	4249	3	444	
3967	9464	A	4250	3	828	VKGVPGVKAERF*RMTAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFIDS VKALAVKQQRVTYRLTLVKA\WNV VSLQAYAYQLGSLGNPDFIEVKGVT YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYEIACEHEHSNCLLIA HRKFKIGGEWWTWIDYNRFQELIQ EYEDSGGSKTFSKDYMARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC
3968	9465	A	4251	1	384	
3969	9466	A	4252	3	1225	
3970	9467	A	4253	1	864	
3971	9468	A	4254	1	1266	GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQIGFTTDPMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVVDLCY RRNGHNEMDEPMFTQPLMYKQIRK QKPV\QKYAELLVSQGVVNQPEYE

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						CVSMHGVRNKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDGIEPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCEPLERK GFGL*GVPCFHLRFPRVLCVQGGEL QQRH\NGNWWAS\PILWGRKFERLK NFHP*KPYGSPGILSPWQAGPQTQ MVPQFFICTAQDCSGWNGQAMWV FGTSEKAMNIVEAHWSRFG\SR\N GKTQQRSPFADCGQLLISLTCVFIF NHPDHSLL
3972	9469	A	4255	3	275	
3973	9470	A	4256	125	315	
3974	9471	A	4257	3	292	
3975	9472	A	4259	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEA\INSLPTKKKSRTRWIHSRI LPEVQGGAEKEGILPNSFYEASIIIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIIQHINRTNDKNHMI ISIDAEKPFDKIQQHFMKLTNLKLA QNLLKLIGNFSKVSGYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W\NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYAAKHKMKK CSSSLVIREIQIKTTMRYHLTPVRMA IHKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS\WRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPIVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQ SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPC DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAVHHKLKVLHWRS SLSNNKGTGRLYEQVA
3976	9473	A	4260	1	2526	
3977	9474	A	4261	1	3111	

MISSING AT THE TIME OF PUBLICATION

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						VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPSIVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPPEYGWEEAFLALRKCSQ CPEDAVAASGAVALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGSLIHLPSKT QSQCPLGFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLLDLASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGPSCLGVSFQKGLCQEM VYISTRGSSSGLRPLVLSLHGWAVD TAIHTCIPFPTDIIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSGVH
3980	9477	A	4264	1	2653	MGDFTPLSTLDRSMRQKVNKDIQ ELNSALHQADLIDIYRNLPPESTEYT FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKKLTQ NRSTTWKLNLLNLDYVWHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTTHSKASRRQEIS KIRGELKEIETQKTLQKINESRGWFF EKINKIDRLARLIKKKREKNQIHAI KNDKGDMSNHTIEIQTIREYYKHL YANKLENLKEIDKFLETYSPLRLNQ EEVESLNRPITGSEIEAIIINSLPNKRS PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKNKAG GIMLPDFKLYYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVPRPKTIKLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFTAKETTIRLNRPTEWEKIFA IYSSDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYA AKRH MKKCASSLAIREIQTMMRYHLTP VRMAIHKSGNNRCWRGCGEIGTLL HCWWDCKL VQPLWKS VWRFLRDL ELEIPFDPAIPLGIYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTM EYYADIKKDE FMSFVRTRMKLETIILSKISQEKKT KHRMFSLIGGN
3981	9478	A	4265	1	2988	
3982	9479	A	4266	1	2515	MGDFTPLSTLDRSTRQKVNKDTQ ELNSAPHQADLIDIYRTLHPKST EYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT

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						QNRSTTWKLNLLDDYVWHNEM KAEIKMFFETNENKDTTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLEKEKQEQTHSKASRRQE ITKIRAELEIETQKTVQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITDPTEIQTIREYYKH LYANKLENLEEMDKFLDTYTLPR NQEEVESLNRPIITGSEIVAIHNSLTK KSPGPDGFTAIFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLLKEI KEDTNKWKNIPCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQKRAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWYWY QNRDIDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSLFNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKTLEENLGITQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFCTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYH LTLVRMAIHKSGNNRCWRGRGEIG TLLHCWWDCKLVQSLWKSVMQFL RDLELEIPFDPAIPLL
3983	9480	B	4267	1	2634	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGLDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEITNDLSDHSAIKLELRIKNLTQ NCATTQKLNNLLNDYVWHNEMK AEIKMFFETNENKDTTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITDPTEIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPIITGAEIVAIHNSLPTKK SPGPDGFTAIFYQRFKGLRQNSTT FMPKTLNKLIGDGYLKIRAIYDKP TANIILNGQKLEAFPLKTGRQGW LSPLLFNIVLEVLAIRAEKEIKGIQ LGKEEVKLSLFADDMIVYLENPIVS AQNLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGQLTRDVKDLFKENYKPLLK KIKEDTNKWKNIPCSWVGRINIVKMAI AILPKVIYRFHAIPKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAIVTKTAWYWY QNRDIDQWIRTEPSEITLHIYKYLIF DKPEKNKQWGKDSLFNKWYWEN WLAICRKLKLDPFLTPYTKINSRWI

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						KDLNIRPKTIKTLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAA KKHMKKCSPSLAIREMQIKTTMRY HLTPVRMTIISQETTGADEDVEK*
3984	9481	A	4268	1	2429	
3985	9482	A	4269	1	2745	
3986	9483	A	4270	1	3210	MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEIITNC LSDHSAIKLELRIKNLTQNRSTTWK LNNLLNDYVWHNEMKAEIKMFFE TNENKDTTYQNLWDTFKAVCRGKF IALNAHKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAEKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDI TDPTEIQTIREYYKHLIYANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQSIEKEGI LPNSFYEASIIIPKPGRDTTKKENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIPGMQGWFNIRKSINVI QHINRAKDKNHMIIISIDA EKA FDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINI QKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENHKPLLN EIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIASILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSETPHIYNYL IFDKREKNKQWKGDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKINSRW IKDLNVRPKTIKTLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFC TAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGCGEIG TLLHCWWDC KL VQPLWKAVWRFL RDLELEIPFDP AIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPEQA KPYPPTLPTLAQDF
3987	9484	A	4271	3	3655	
3988	9485	A	4272	1	3615	
3989	9486	A	4273	1	4038	
3990	9487	A	4274	1	3317	MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLDIYRTLQPKSTEYT FFSAPHHTYSKIDHIVGSKALLSKCK

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						RTEIITNYLSDHSAIKLELRKNTQS RSTTWKLNLLNDYWVHNEMKA EIKMFFETNENKDDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQLEKEKQEQTTHSKASRRQEITKI RAELKEIETQKTLQKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITDPTEIQTIREYYKHLA NKLENLEMDKFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEASIIIPKLGRDT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGW NIRKSINVIQHINRGKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTTRQGCPLSPLFNIVLEVLAR AIRQEKEIKAQNLLKLISNFRKVS KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNI PCSWI GRINIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTAWYWYQKRDIQWNRIELSEIIP HIYNHLIFDKPDKNKKWGKDSVFN KRCWENWLAICRKLKLDFTLTPYT KINSRWIKDLHVRPKAIKTLEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLSFCTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSSLAIREMQIKT TMRYHLTPVRKAIKKSGNNRCWR GCGEIGTLLHCWWDCCLVQPLWK TVWQFLRDLELEIPFYPAIPLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQKTKHGIFSLIGGN
3991	9488	A	4275	959	2955	
3992	9489	A	4276	1	2870	MKAIEIKMFFDTSSENKDDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKEKQEQTTHSKASRR QEITKIRAELEIETQKTLQKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITDPTEIQTIREYYK HLYANKLENLEMDKFLDYTLPR LNQEEVESLNRPTGSEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFNIRK SINVTQHINRAKDKNHMISIDA EKA FDKIQPFMLKTLNKLIGDGT YFKIIRAIYDNPTANIILNGQKLEAFP LKTGTTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSL FADNMIVY

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						LENPIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNNRQTESQIMSQLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSGEG RINIVKMAILPKNWKKTTLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYWYQNRDLQW NRTEPSEITPHIYNLIFDKPKDNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIHK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKS VWRFLRDLELEIPFD PAIPLLGIHPKDYKSCCYNDTCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTMYYAAIKNDEFVSFVGT WMKLEIIILSKLSQEQTTHRIFSLIG GN
3993	9490	A	4277	1	2982	
3994	9491	A	4278	1614	4577	TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAIQKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNIPCSWVGRNIV KMAILPKVIYRFNAIPIKLPMPPFTE LEKTTLKFIWNQKRACIAKSILSQK NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCPSLAIREMQIKTTM RYHLTPVRMAIHKSGNNRCWRGCG GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCTRM TITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSL GKVPFWLYLGSRLATPTSSQLFFIG GKERSPDEQVDILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTIN KPSFRLTRCGIRMTSSNMPLPASST QRIVQGRETAMEGEWPWQASLQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWIATFGATITPPAVKRN RKIILHENYHRETNDIALVQLSTG VEFSNIVQRVCLPDSSIKLPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS

MISSING AT THE TIME OF PUBLICATION

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						LPCLMIPSQMLLENFSAIIPGHRWC THMLDNGSAVSTNMTPKALLTISIP PGPNQGP HQCRRFRQPQWQLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFIWGLLSYRFGRKPMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAF GMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCAFSAGQAALGGL AFALRDWRTLQLAASVPFFAISLIS WWLPESARWLIIGKPKDQALQELR KVARINGHKEAKNLTETPPPPPIPI PSPTAPPLSTPTITFTAITPSPAPPIS LTPQPPSLQNISTTTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARTHLMGVL DVSGETECVYLKVLMSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFLLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCGISLTCLTIYKAELFPTPV RMTADGILHTVGRLGAMMGPIILM SRQALPLLPLL YGVISIASSLVVLF LPETQGLPLPDTIQDLESQKSTAAQ GNRQEA V TVESTSL
4009	9506	A	4293	3672	3967	LQPPPHGRRGLLHHLSPGHGPHHP VTPQTRSPAQP/PGQMGPRAPLGCC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA
4010	9507	A	4294	1773	2213	AHWLHL PRLPHHRAQWAAALQPG PAGWGWSWQPQLCSAGRLLCHGAI GRP/LSIFCWTWDLGASSCGHPAAR SMMASGVTWTSRGMGEKRVSSSTPF PIFFPAASPPPPSRLPNCPFCHRTLAE RAQH LASVRPGLHLSSPTCCMKCSC
4011	9508	A	4295	1	616	
4012	9509	A	4296	93	502	EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQLCLEVRLARGVCRRAHLS PPVCIQSPLSQGH*LLCSK*SASIIGA GLANFQGTDSLVAEHPVSWIHNNSN FVFHPGYFRL
4013	9510	A	4297	1537	2360	TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLLSRR*LVWPMRSASLQSM PLASPPVCPPGLLFLWP*QALL\PS DCG/PLSLTRLR*GGVPPRPHWCSR FRWLCARVLL
4014	9511	A	4298	1	493	MEAPAE LLAALPALATALALLAW LLVRRGAAASPEPARAPPEPAPAE ATGAPAPSRCAPEPAASPAGPEEP GEPAGLGELGEPAGPEGEPEGDPDA AAPAEAE/PGGGGEAGTHRGPRGP LPTPGAPAAA VPRRARERGRGLQ PRLPPGSAEPAARRKCR
4015	9512	A	4299	2	418	
4016	9513	A	4300	8808	9100	RKVLFFFFFEMKRSRVA RLGCSTI

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						SAHCNLCPLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVGQA GLELLT*VIHPPQSPKVLGLQV
4017	9514	A	4301	3	101	
4018	9515	C	4302	5673	5894	MWQLTPAILALGEIEAGGLFEPRRV KLA WPAQEELVSTKNTKISWVWW RAPVVPATQEA EVGGSLELERSRLQ *
4019	9516	A	4303	1	241	
4020	9517	A	4304	58	180	
4021	9518	A	4305	2	325	FFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCLSLPSS\WIYR HVPPCPANFFFFLVETGFHHVGQAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS
4022	9519	A	4306	206	386	
4023	9520	A	4307	2	260	
4024	9521	A	4308	5	227	
4025	9522	A	4309	676	1076	FLLCFPPCLSPKFFFLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSM/RLFF ELLVKSLPVASPVPLSVIAEQSSQI CPCHGI
4026	9523	A	4310	3	205	
4027	9524	A	4311	3	345	
4028	9525	A	4312	118	7473	
4029	9526	A	4313	1	297	
4030	9527	A	4314	366	504	
4031	9528	A	4315	1	2899	MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVLPSYIRVLEAAV RNCDFGLMKKEDVMNILDWKTQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDHSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKLPCRQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQPVPEPETVLKNQEV EFG RNRERLQFFKWSSRVLKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTD SHITMVNGLGILGWVG GIETEAVMLGLPVSLTLPEVVGCEL TGSSNPFVTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRRTIA NMCPEYGAILSFFPVDNVT LKHEH TGFSKAKLESMETYLKAVKLFRND QNSSGEPEYSQVIQINLSIVPSVSG PKRPQDRVAVTDMKSDFQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAAVISCTNNCNP SVM LAAGLLAKKAVEAGLRVKPYIRTS SPGSGMVTHYLSSSGVLPYLSKLG EIVGYGCSTCVGNTAPLSDAVLNA VKQGD LVTCGNFIWK\KNFEGRLC DCVRANYLASPLVVAIAGTVNI DFQTEPLGTDPTGKNIYLHDIWPSR EEVHRVEEEHVILSMFKALKDKIEM

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						GNKRWNSLEAPDSVLFPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDDHISFAGSIARNSAAA KYL TNRGLTPREFNSYGARRGND VMTRGTFANIKLFNKF IGKPAKPTIH FPSGQTL DVFEAAEL YQKEGIPLIIL AGKKY GSGNSRDWAAKGPYLLGV KAVLAESYEKIH KDHLIGIGIAPLQF LPGENADSLGLSGRETFSLTFPEELS PGUTLNIQTSTGKVFSVIASFEDDV EITL\YKHG\GLLN FV\ARKFS
4032	9529	A	4316	1	178	
4033	9530	A	4317	165	403	PSSRSRAPSPPTLCGASCCPTCPAC FPAPSR RAGAAGGAG *RPRGGPTST TCYGPTETWLYQLQTVGSRNTTRT PKST
4034	9531	A	4318	3	404	
4035	9532	A	4319	3	217	
4036	9533	A	4320	3	423	SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFAKTPS/CQQGQCDKTRSRV TLQEWNDPLDHDLEAQLIYRHLLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPSEPNCLELQ
4037	9534	A	4321	2	3040	DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIIRTATVWKTLCPFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFGSWAHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGRTRETSIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLVS RNDFLGKVVIDVQRLRVVQEEGW FRLQPDQSKSRRHDEGNLGSLLQLEV RLRDETVLPSSYYQPLVHLLCHEVK LGMQPGQQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFLDLLFQLE LSRTSETNTLFRSNLASKSMESFLK VAGMQYLHGV LGPIINKVFEEKKY VELDPSKVEVKDVGC SGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVVRATFRQLFRRVRERFPG AQHENVPFIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGV AQLKDFITKLVDIEEKDE LDLQRTLSL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAK MPSSKKSALIKLANIRAAEKVEEKS FGGSHVMQVIYTD DAGRPQTAYLQ C/KGV PFCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQPTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTD TDF RSVPQTGVQWRDLGSLQSPPRVK QFSCLNLPSSWDDRHSPPSLANFFV

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						F*LEMGFHHVSQAALVLLLLLLLL FDTESRSIIQAGVQWCNLSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL IYRHLLGVEAMLWERHRELSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPPSEPNCLLELQT
4038	9535	A	4322	308	658	
4039	9536	A	4323	1	2662	MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIVKVDNEPIIRYPHPQDRGA LSLSSARALPAKGATVWKTLCPF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRL VWPGARACRLRCSVLEARDLAPKD RNGTSDPFVRVRYKGRTRETSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIDVQR LRVVQQEEGWFRLLQPDQSKSRRHD EGNLSLQLEVRLRDETVPSSYYQ PLVHLLCHEVKLGMQGGPQLIPLIE ETTSTECRQDVATNLLKFLGQGLA KDFLDLLFQLELSRTSETNLFRRNS LASKSMESFLKFALHVVYLAWSAD TAGKRCKGGCREKVGWSGTGGD RINVTCCGGPQVAGMQYLHGVLPPI NKVFEEKKYVELDPSKVEVKDVG SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPIAVTSFLC LRFSPAIMSPKLFHLRERHADARTS RTLALLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGVQQLKDFITK LVDIEEKDELDLQRTLSLQAPPVKE GPLFIHRTKGKGPLMSSSFKKLYFSL TTEALSFAKTPSSKKSALIKLANIRA AEKVEEKSFGGSHVMQVIYTDAG RPQTAYLOCKCVNELNQWLSALRK VSINNTGLLSYHPGVFRGDKWSC CHQI*ITGQG\CDKTRVTG*PCREW NDLLDRDLE\SLIYRHLLGVEAML WERHRELSGGAEAGTVPTKPLAKV PEDSLARLAPGCLQDLREAHSSSPA GSPSPSEPNLASLEAADVRPALRSPC
4040	9537	A	4324	69	194	
4041	9538	A	4325	1350	2203	TWRLDPQIISSPKPQPGGTYTLEV KSSKSKKVLSPHP*WPPLRLWQRIG GSPEGGTQAPDGS�PPPPRPKSERV GSPKLSGGKR/EGSHPGGPPHITH/ DGEEKAKSSWFGLREAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLTVTSGSIQPVTPAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLQRRERELSQRDEH VQELSYIDRLVRIMETSPTLLQIPP GPPK
4042	9539	A	4326	2	761	
4043	9540	A	4327	2	410	

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4044	9541	A	4328	295	780	
4045	9542	A	4329	1	2203	
4046	9543	A	4330	1	190	RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFRNW AFRLLLQCHSPDF
4047	9544	A	4331	2	269	
4048	9545	A	4332	3	223	DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR
4049	9546	A	4333	2	366	PCSEPTRRSRGATPSHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCSTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN
4050	9547	A	4334	3	131	
4051	9548	A	4335	923	1442	GGPCLCRPSWPAVLQVRSGLPTSIPS PWPLFCLPQSILLGPLEMPG*RPLLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDFTTNDSSSTG *AKPSALLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM
4052	9549	A	4336	1	137	
4053	9550	A	4337	876	1012	
4054	9551	A	4338	148	278	
4055	9552	B	4339	7	673	MVEVTILMIMGLYRIYGFAVAVVS MILSYNVCSEGEVVSVMFSFVVTSS SCGMHRSTLLSSVYSHLIFDSAYVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETA VINHKRKNPRI VQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX *
4056	9553	A	4340	786	1088	
4057	9554	A	4342	1	66	
4058	9555	A	4343	2	80	
4059	9556	A	4344	8	258	
4060	9557	A	4345	5	383	
4061	9558	A	4346	99	634	TTTMSSKRTKTKTKKRPQRATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGK\NPTDAY LDAMMNEAPGPINFTMFLTMFGEK LNGTDPEDVIRNAFACFDEEA\TG QEDYLRE\LLTGMGDRFTDEE\DEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD
4062	9559	A	4347	1	966	
4063	9560	A	4348	3	215	
4064	9561	A	4349	1	1416	NSGGSGGGTSGSGSSSGQKMGQS QSGGHGPGGGKKDDKDKKKYEP VPTRVGKKKKKTKGPDAASKPLV TPHTQCRLKLLKLERIKDYLLMEEE FIRNQEQMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIIDDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLAKAVANQTSASFLR WVGVELIQKYLGDGPKLVRELFV A\EEHAPSIVFIDEIDAIGTKRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DVVKVFPWATNR\ETL\DPALI RPGRI\DR\KNEFPLPDEKTKKRIFI HTSRMTLADDVTL\DDLIHGLKIDLS GA\DI\KAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL
4065	9562	A	4350	2	70	
4066	9563	A	4351	1	1605	
4067	9564	A	4352	3	193	
4068	9565	A	4353	3	127	LFHPCQDSQQHH*CVCCRLTGHA A*VHGPCQAVQTYRASH
4069	9566	A	4354	2	323	
4070	9567	A	4355	3	85	
4071	9568	A	4356	49	413	
4072	9569	A	4357	3	338	
4073	9570	A	4358	1	3735	
4074	9571	A	4359	2	317	
4075	9572	B	4360	2576	2685	MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRSSSQSKTFNMPPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKINLNHLLNFTFEPR GQTGHFEGSGHGSWGKRKNWGHK PFNKELFLQANCQFVVEDQDYTA HFADPDTLVNWDVFVEQVRICSHEV PSCPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTWSKPCICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGVLVALPKSKWMNVDPHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEEKHTPESCFIEA AIQELKTREEALSLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEA VSEPEPEGLPEACDDLE LADDNLKEGTICTESSQQEPITKSGF TRLSSSPCYFYFYQAEDGQHMFLLHP VNVRCLVREYGLERSPEKISATVV EIAGYSMSSEVRQRHRYLSHLPLTC EFSICELALQPPVVSKEITLEMFSDDI EKRRQRQKKAREERRRERRIEIEE NKKQKGCPEVHIPLNLQFPFAKF LYLLLFEKPRKETGKNVAMKAENR CRRRPPALNAMSGLGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLRLFGQQQRATAAPLRL GGASRRV*
4076	9573	A	4361	3	93	
4077	9574	A	4362	1	289	VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						T/LRTSKEAVSQRLCELLSAQF
4078	9575	A	4363	1	275	
4079	9576	A	4364	2	2803	RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCIA VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLRLYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYFVPAPWLSV KLLRLLQCYPPDPAPVRGRLTECLE TILNKAQEPKSKKVQHSNAKNAV LFEAISLIHHDSEPNLLVRACNQLG QFLQHRETNRLRYLALESMTLASSE FSHEAVKTHIETVINALKTERDVSV RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAIAEKY AVDYTWYVDITLNLIRIAGDYVSEE VWYRVIIQVINRDDVQGYAAKTVF EALQAPACHENLVKVGGYILGEFG NLIAGDPRSSPLIQFLLHSHKFLCS VPTRALLSTYIKFVNLFPEVKPTIQ DVLRSDSQLRNADVELQQRAVEYL RLSTVASTDILATVLEEMPPFERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTAVSTPSPSA DLLGLGAAPPAPAGPPSSGGSGLL VDVFSDSASVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGTFQMVSLQLPITLNKFFQPTKEK FCQDFFQRWKQTSNPQQEVHNIK AKHPMDTEFTKAKIIGFGSELLAE VDPNPANFVGAGIHTKTTQIGCP LRL*PNLQAQMYRLTLRTSKEAVS\ QRLCELLSAQF
4080	9577	A	4365	2	231	
4081	9578	A	4366	1	224	
4082	9579	A	4373	131	381	
4083	9580	A	4374	93	449	
4084	9581	A	4375	11	594	
4085	9582	A	4376	1	1410	
4086	9583	A	4377	1	66	
4087	9584	A	4378	1	553	RRGPLSQNGSFGSPVSGGECSPPLT VEPPVRPLSATLNRDMPRSEFGSV DGPLPHPRWSAEASGKPSDPGSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPFPFVPLMSTPMGGPVPPPI RYGPPFQLCGPFGPRALPPFPGPM RPPLCLRE
4088	9585	A	4379	1	3589	AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFFERSDFSISIKITP ELGEVFQNKDSDYLKNDNPEEHLK TSGLAGEPGELSKEDEHGNTKEYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLISSFFKEQQLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPHTL DQRVIGDTHASEVSQKPNTKDLDP GPVTTEDTPMDAIDANKQPETAEE PASVTPLENAILLIYSFMFYLTSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGASFALFLWRTVLVVKDRVYQV TEQQISEKLKTIMKENTELVQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEKVKSECHRVQEENARLKKKK EQLQQEIEDWSKLHAESEQIKSFE KSQKDLEVALTHKDDNINALTNCIT QNLLECESESEGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTAISVVEEDLKLQLKLRSV STKCNLEDQVKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQOKE MALQKKLSQEEYERQEREHLSAA DEKAVSAAEEVKTYKRRIEMEDE LQKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREAANLRHKLL ELTQKMAMLQEEPVIKPMGKPN TQNPPRRGPLSQNGSFGSPVSGGE CSPPLTVEPPVRPLSATLNRDMPR SEFGSVDGPLPHRWSAEASGKPS SDPGSGTATMMNSSRGSSPTARVL DEGK\VNMGPK\GAPSPKEFPLMS TPMGGPV\PPPIRYGPPQLCGPFGP RHLPPFGPGMRPPLGLREFAPGVP PGRRLPLHPRGFLPGHAPFRPLGS LGPREYFIPGTRLPPPTHGPQEYPPP PAVRDLLPSGSRDEPPASQSTSQD CSQALKQSP
4089	9586	A	4380	3	148	
4090	9587	A	4381	1885	2826	CLQEAIMDGTETIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSG PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTGPPSPPGA PSPPEPGDPYLQSSSEALWL*ACPP SHSRYVKTTGNATVDHLSKYLALRI ALERRQQEAGEPGGPGGGASDTG GPDGCGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPSLPPQTNLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTLELVNSPRRPLPRQGLTLRALSLP GSPQHPPGKLLTGGCALGFSTPATLH TGKQPYVCAT
4091	9588	A	4382	2	456	DRGGTLGGGTGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSRY VKTTGNATVDHLSKYLALRIALERR QQQEAGEPGGPGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPSLPPQTLLNGSLTLEL V
4092	9589	A	4383	58	1262	CLQEAIMDGTETIAVSPRSLHSELMC PICLDMLKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQALSSSIEEGLRMQA MHRAQRVRRPIPGSDQTTTMSGGE GEPGEGEGDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTGPG PSPPGAPSPPEPGGEIELVFRPHLLV EKGEYCQTRYVKTGNATVDHLSK YLALRIALERRQQQEAGEPGGPGG GAS\NTEELNVC GGEGGGAGGGDG\N PKEPA\PSLEGVSEKQYTIYIAPGG GAFTTLNGSLTLELVNE\KFWKVS RPALELCYAPHRIQSDPHPGDKPEE RGPLG
4093	9590	A	4384	3	221	
4094	9591	A	4386	2	271	
4095	9592	A	4387	54	990	HSIMMKIPWGSIPVLMLLLLGLIDI SQAQLSCTGPPAIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDWPWPGNPGKVGPKGPMGPKGG PGAPGAPGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQTVIRFRPCITN MNTNYE\PRSGKFTLQGCPLY*FN LSTPSSRG\NLCVNLMRGRERAQE/ VWVTFCDYCLTNTPGSPQGGNGP QLKKAPKGGGGGEKKTVPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WEGLTCLASHPTPAPPAQQRSLYP QQQPYDQAKCTQ
4096	9593	A	4388	3	493	
4097	9594	B	4389	272	2158	MGPLMVLFCLLFLYPGLADSAPSCP QNVNISGGTFTLSHGWPAGSLLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRSLSKAVCKPVRCPAPVSFENGIV TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNGMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDKV RYRCSSNLVLTGSSERECQNGVW SGTEPICRQPYSYDFPEDVAPALGTS FSHMLGATNPTQKTESLGRKIQIQ RSGHLNLYLLDCSQSVSENDFLIF KESASLMVDRIFSFEINVSAIITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTTGNTYAALNSVYL MMNNQMRLGMMETMAWQEIRHAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDDGERHAFILQDTKAL HQVFEHMLDVSKLTDITCGVGNMS ANASDQERTPWVHTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSWGKEFLIEKAAIS PGFDVFAKKNQGILEFYGDDIALLK LAQKVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNKSGPKI*
4098	9595	A	4390	2	201	
4099	9596	A	4391	1	130	
4100	9597	A	4392	2	215	
4101	9598	A	4393	3	300	
4102	9599	A	4394	3	310	
4103	9600	A	4395	2	228	
4104	9601	A	4396	2	448	PRVRKDAVRDGLRAVKNAIDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVLQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAEAGI\WDNDCVKK QLLHSCVTIATNILLVDEIMRAGMS SLKG
4105	9602	A	4397	2	100	
4106	9603	A	4398	3	174	
4107	9604	A	4399	1	147	
4108	9605	A	4400	1	104	
4109	9606	A	4401	153	480	TTLKQQFSFMSYKAVKLKVFLIMSC YPRNPSHFP*CGA/WVMCLRVGSE RRLCPFMATS\QSLSNKFHNRKIFMS REIKFRNLLKKNETQLMYLQIFRW YTKQRLFLF
4110	9607	A	4402	1	186	
4111	9608	A	4403	3	478	
4112	9609	B	4404	56	390	XAAYVQPFLDKSGLEKYLYPASAA APFLLYPGIPAAAAAFCLSSVLSP PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPRESSAQ EDPSQPGKEAP*
4113	9610	A	4405	2	485	
4114	9611	A	4406	105	183	
4115	9612	A	4407	1	1560	MLRKKEKANYRLLAERTRKRPRKA SAELQRKHLYPMLRGHLRLFLPGRL RPLPSNPRLAFPAAERGGGHCGPMR HFPVSTQERGTADPVHPASPLPPNQ APNAGHSPPTPRSPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAFSARRQSV GGGANWEGGGAKRARRGTGPAG WRAEGGGAACRGASARASPAFRGRG PLPPFASGRVPGRQCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKPCDSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTVDKIVGRGGGSGNFMGRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNFGGGGGNFGRGGNFGGRRGGYG GGGGGSRGSYGGGDDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGY GNQGGGYGG/G/GGGYDGYNEGNN FGGGNYGGGGNYNDFAGNYSG\QQ QS\NYGPMKGGSLGGRSSGSPYGG GYGSG\G\SGGGYGSRRF
4116	9613	A	4408	2	370	
4117	9614	A	4409	1	159	
4118	9615	A	4410	3	261	
4119	9616	A	4411	1	8748	
4120	9617	A	4412	1	2176	
4121	9618	A	4413	37	441	
4122	9619	A	4414	1	1940	PVLRHAVWLKSEKSSFLCAPLR KGSFLQKSWIFRPVMADKLTRIAI VNHDCKPKKCRQECKKSCPVR MGKLCIEVTPQSKIAWISLTCIGCG ICIKKCPFGALSIVNLPNLEKETTH RYCANAFKLHRLPIPRPGEVLGLVG TNGIGKSAALKILAGKQKPNLGKY DDPPDWQEILTYFRGSELQNYFTKI LEDDLKAIKPYVDQIPKAAKGTV GSILDRKDETKTQAIVCQQLDLTHL KERNVEDLSGGELQRFACAVVCIQ KADIFMFDEPSSYLDVKQRLKAAITI RSLINPDRIIVVEHDLVLDYLSDFI CCLYGVPSAYGVVTMPFSVREGINI FLDGYVPTENLRFRDASLVFKVAET ANEEVKKMCMYKYPGMKKKMG EFELAIVAGEFTDSEIMVMMLGENG MGKTTFIRMLAGRLEPDEEGEVPVL NVSYKLQKISPKSTGSRQLLREKIR DAYTHPQFVTNVMKPLQIENIIDQE VQTLSSGGELQRVTLAL*LGQNLDP VYL\DEPPA\YLDSEQLMAARVV KRFIPHAKKTA\FVVGTVTFIMATY L\ADRVIVFDGVPSTKNTVANSPTQ LLAGMKNKFLSQLEITFRDPNNYRP RINKLNSIKDVEQKSGN\YFFLDD
4123	9620	A	4415	1	122	
4124	9621	A	4416	2	1382	
4125	9622	A	4417	135	282	
4126	9623	A	4418	2	1652	
4127	9624	A	4419	3	279	
4128	9625	A	4420	8	353	
4129	9626	A	4421	1	1542	
4130	9627	A	4422	1	496	
4131	9628	A	4423	70	365	
4132	9629	A	4424	1	3771	
4133	9630	A	4425	2	285	
4134	9631	A	4426	1	724	
4135	9632	A	4427	58	197	
4136	9633	A	4428	640	813	
4137	9634	A	4429	3	268	
4138	9635	A	4430	1	1512	
4139	9636	A	4431	3	1625	
4140	9637	A	4432	1	330	GKTITLEVEPSDTIENVKAKIQDKEG

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						IPPDQQRLLIFAGKQLEDGRTLSDYNI QKESTLHLVLRRLRGGIKYNC DKMI CRKCYARLHPRAVNC RKKKCGHT NNLRPKKKVK
4141	9638	A	4433	2	544	DPRLQFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKTL\TGKNLHPL RYETQ*HPLKNVQPKISRTKEGIP\ PDQAAS**FAGK\QLE\DGRTLSDY\ NIQKESTRAPWLLRLR\GGIIEPFSP GLPKKYN\CDKM\CRKCYAR\LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP
4142	9639	A	4434	385	499	
4143	9640	A	4435	2	127	
4144	9641	A	4436	3	424	
4145	9642	A	4437	1	110	
4146	9643	A	4438	1	110	
4147	9644	A	4439	1	110	
4148	9645	A	4440	1	110	
4149	9646	A	4441	1	108	
4150	9647	A	4442	3429	7466	
4151	9648	A	4443	4048	4181	
4152	9649	A	4444	682	829	
4153	9650	A	4445	163	320	EFEGFNPLKLGEAGWARWLTPVIPAL *ETEAGGSRGQEIETILANTVKPHLY
4154	9651	A	4446	1122	1446	
4155	9652	B	4447	124	27844	XRSTVPPRISAYERPVWPGEWNDP RGPGRRASAVVSPREGNWGVLRDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLL KLLKSVAQKQDQTYTMKEVLFYLGQ YIMTKRLYDEKQQHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIRNLV VVNQESSDSGTSVSENCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETEENSDELSEGERQKRH KSDSISLSFDESALCVIREICCERSS SSESTGTPSNPDLDAGVSEHSGDWL DQDSVSDQFSVEFEVESLDSYSL SEEGQELSDEDEVEYQVTYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEFGDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESDYSPSTSSSIYSSQEDV KEFEREETQDKEESVESSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCPVLTGHIRTEQ PIIILPKKHKKKKERKSLPEEDVAVS SNVDFFTLTKKKVYLNKLERKSV FKGFQGMGQHWGTGFINDKPSNPS SHEVVAWIRILRVEKTGHSGTLDP KVTGCLIVCIERATRLVKSQQSAGK EYVGIVRLHNAIEGGTQLSRALETL TGALFQRPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR

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						TLCVHLG LLLGVGGQMQLRRVRS GVMSEKDHMTMHDVLDQAQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGLVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVVPNRHNLGLQL SVETLDGQTINPKLAGLGRHGPQN KQPFMVAFKATEVHFRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGLIVTLQSLFEKRTAAGTRG RPCCKHELYVSFRDLGWQDWIAPG GYARYYCEGECAPPLNSYMNATNH AIVQTLVHFINPETVPKPCCAPTQLN AISVLYFDDSSNVILKKYRNMVVRA CGCH*
4156	9653	A	4448	2	129	
4157	9654	B	4449	1	462	MSQQYYVRLCQIQSPSRSVGRENL VLVGDFPDPTTELKRVKGRGCAHCG LTDLPEPTAQVLVEQGQDEALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDRALK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE*
4158	9655	A	4450	3	366	
4159	9656	A	4451	1	167	
4160	9657	A	4452	2	382	TMVLSPADKTNVCAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKL RVDVPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4161	9658	A	4453	2	252	
4162	9659	B	4454	31	449	MVLSPADKTNVKAAWGKTYFPHF DLSPGSAQVKGHGKKVADALTNA VAHVDDNAQRAVRPKRPCTRTSFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPQVPGFCYAPC*
4163	9660	A	4455	2	81	
4164	9661	A	4456	2	81	
4165	9662	A	4457	3	452	
4166	9663	A	4458	1	493	RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLER/M FLSFPTTKTYFPQLRTL SHGF/SQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLHAHKL RVDVPVNFKLL SHCLLVTLAAHLPAEFTPAVHAYL DKFLASVSTVLTSKYR
4167	9664	B	4459	208	420	MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTSLAIHFGIEFTPE*
4168	9665	A	4460	40	534	SRRHGSVSHREAKATIASLWGKVN VEDAGGETMIRLLVVYPWPQRSF ASFSSLFSAIMGNPKVKA/HGKK VLTSLGDAIKHLDDLKGTFAQLSEL

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						HCDKLHVDPENFKLLGNVLVTVLA IHFVGKEFTPEVQA\SWQKM\VTGV ANA\LSSTYHLNSLPMQNF
4169	9666	A	4461	2	171	
4170	9667	B	4462	10	351	MAPRTLVLALLSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRIA VGYV DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWRNTRNVKAHSQTDR VDLGLTRGYRCVSHSL*
4171	9668	A	4463	1	986	
4172	9669	A	4464	3	1282	
4173	9670	A	4465	1	1004	MAVMAPRTLLLLLLGALALTQTWA GSHSMRYFTTSVSRPGRGEPRIA V GYVDDTQFVRFDSDAASQRMEPRA PWIEQEGPEYWRNTRNVKAHSQI DRVDLGLTRGYYNQSEAGSHTIQM MYGCDVGS DGRFLRGYQQDAYDG KDYIALNEDLRSWTAADMAAQITQ RKWEAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMTH HAVSDHEATLRCWALSFP AEITLT WQRDGEDQTHTCHVQHEGLPKPL TLRWEPSQPTIPVGHAGLVLF GAV ITGAVVAAMWRRKSSDRKGGSYS QAASSDSAQGS DVS LTACKV
4174	9671	A	4466	1090	2175	
4175	9672	A	4467	1	780	
4176	9673	A	4468	59	169	
4177	9674	A	4469	89	134	
4178	9675	A	4470	864	1885	
4179	9676	A	4471	89	176	
4180	9677	A	4472	1	1127	
4181	9678	A	4473	1	405	
4182	9679	A	4474	3	199	
4183	9680	A	4475	3	607	
4184	9681	A	4476	1017	2029	
4185	9682	A	4477	844	1572	
4186	9683	A	4478	1	846	
4187	9684	A	4479	452	1220	
4188	9685	A	4480	1	1254	
4189	9686	A	4481	1	1383	
4190	9687	A	4482	1	1290	
4191	9688	A	4483	666	1606	
4192	9689	A	4484	1	1236	
4193	9690	A	4485	1	1269	
4194	9691	A	4486	719	1175	
4195	9692	A	4487	1	1182	
4196	9693	A	4488	1	1377	
4197	9694	A	4489	1	1335	
4198	9695	A	4490	1	2456	
4199	9696	A	4491	1	1827	
4200	9697	A	4492	1	1011	
4201	9698	A	4493	452	950	
4202	9699	A	4494	1	1433	
4203	9700	A	4495	1	1933	
4204	9701	A	4496	641	2107	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4205	9702	A	4497	1	2582	
4206	9703	A	4498	1	1095	
4207	9704	A	4499	1544	525	
4208	9705	A	4500	2	161	
4209	9706	A	4501	3	452	
4210	9707	A	4502	25	622	EFHRLRENPPWFLFPAAKTNVRAA WG*RSGAHAG\EYGAELER\MVLF PPPTPKPYFPELRT*AHGFCPKVKGP TAKKVAERA*PNAVAIHVDGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTL\AAHLPAEFTPAVHA SLGQVPGLSVSTVLTSTKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTVPGL
4211	9708	A	4505	2	213	
4212	9709	A	4506	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV TAAHLPAEFTPAVHASLDKFLASV TVLTSTKYR
4213	9710	A	4507	2	252	
4214	9711	A	4508	1	466	WSPQTQREPTMVLSPADKTNVKAA WGKVGAGHAGEYGAELGR\IFLSFP PTKTYFPHFDLSPGSAQVKGHGKK VADALTNAGAHVDDMPNALSSPE ATLHAHKLRVDPVNFKLLSHCLLV TAAHLPAEFTPAVHASLDKFLASV STVLTSTKYR
4215	9712	A	4509	256	391	NELHAENLKNEDDVTGLLGFWT LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWITIRI LDSTYNIPNCWILLQLFLSDLL
4216	9713	A	4510	2	490	
4217	9714	A	4511	1	160	
4218	9715	A	4512	1	150	
4219	9716	A	4513	1	73	
4220	9717	A	4514	2	213	ISPFYHLCQMLKTADVLRRLMALWR CRDALLS*GGSSIEIPLFLLYGSREL LGFCFTGMNHCAQSIYNRF
4221	9718	C	4515	186	365	MFQLLYDSLXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXIYNRF*
4222	9719	A	4516	251	454	GGSSIEIPLFLLYGSRARTWILF*EM AAGRVQWLTSVIPALWEAEAGGS RQGEFKTSLAKRVKPHLY
4223	9720	A	4517	3	192	
4224	9721	A	4518	1	129	
4225	9722	A	4519	23	115	
4226	9723	A	4520	1	1582	GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSRRAEMGTAD LGPSVPTPTNVTIESYNMNPVYW EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFNVDGEQVDYDPETTCYIRVY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGLV HVWGVTTTEKSKEVCITIFNSSIKGSL WIPVVAALLFLVLSLVFICFYIKKI NPLKEKSIILPKSLISVVRSATLETKP ESKYVSLITSYQPFSLKEVVCCEPL SPATVPGMHTEDNPGKVEHTEELSS ITEVVTTEENIPDVVPGSHLTPIERE SSSPLSSNQSEPGSIALNSYHSRNC ESDHSRNGFDTDSSCLESHSSLSDSE FPPNNKGEIKTEGQELITVIKSPPPSF CYDKP\HVLVDLLVDDSGKESLAIG YRPT\EDSQRFHEISLSCTQL
4227	9724	A	4521	1	408	
4228	9725	A	4522	2	377	
4229	9726	A	4523	50	326	
4230	9727	A	4524	3	1948	AAAAAAVPASFGLCSDPAPPQP ASMSGIKKQKTENQQKSTNVVYQA HHVSRNKRQGVVGTRGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVRHGLNRNLGFSPGD REENIRRIAEVAKLFADAGLVCITSF ISPFADRENARKIHESAGLPFEIFV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPEPVERVLKTNLST VSDCVHQVVELLQEQNIVPYTIKDI HELFVPENKLDHVRAEATLPSLSIT KLDLQWVQVLSEGWATPLKGFM EKEYLQVMHFDTLDDGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL A\HGGRRVAYLTETAEF/HTEHRKE ERCS/RVFWGTTCTKHPHIK/MVME SGDWLVGGDLQVLEKIRWNDGLD QYRLTPLELKQCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLLHPLGGWTKDDDVPLD WRMKQHAAVLEEGVLDPKSTIVAI FSPMLYAGPTEVQWHCSRMIAG ANFYIVGRDPAGMPHPETKKDLYE PTHGGKVLSPAGLTSVEIIPFVA AYNKAKKAMDFYDLARHNEFDNIS GTRMRKLAREGENPPDGFMAPKA WKVLTDYRSLEKN
4231	9728	A	4525	1	626	
4232	9729	A	4526	66	409	LGLLQVTTTNPPSPNTYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRQRPIH LSFDIDAFDPTLA\PATGTPVVGGLT YREGMYIAEEIH
4233	9730	A	4527	1	1257	
4234	9731	A	4528	3	1086	FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSVAVIGAPFSQGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTVPKDDLYNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVTLGG DHSLAIGTISGHARHCPDLCVWV DAHADINTPLTTSSGNLHGQPVFSL LRELQDKVPQLPGFSWIKPCISSASI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VYIGLRDVPPEHFILKNYDIQ/YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIHNTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI
4235	9732	A	4529	1	128	
4236	9733	A	4530	3	126	
4237	9734	A	4531	1	79	
4238	9735	B	4532	214	268	XELEKLVQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDYIVDHSIAIY LLNSDGLFTDYYGRSRSAEQISDSV RRHMAAFRSVLS*
4239	9736	A	4533	23	257	AYLIDDTEAQSRGSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCLLMTA LKAI/TQIQLPATSHSAARLRGVLPR AIR
4240	9737	A	4534	3	229	
4241	9738	A	4535	1	297	
4242	9739	A	4536	67	552	GPWRFCFSEAVSEPTTVAFDVRPGG VVHFSFHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTSEDHQHFTCT IWRPPRGKSYLYFT/QFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEVTKTAVGSQGPAGFKLTC PKLVIVAKAS\RTTEL
4243	9740	A	4537	2	232	RDGTVHARAANKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWKR NNK
4244	9741	A	4538	2	1094	RHPVCLLVLMAGSGKTTFFVQRLT GHLHAQGTTPPYVINLDPVHEVFPF ANIDIRDTVKYKEVMKQYGLGPNG GIVTSLNLFATRFDQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTIIT EALASSFTVVIIYVMDTSRSTNPVT FMSNMLYACSILYKTKLPFIVVMNK TDIIDHSFAVEWMQDFAFQDALN QETTYVSNLRSMSLVLDEFYSSLR VVGVS AVLGTLDEL FVQVTSAAE EYEREYRPEYERLKKSLANAES\QQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEPAF QNFMQESMAQYWKRNNK
4245	9742	A	4539	710	1053	
4246	9743	A	4540	3	281	
4247	9744	A	4541	30	320	
4248	9745	A	4542	3	115	
4249	9746	A	4543	1	137	
4250	9747	A	4544	3	32	
4251	9748	A	4545	1	135	
4252	9749	A	4546	1	2694	
4253	9750	A	4547	3	544	
4254	9751	A	4548	2	323	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4255	9752	A	4549	1	384	
4256	9753	A	4550	1	1299	MASPVAAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLEQYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCDAKINFDDNAEF RQKDIFAMDDKSENEPIENEAAYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIIANGITKACRELELKVPLVVR EGANVQEAQKILNNS\GLPITSAILD EDAACKAVASVAMK
4257	9754	A	4551	1	590	RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIIANGIPKACRELELK VPLVVRLEGTVNVEAQKILNNSGLP ITSAIDLEDA\AKKAVA\SVAKK
4258	9755	A	4552	3	168	
4259	9756	A	4553	3	95	
4260	9757	A	4554	3	354	
4261	9758	A	4556	1	95	
4262	9759	A	4557	156	364	GPVE*KPVEEESRGLLD*GLPGMD WGWVFGKGGDPPLAQSLNCPSFTV SEIIGRDLSGFPAPPGEPPA
4263	9760	A	4558	1	2523	
4264	9761	A	4559	3	469	
4265	9762	A	4560	3	132	
4266	9763	A	4561	1	2961	MGAASCEDEEFLKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPISIRISPTPEPP AALEDNPDAWGDGSPRDYPPPEGF GGYREAGAQGGGAFFSPSPGSSSL SWSFFSDASDEAALYAACDEVESEL NEAASRFGLGSPLSPRASRPWTPE DPWSLYGSPGGRGPEDSWLLSAP GPTPASPRPASPCGKRRYSSTGTPSS ASPALSRRGSLGEEGSEPPPPPLPL ARDPGSPGPFYVVGAPPAESIPQKT RRTSSEQAVALPRSEEPASCNGKLP LGAEESVAPPGSRKEVAGMDYLA VPSPLAWSKARIGGHSPIFRTSALPP LDWPLPSQYEQLRLIEVQPRAHHR AHYETEGSRGAVKAAPGGHPVVKL LGYSEKPLTLQMFIGHTADERNLRPH AFYQVHRITGKMVATASYEAVVSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPQGGGKVVSVQAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEETVNRLQSNEVTLTTLTV PEYSNKRVS RPVQVYFYVSNRRK RSPTQSFRFLPVICKEEPLDSSLRGF PSASATPFGTDMDFSPRPYPSPYH EDPACETPYLSEFGYGMPLYPQT GPPPSYRPLRMFPETRGTGCAQP PAVSFLPRFPSPDYGGRGSSFFPLGL PFSPPAPFRPPPLPASPPLEGPFPSQS DVHPLPAEGYNKVGPGYGPGE GAP EQEKSRGGYSSGFRDSVPIQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLAALEGLGGKECVE EGGG
4267	9764	A	4562	19	387	
4268	9765	A	4563	1	373	
4269	9766	A	4564	2	343	
4270	9767	B	4565	19	507	MEANGLGPQGPELKNDFLRAAW GEETDYPVWCMRQAGRYLPEFRE TRAAQDFSTCRSPEACCELTLQPL RRFPLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAITPYPTTGWWDV CRLIGFCWCPHGP*
4271	9768	A	4566	3	339	
4272	9769	A	4567	3	679	
4273	9770	A	4568	1	139	
4274	9771	A	4569	1	526	HERFETTYFKKFP\GYVVTGDGCQR DQDGYWITGRIDDMNLVSGHLLS TAEVESALVEH*RLLQEA\AVVGHP HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKTRSGKIMRRVLRKICS/VT DHDLDGMSTVADPS\VISHLFSHRC LTIQ
4275	9772	A	4570	537	2357	GVCHQRR LAPQAWPGAGTDSL LLA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQASAGPPGGLLWERHSRE YIKTWRPR/YFLKSDGSFIGYKERP/ EAPDQTLPLNNFSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVAVSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNTRHPFLTALKYAFQTHD RL/CFVMEYANGAVFHLSRERV FTE ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTQVSTVRGTS DP/AVECS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSGTPHSSWNEQLHHTTVWTRLIG YVEGKPHRGAVPRYMGVQQRVLE DN/DYGRAVDW/WGLGVVME/MM CGRLPFYNQDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFPAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS
4276	9773	A	4571	64	1537	VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLLKSDGSFIGYKE RPEAPDQTLPLNNSVAECQLMKT ERPRPNTFVIRCLQWTTVIERTFHV DSPDEREEWMRAIQMVANSCLKQRA PGEDPMDYKCGSPSDSSTTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTSRVLQNRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTTEERARFYGAIVS ALEYLHSRDVVYRDIKLENMLDK DGHKIDTDFGLCKEGISDGATMKT CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMEYEMMCGRLPFYQDHE RLFELILMEEIRFPRTLSPKASLLA GLL\KKDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLE\LDQRT\HFP\QFSYSASIRE
4277	9774	A	4572	2	423	
4278	9775	A	4573	1	106	
4279	9776	A	4574	3	58	
4280	9777	A	4575	1	191	
4281	9778	A	4576	3	325	
4282	9779	A	4577	3	277	
4283	9780	C	4578	77	292	MVDFCPCSI CXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXHWSIC IS*
4284	9781	A	4579	645	849	
4285	9782	A	4580	3	140	EANKENREAQMAAKLERLPEKD*A /HLEEV RKNK\ESKDPADETead
4286	9783	A	4581	49	605	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASQAFELILSP RSKESVPEFPLSPKKEGFFPGGKFR EN*EAAEERRQSP*SCSS*RQLAEKR E\HGKEVL\QKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKNKESQRP CPRDLKPD
4287	9784	A	4582	1	567	VVREPAFSLA/EAQFTARYFSTSSIP NV\NKA PV\RI RRSKHM*QGVTL PVI E\HYHEGTD SL*TALV*ARVGNQLA KLKR\NYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPRIERT LAYIITELDEREREFEYRLKKIQEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KILKEKSEKDLEQRRRAAGEVLEPANLLAEKDEDLLFE
4288	9785	A	4583	1	748	MSGKDRIEIFPSRMAQTIMKARLKG AQTGRNLLKKKSDALTLRFRQILKK IETKMLMGVEMREAAFLAEAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLPVFEHYHEGTDSELTG LARGGEQLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKITNRRVNAI EHVHPRIERTLAYIITELDERVREEF YRLKKIQEKKILKEKSEKDLEQRR AAGEVLEPANLLAEKDEDLLFE
4289	9786	A	4584	166	238	
4290	9787	A	4585	53	203	
4291	9788	A	4586	357	498	
4292	9789	A	4587	262	397	
4293	9790	A	4588	68	422	
4294	9791	A	4589	70	361	
4295	9792	A	4590	259	2603	
4296	9793	A	4591	246	667	
4297	9794	A	4592	25	471	
4298	9795	A	4593	2	3788	
4299	9796	A	4594	1	700	
4300	9797	A	4595	604	1047	SNRRTDNPTSVAYLSKETDVVAKG WPHCLWVVAVAILVLEAIKIIQKG DFTVWTSHDVNGILGAKGNSWLS KRLRLRYQALLLEGPVLQIHTCV PAIFLPEDGEPIKHDYQQIVAQTYVT *EDLLEVPLANPDNLNTNGSSV
4301	9798	A	4596	1	1410	
4302	9799	A	4597	510	755	
4303	9800	A	4598	59	411	SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFRDSPH LFGQALAQDLGHFSSPGTLVLQYV DDLALATSEASCQATLALLNFLA NQGYK/LSRSKAQLCLQVKYLCL
4304	9801	A	4599	1	565	
4305	9802	A	4600	126	492	CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV
4306	9803	A	4601	1	342	
4307	9804	A	4602	55	219	LGNKHLLGSIDPRGSWVTGEYIFLR PPIAA*GRQ*DFLPFELWWTSLNNS WAFS
4308	9805	A	4603	339	1371	ASHPLRGLLCGPSLPNEPCPLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAQRAKLGDRLDIPDR RKSSTILGRAGDLQAMPEPPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPSDGVVGD TAGT VWPGLKGEPCHLGTCYRCVLD PH PTPSESDTIQGIHVQVCYMS TLHDA DVCDTNDPVTHNTKKYI YSTEIFTS NNPELRSEDET VFRALEKWK TSEQT IGEMDFYIC NDPHPDSALYQNGLSK MQDTVSL SVFSPSVAA
4309	9806	A	4604	749	1002	QLKKG TNSLLVSKPSPVWIPTG TLT QIMGTGVANIC*PVF*KD* GELGKM NYAMMSTITQGKEEN PAFLKWLWE ALRKYTPLSP
4310	9807	A	4605	1	1632	
4311	9808	A	4606	307	543	
4312	9809	A	4607	1	1149	
4313	9810	A	4608	119	409	GDICHHLGLTPVGSHSLSCSR*QV A*VGAVTAATIGTGILLQQLAFL VC NWLLSGSSENFPRSALICFK SEREK GTCIQVGPNSPPPTACKG HN
4314	9811	A	4609	1	2433	
4315	9812	B	4610	97	1065	MHAVHTSLLVERTILTTTKERG STL QYPLRPGAHKGLQDIVKRF KAQALI RKCSSPCNTPILGVQK PNGQWRLV QDLRLINEAVIPL YPVVPNPYNLLSQ IPEEAEWFT VLDLKD AFFCIPLHSDS QFLFA FEDPTDHTS QLTWTVLPPGF RDSPLFGQALAQDLGHFSSPGTL V LQYVDDLLATSSEASCQATL DLL NFLANQGYKTHSRDSDAPV GFTDR HLVATEKIPRGREPLSSL AVYTRGR PTRTGARRTIVSRIR DRFFRYLA QREPPLYQQSLIHL QLDSQPALS VIGKVPNVVELTP NFGTAAQV*
4316	9813	A	4611	1	2403	
4317	9814	A	4612	1	2838	
4318	9815	A	4613	1908	4698	SNDRTEDDCGKHPFMSSPPATEP WV CLIEGQEIDFLDGTTFSVLIP CLG RLSSRSVTIQGILGQPVT RYFSHLLS CNWETLLFSHAFL VMPESPTPLGR DILAKAGAIIS MKTGNKLPICCPLE GINPEVWA LEGQFGRAKNAHPLQIR LKDP ISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSSPCNTPIL GVQ KLNSQWRLVQDLRLINEA VIPLYPV VRNPYTLSSQVPEE AEWFTVLDLK DAFFCIPLHSDS QFLFAFEDPTDHTS QLMWMVLP QRFDRDSPHLFGQAQA QDLGH FSSPGTLVLQYSEIAKTLYT LIKEMERANTHLVEWEPEAETA FET LKQALVQAPALSLPTGQNF ALYVIE RAGIALGVLTQTHRT TPQPVA YLSK EIDVVAKGWPH CLRTVVAVAVLVS EAIKIIQK DFTVWTT HDVNGILGA KGG LWPSDNCLLRYQALLLEEPVL QIHMCIAINPATFLPEDGEPIK HDCQ QIIVQTYATQDDLLEV PLANPDFNL YNSGSSFVENGI QRAGYAIVSDVTV

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						LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTD SKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLAVVHEEICS MGCKDPGWNSLKVSEEDRKMQUES LETSRDLLNGFDQNVNDNDMSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIIVIEK AVKAIKPETINSCQRNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRLSPHNKLLKFY KPEFYSSYPLVSCLDHYVDQVGARI SMSFCVTTVTEASGSGSWTCGVSQ LKLSYAD
4319	9816	A	4614	1529	2945	
4320	9817	A	4615	3	374	
4321	9818	A	4617	3	112	
4322	9819	A	4618	359	465	
4323	9820	A	4619	3	381	MRILMVGLDAAGKTTILYKLLGEI VTTIPTIG\FIFVVSNDREIRIQEVAD ELQKMLLVDEL RDAVLLL FANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR
4324	9821	A	4620	395	552	
4325	9822	B	4621	1289	1603	MVVTISPNSFLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPM AVVA LVMGRSRRGLGRPRAFSQAPRQT KREGREAAEEERGRQRLSGPCAD EDPAQE*
4326	9823	A	4622	2	116	
4327	9824	A	4623	156	403	
4328	9825	A	4624	8	2648	WIQYSSTTL PNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVG\YCRVRLGFPDQECCIEVINNTT VQLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDVVANPLVND LIHGKNGLLFTYGV TSGKTHMT GSPGEGGLLPRCLDMIFNSIGSFQAK RYVFKSNDNRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAAEVEDSDSVYGVFVS YIEIYNNYIYDLLEEVFPDP/IKPKPP QSKLLRED\KNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKLVQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTRLTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPPPLSCEILDINDE QTLPRLEALEKRNHLRQMMIDEFN KQSNAFKALLQEFDNAVLSKENHM

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						QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLQQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLVVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFPDQNPPIRLRHRRSRSAG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKDIYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EWTDV\ETRCVGC GR*GAGSQLGPGYQHHAQPKRKK P
4329	9826	A	4625	1	331	
4330	9827	A	4626	142	461	
4331	9828	B	4627	136	906	XPELKPVDKSEVVMKFPDGFEEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL*
4332	9829	A	4628	1	233	
4333	9830	A	4629	1	312	
4334	9831	A	4630	2	119	
4335	9832	A	4631	1	145	
4336	9833	B	4632	78	236	MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFS DK*
4337	9834	A	4633	102	583	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALQ IGDKIMQVNGWDMTMVTHDQAR KRLHQA LRRRLVRL\VTRQSLQK\ AVQQSMPVLAATTILRLPAASLYS NATSTLWSPSGFC
4338	9835	A	4634	1	373	
4339	9836	A	4635	3	86	
4340	9837	A	4636	1	204	
4341	9838	A	4637	1	767	
4342	9839	A	4638	20	515	
4343	9840	A	4639	3	391	HEESRSVSQAGVQWRYLGSLQRPP PRFKRFSCLSPPSSWDHRCCTS*LAN F*YLVETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWALNVFKDG CESPWPHNKLEFYTAYYFFNTGTT LRPPL
4344	9841	C	4640	201	368	MGKSKXAFRXKXGIVFIQGTFFPX YNXXPRGIKVSQEXNXXXXCXKI GGEDVX*
4345	9842	A	4641	1	307	RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSCLSLPGS*DYRRL LHPANF*FSVETGFHHVQGAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST

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4346	9843	A	4642	1	310	
4347	9844	A	4643	49	360	DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLLSSWDYRRPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSQPFF FF
4348	9845	A	4644	2	119	
4349	9846	A	4645	1	276	FFFFFFFFLTQSLTHSVTRLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA
4350	9847	A	4646	2	273	LRQFSLLLPRVECSGAISAHCNLCCL GSSDSPASASRVSGITGTHHQTWLT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPPKVLGLQA
4351	9848	A	4647	1	106	
4352	9849	A	4648	1	485	SSIDTLGRRVGQPAPGSPGASNHLC CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGQASSGSC TCWGCPTAQAAQAPSSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPGSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS
4353	9850	A	4649	1	623	CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSAYE/GEQ*NVSFGQ L*SENHNQYVNPSSGRSHLLERHSK RSF/FRQSGVKVESVDHSDCVHGPC QNGGSCLRRLAVSSVLKSRESLPVII VANEPLQPFCKCLPGYAGSWCEID IDECLPSP
4354	9851	A	4650	1	446	LMLRPRLKLQEPVPHHHLGFQCPSS PLLPPGPPPHKV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPAWLLPSLIVPLIVHQPVS LQPIRHDLPAPGDGTHSSAYC
4355	9852	A	4651	2	388	SHGSYVMYHDQVEFISGMKHW/FN TKIQTIIY*KNEEKNKMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQGGQWGGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL
4356	9853	A	4652	115	413	LHIYSQPKFRKGTKKIH*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPMQLIQENTG/IMLQDI GFGKDYLSTSKAQATKQK*TRKH WEMLQDIGFGKDYLSTSKAQATK QK
4357	9854	A	4653	3	129	NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPTYTKIKSLIKNLKVRPET MQLIQENTG/IMLQDIGFGKDYLST SKAQATKPK*TRLLSLTIYKNQVK VD
4358	9855	A	4654	1	405	LTLKPNSGFRFPFQVATR*IKYPGIH PAKEVKDLYRKT*KTLKGITDGP

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						Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMFAVITQLEKTIQKFIWN QKGAQIAKRILSKKTNSTSHITVL QTIRI
4359	9856	A	4655	3	448	FFFFFAFLLLGLLHQIPDVSPGKYT TLLPLMIILMISGIKEVIYIINDMADK IVKEHKTVMTRLWDTFKWKEVKC GLNTVKALEMGELPSLQDTSDFVI *QHSNPG*RDCKTRQGFDREQLLY QCRDILPPRQQAFLQLSLRAQP
4360	9857	A	4656	2	502	KKKKERKRKRTPAIKKWAKDDRHF TGDKIKMVNKNIKISISLVIS*MQI KAITIHPTRLAKVKCLPRMGR/KGIL FYCWWARKLEQ/SFRKIFIP*NPQVR LLSTNPRKICAPFAKNTRASETWTK LLLAALCVVTPN*KQTNCSTAGMS NLLASMDHTGRTVSGHA
4361	9858	A	4657	61	364	KTVWFCAVEGQGNLQ*WKPRLP GLKHFPGLSSQ/WNRKLPDGPNTPG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR
4362	9859	A	4658	2	436	KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLT\WIQELYEKIYKSVM KNIKELNKWRSSYGKGKSSSSSSSS SSSLDIACSWLRRLKIVKISGLHNL YRFNIVPIEIPETYLVDVNKLIPQFIW RGRHRIVNKIVE
4363	9860	A	4659	3	480	GSHDFDKLILKFIWNSRPRIAKTIL KKKNKVGGLTLCDFKTYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYCQLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV
4364	9861	A	4660	362	408	CQVISVLWFYSSVLGWLWVIFCFSL KF*/WKSRSRQANPILKNKTRVLIL PDIKTPKAVGVIPVW*QCS*KVW GEKVWYVQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSLFNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKITINLL
4365	9862	A	4661	93	367	KVWGEKVWYVQKMTQIVQWDRTE SPQIDN*SLTKEIQWRKDSLFNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKITIKLL
4366	9863	A	4662	123	397	KVWGEKVWYVQKMTQIVQWRDRA ESPQIGH*SLAKEIQWRKNSLFNKW *GDHWAAAFSSSSSI*TKTLQP/CTKI KSKWVTDLNVKRTIQLL
4367	9864	A	4663	2	433	ETADFGPLVLDSDDDSVDRDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPKLVPGSGGGPGSVRSSED*GS AFPVRASSNDSFEQSIKAEIEQLLNE KR*HATPKCDG/SIDKKPDP
4368	9865	A	4664	94	445	HHQLTLESLGKSKNSPRLSPSLGAC

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						LSCIIWQPAKGQG\SGDGGNWRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAEHPQA/GG TYRDLHPDPTWKTGWCHFVFC
4369	9866	A	4665	52	119	
4370	9867	A	4666	987	1324	VSNTPSARNQGRASSPGNSSPE/SSS ESAPAAATANGCDEAHLIPGGKFREP LKGQRGPPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN
4371	9868	B	4667	3888	8771	MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPRAGRPPRPAAGPATCA TRGPRPPRLAAAAAAGRAWAVR VPRRRQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAFTLQ VWLRAEGGQRSPAVITGLYDKCSYI SRDRGWVVGIIHTISDQDNKDPYFF SLKTDRARQVTTINAHRSYLPQW VYLAATYDGQFMKLYVNGAQVAT SGEQVGGIFSPLTQKCKVLMLGSA LNHNRYRGYIEHFSWKVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGSSPKVEFSNAHGF LLDTSLEPPLCGQTLCDNTEVIASY NQLSSFRQPKVVRYRVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSSLRRRLILANC DISKIGDENCDEPNHTLTGHDGGD CRHLRHAPAFVKKQHNGVCDMDCN YERFNFDGGECCDPEITNVTQTCFD PDSPHRAYLDVNELKNILKLDGSTH LNIFFAKSSEELAGVATWPWDKE ALMHLGGIVLNPSTFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCDNTNPAPKHKSC GDPGPGNDTCGFHSFFNTYPNNFMS YADDCTDSFTPNQVARMHCYLDL VYQGWQPSRKAPVALAPQVLGHT TDSVTLEWFPPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTIWTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEEVYGIQIYTL EHLEIDAAMLTSTADTPLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGSVYQYVWITISGTEESE PSPAVTYIHGRGYCGDGIIQKDQGE QCDDMNKINGDGCSLFCRQEVSN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIGQPAASQVCRTKVID LSEGISQHAWYPCTISYPYSQLAQT TFWLRA YFSQPMVAAAIVHLVTD GTYYGDQKQETISVQLLDTKDQSH DLGLHVLSCRNNPLIIPVVHDLSPF YHSQAVRVFSFSSPLVAISGVALRSF

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						DNFDPVTLSSCQRGETYSPAEQSCV HFACEKTDCELA VENASLNCSSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSGTGPSVTVTCTEGKWNKQVA CEPVDCSIPDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNLLTC MEDGLWSFPEALCELMCLAPPPVP NADLQTARCRENKHKVGSFCKYKC KPGYHVPGSSRKS KRAFKTQCTQ DGSWQEGACVPVTCPPPKFHGL YQCTNGFQFNSECRKCEDSDASQG LGSNVIHCRKDGTWNGSFHVCQEM QGQCSVPNELNSNLKLQCPDGYAIG SECATSCLDHNSESIILPMNVTVRDI PHWLNPTRVRRVCTAGLKWYPHP ALIHCVKGCEPFMGDNYCDAINNR AFCNYDGGDCCTSTVKTKKVTFPF MSCDLQGDCA CRDPQAQEHSRKDL RGYSHG*
4372	9869	A	4668	1	183	GRDGVLPCCPGWP*SPELKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPCLTSCQYSKC
4373	9870	A	4669	3	462	TYQSFSPSHMPLRGYDVW*TTLFQN P*HG*PGLQRFLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPPE*YV EPSGTK\CIAGWGETKGTGNDTVLN VSLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG
4374	9871	A	4670	1	360	ARGPQRSERSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRWH/AGVLS PPAAPPPSSSSVPEAGGPIKKQKAD VTLSALNDS DAHSDV VDM
4375	9872	A	4671	70	631	RQRPQRSERYWRAPPS*GDKVG PQMASQQPSASLYPYPSTSHITAGS RLGEFHELGWLEVRWFVVDPLAC RENCETGVWAMGLSVFLSVIHLT QRSFINTDSVLCHAQRETNVCPCAR EGPCL*PSPSARSQRPRSPGSRTPQ EKSRRDAAASSAPRAS*RRRRPPII PLRPLWTLTSWPRAPPHGDAAAAA TREPEFHL
4376	9873	A	4672	93	338	
4377	9874	A	4673	1	660	FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVDPRNILLTNEQLESA RKIVHDYRQGI VPPGLTENELWRA KYYIDSAFHPDTGE\KMILIGKNGQ AQGF PWNMT\TGTGCM DGRFTGTP AVLFWQWINQSFNAV VNYTNRSGD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPFGPFACVA
4378	9875	A	4674	1	387	FFF*RWVSHSVAQA AVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGP HLSMFPK MVLNSRPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI

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						HFKRTK
4379	9876	A	4675	3	383	GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPECP*A PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTRK RNGE
4380	9877	A	4676	490	1013	WASCSSSREYQCCFQTVPPGFSRVM KFFTFPPGSKHFPAPL\PAPQACTSF GLAGLPPNALPLILVPAPPA/SSLAN PQLVQPPVPGLVPRPSRSCSAA/RP SA/RLARPPETPAR\PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDASGSWRVLRP
4381	9878	A	4677	1	447	KKFVIPDFEFTGHVDRIFEDVKELT GGKVAAAYIPQLAKSNPDLWGVSLC TVDGQRHSEGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAI VVS SLIKMDCNKA*KFDFVLQYLNKMA
4382	9879	A	4678	3	284	QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SQLLRSLRQKNLLNPGGRS CSEPLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSR
4383	9880	A	4679	122	196	CWFENVNSKSGFWVLF*FKAKLVN
4384	9881	A	4680	2575	2786	ADTESITL*FYHFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM/G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAQPTFIPK
4385	9882	A	4681	3	512	YNQKVDLFSLGIIFFEMSYHPMVTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFISWLLNHDPAKRPTATEL IKSEL\LPPPQMEESL\HEVL\HHTL\ ANVDGEGPYRTIDGPRSFRQRISPAI DYTYDQRHS*KGTSSIRA\AKLLHL VRETMIRICTRHGACQT
4386	9883	A	4682	1	382	EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSSQLNVTSMQLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL EC\HRLDIRAELDESVDVHNMW S
4387	9884	A	4683	1	472	GIMLPDLKLYDIAMVAKS AWYWH KNGHKVLWNKMAQN/HIYGQLVF VKVPKYTQWGKGS LFNEWNQEN/ WISACRRMKLDPY\STKINSKWIK AYTIR/PETVKLLEENIGKKLID/ GP G**FLALAPQTQATKA*IDKWDFIK VKTFTARETVNTEKRH
4388	9885	A	4684	182	345	RFPLCSFPPTLPCEGICFPFA\FCHDC KFPEAFPTRLPEPAEL*VNSTSSLH KL
4389	9886	A	4685	205	395	VNLGIFGKNGAPPG/PEGRGGILGHR NPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQGGTTGLDPLGPPK

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						KGFNNHPGGIREFPGN
4390	9887	A	4686	35	389	NLFYKVLQSAGFFSMDHEDDVDFL ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHLADQ QKAGAAAIMSVATKELMMKT
4391	9888	A	4687	3	547	GGAGRRAWAGVGGAPGAGGGPAE AGAAAEEGAEHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAV SLPTSSVPETRGAPAGPIRG/PAPGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF
4392	9889	A	4688	65	414	WKCADTNVAQGPVRVQVQLRGT PIPNHCALCLLREKQRQLCPRGSNG PAERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKPF
4393	9890	A	4689	75	787	HVAFASGQRCNKS LPTPKVVPRVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPEGKRLPFVSPS GHRARSTWAETRPQGPRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPAPPPP*RPDK DGGGGS\PDQRAGRTRKAEVGGCL ASMRPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTPAPRPRPYALRR
4394	9891	A	4690	8	382	QEYWE*LYAYTF*NRDELDEFDRH ILPNFTQEEYTT*NNPVSVEIEFVI NNISTPKKNPK*TSDDDFTSKFC*T FKEELIPVLYKHFQKIVEEEVLPFLF CELSITFLKLDRRCEVRLHR
4395	9892	A	4691	2	389	NRKRIELTRKVL FELKHMRDVQNE HLTRFVGACTDPPNICILTEYCPRGS LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNLNSFNSVLIR DLSRFN*FSFSSESPVNCIQIIVIIISP
4396	9893	A	4692	2	544	TKAPKYIKQTLIDPKGEVDYNNIIV G/DANTPLSKTDRSSIQ*INKETVEL NHILD LIGLTAIYRTFHPTATE/YFFS SAHGTL SRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELEINNKR\SENT NTWKLNNMFLKD*WINEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFIT
4397	9894	A	4693	1	373	MPHSVPGLMSPGIIPPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGANSHQGDMSRVAL DLPLSILPNLYTMPLVLQHSHTYN HLTYS*LHNLQTIP*INLDQRAPSLP
4398	9895	A	4694	185	417	NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGW\WIRSGVRDQP *PHG
4399	9896	A	4695	88	432	TDLFLFVCLRLSLLSVAQAGVQWF

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						DLSSQPPPPRFKRFSCSLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVIS*PCDLPTSASQSAGITGINCR TQTTY*F*KFSVDSL
4400	9897	A	4696	3	390	YRIPYYVSTDCENLLKRFELENPVK RLTLKQIMNDRWINARHEEDELKPF AEP*LADILDQKGIYIIGMGYSQEEI WESLTKMKYDEITATYLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG
4401	9898	A	4697	289	365	SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPGFK*FSRLSLQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL
4402	9899	A	4698	33	397	NAYNQLKVCASSPWLFCCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSLPEVVIVHGSQDNNATA
4403	9900	A	4699	2	371	LNTVIANGVAMASRPYQPTHVNVH IHQUESTLTHLLKAGGTLKKTLEHPG DVSSTATIGYEQALWVTQILLGR *E/CVILECVLILGPWTALSASRCF WAESVEIVPRAGAIVHDKQPVKLA
4404	9901	A	4700	3	441	GFEDKVFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNIEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYIRPE GQDSAFSWTDLLLKNNSSELLNNLG NFINRAGMFVSKFFGGYVPEMVLTP
4405	9902	A	4701	2	375	CITRDLKWGTPVPLEGFEDKVFYV WFDATIGYLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR
4406	9903	A	4702	1	3093	
4407	9904	A	4703	2	2717	GEMRLFVSDGVPGLPVLAAAGRA RGRAEVLSTVGPEDCVVPFLTRPK VPVLQVDSGNYLFSTSAICRYFFLLS GWEQDDL TNQWLEWEATELQPAL SAPLYYL VVQGKKGEDVLGSVRR LTHIDHLSLRQNCPLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPQRAAETVLKQGG VLALRPYLQKQPQSPAEGRAVTNE PEEEELATLSEEEIAMAVTAWEKGL ESLPPLRPQQNPVLPVAGERNVLITS ALPYVNNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICDKYHIIHADIYR WFNISFDIFGRITTPQQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFVEGVCPFCGYEEARGDCQD KCGKLINAVELKKPQCKVCRSCP VQSSQHLFLDLPKLEKRLLEEWLGR

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						LPGSDWTPNAQFITRSWLRDGLKPR CITRDLK WGTVPVPLEGFEDK\VFYV WFDATIGCLSNITANYTDQERWW\ KNPEQVDLYQFM\AKDNVPFHSLVF PCSA\GAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGFGDMAHDTG IPPDISR FYL\LYIRPEGQDSAFSWTD LLKNNSELLNNLGNFINRAGMFVS KFFGGYVPEMVLTDDQRLGHVT LELQHYHQLLEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMLQPYM PTVSATIQALQLPPAC SILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVAEVAKLLDLKKQL AVAEGKPPEAPKGGKKK
4408	9905	A	4704	180	490	VENGNNSLTIMNRRARQKINKE\TA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF
4409	9906	A	4705	2	405	KNLNNRLFIFF*IKKEIKRQIRK*FEW NEKEKTIYQNLWDAPKAKLKEKCI VLYV\KEETSQITDLSFHLKTPEKEE HVKPKVNRMEIIRAEIIAVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD
4410	9907	C	4706	217	486	MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHWGRGKPPRGRV PAAALGA AVVAAMASDPWAPGP KQPGRWADLAALLCGLRPA*
4411	9908	C	4707	13	216	MLYWDCKRYKVVDKTAQWDFAG NISVKGAELSQTAAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC*
4412	9909	A	4708	132	1424	VKHGPQGGPRRQAQGGDIQVFGVG LPGEWPEEGTQKGGPPLKTLTGTD GDKIGEPPTRAP\RFRTGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVGCP*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMFPNGPIQALFEG DLWDLGRTGHGTTGGGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGKPESESPCPNP*APPVVC YGITRPVGFGRGPSQPG/LMGRPGSS ALWA*NPELPNCPGLPQPCPQEV QSFPGPVGRGLKGGQDCHRG EGSSKCAQGGHPAPA*WNPLVYTP ASPFPRPASGKPRS/RPSCGLRAPS* HLRRPCLTPFRPQGLLGSSPCPKP APDSGLLHSP LTPSRGLSGQCNP LHPQLNQSNRDR
4413	9910	A	4709	1	340	RHEERTTGILTSVGLASDTSLICVIE DFFDTALIISRSSSEGKIQMLDSFLLS L*LLVTEETVNHLLQQEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDL

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						HIWYDDESIV
4414	9911	A	4710	12	398	TYLDLPLPGFCIYDF/VPPFSSECFIF VFMVCFFLAFILSFSSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFQFIFKQLAFFH HV*ETFSPVFLICKYWDD*TYFS
4415	9912	A	4711	111	453	YPIIITFNTLGVAGNCL/KLTYTI** MPTANILKCLKAFSLR*RTR/H/GCP QSI*ARRII*DIQAKEDVKLYLFTDD MILYVENPEESTQKDLLANKVNKVS GYNINMIIRCISM
4416	9913	A	4712	1	184	SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQD\ELAAARRRSLPGLASS VKEPLQAT
4417	9914	A	4713	1	1630	MALTRPVRLFSLVTRLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPVPVLRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQEAPAVRKLSS KGSFADLGLLEPRVLHALQEAPEV VQPTTVQSSTIPSLLRGRHVCAAE TGSGKTL SYLLPLLQRLLGQPSLDS LPIAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLDESLE LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPE\GVGQLLNKVAS DAVTITSSKLHCIMPHVKQTFRLR KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLGYILDDHK IQHLRLQGQMPALMRVGIF\QSFQK SSRDILLCTDIASRGLDSTGV\ELV VNY\DFPPTL\QDYIHRAGRVGRVG SEVPGTVISFVTHPVDVSLVQKIEP AARRRSLPGLASSVKEPLQAT
4418	9915	A	4714	79	410	IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPOEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EMEI LNNCRNQGV*RMSKDRRETLETYQ QL/L*LLQTSPLYLA
4419	9916	A	4715	185	449	TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRL ALCSLQLGRK\ETITIIYDCEGLGL KHLWKPAVEAYG
4420	9917	A	4716	154	364	MWRWFSLPPFSLAGVELAPPVSR SPRGP/TPYGLPRVPLWPLHSTALYC P\PSRPTSAPFTPHPLPKLRG
4421	9918	A	4717	9	1805	SPATSP*ETAGPVKRSRNGSSPAADP EALSPPTARLQRTVPPI*LNGQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLLQI VYGNYESKKHKQGFLNEENLKSIVP VTKLKSKAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPT GAAFTGQIFTKASPSNHKVIPVYV

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						GVNIKGLHLLNMETKDFQYFYVVD
4422	9919	A	4718	200	529	EDVSKPVPWTLNGSCTSPISHSDN QKCPYFPVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKKREKRYWKRNFKATV K*HKAYWIT
4423	9920	A	4719	177	321	QTCSMDTKWQLYISPHQS**QPMP SIFSSDPSLQCVCLICKRLLS
4424	9921	A	4720	166	627	MWRWFSLPPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSLSHSSFPFRHS SPAQLPVAEKPSVAKRKPS*GFPR PTRAPKAQVSGVGDPPAHLFTVLP SPRTSAPFTPHPLPKLRGPRSSKALA FHSA
4425	9922	A	4721	3	610	STFNNEP*PEKQEQNKHKIRRKQIK IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQDKIRNE KDITTDTAEIQRIRGYEQLYANKL ENLEEIDNS*THTTY*DLQEEIQNL NRLITSNKVEAIKSLPVKKSGLPDG FTAIFYQTFKEELIPILLKF*KVEEE RVLPN*FYEASITLMPKPKDKDT
4426	9923	A	4722	1	454	LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGGVVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNPGKQ SPCLGFPKCDWDYQPDLTMP*FYLL LELEIKFGVHVLWKSFLIKIENYYC
4427	9924	A	4723	1	318	KEECNKEEKESREKK/NEKEKIE*KE EEVRKEEKSLNKDKDKKRRKREK GEGRKKEGILKVKKDGNPSNGHA RMPKER*LYDVRGTPHSSDHGDT AIFQTCIL
4428	9925	A	4724	42	200	LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC
4429	9926	A	4725	50	403	VVYHVMVLLKVVICHHFLTLFFS FRSLJLYLFFILFMISLYLSCFLYNFL FIPSSSIFSICFLMIIVLI*FFFYALFIII FNPIILYLNLYLLSLFLIESLFDYYLCL ISFVIFY
4430	9927	A	4726	3	282	VQGQEPLTASMLVAA/PPQEQQQM LGERLFPLIQTMHNSLAGKITGMLL EIDNSELLHMLESPELSRSKVDEAV AVLQAHAKKEAAQKDSKAK
4431	9928	A	4727	780	1249	LVVFMSIPLCSSTHPSILQGLKLVP EQGQPPPLLFHIVRCSIEQALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTASMLVAGAPPQEQQQML GERLFPLIQTMHNSLAGKITGMLLEI DNSELLHMLESPELSRSKVSWSGSDP AASVLM
4432	9929	A	4728	510	2771	NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPPVSPSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP

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						AAGPIRSPLAGLGVVGGGEMNAAA SSYPMASLYVGDHSDVTEAMLYE KFSPAGPVLSIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFDFVIK GKPIRMWSQRDPSLRKSGVGNVFI KNLDSIDNKALYDTFSAFGNLSLSC KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMMLNDRKVFVGRFKSR KEREAEELGAKAKEFTNVYIKNFGE VDESLEKELFSQFGKTLVSVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLKRFSPFGSITSKAV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPP GFQGMPSAIRQSGPRPTLRHLAPT SECPDRLAMDFGGAGAAQQLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYSLSRH PS/PAVHVQ\QEPLTASMLAACNPP /QKQKQILGERLFPL\PTMHPNLAG K\ITGMLEID\NSELLHMLESPESLR SK\VDEAVA\VLQA\HHAQERSCEP GRCCCCYLLDPRKTDKAK
4433	9930	A	4729	7	365	LYTRHPPSPSCIMTACFGSHIRYRS *VPTPVLRAVIRSVGGGDCSERLG LRPRPI/PELGPHPTRPPPPWQNV QRADPVAVTPCRSREGSQAELPRG RGAVSSSTTRPGLPAPNRP
4434	9931	A	4730	1	1520	AEGACGPRQPNKGAGAPPQGPAT LPGPRSGLSSTATMTANGTAEAVQI QFGLINCGNKYLTAEEAFGKVNAS ASSLKKKQIWTLEQPPDEAGSAAVC LRSHLGRYLAADKDGNTCEREVP GPDCRFLIVAHDDGRWSLQSEHR RYFGGTEDRLSCFAQTVSPAEEKWS VHIAMHPQVNIYSVTRKRYAHLA RPADEIAVDRDVPWGVDSLITLAFQ DQRYSVQTADHRFLRHDGRLVARP EPATGYTLEFRSGKVAFRDCEGRYL APSGPSGTLKAGKATKVKGDELFA LEQSCAQVVLQAAERNVSTRQGM DLSANQDE\RPTRRPSSWRSTATPKS VPSVPTRASTGR*RPFGACSPPPAR MPAATLTSSGVTGASH*GRPMASL* PPRRMGSWPPRWRQQTQSSSS*SS STAPSSCSAGSMASAAAARSRAPWT PTAPAMTSSSWSTMAPTTSKTPQA NTGRWAVTPRSPAAATLLWTSSSS ATITRWPSRWAGAT
4435	9932	A	4731	131	677	PSSLS/CDIFLRSPISTPSPSPLPRTPT TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPTSGSPTNKISTASQISQ GTGSPVPKIHGSSFVTSTVKVIKQE

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						PGEAPHVPATGAASQSPLPQYVTVK GGHMAVSPQKQVITPGEGIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC
4436	9933	A	4732	131	362	PSSLS/CDIFLRSPSTSPSPPLRPTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTSTGTVY*IHICTI*RV
4437	9934	A	4733	1	4461	
4438	9935	A	4734	2	614	STTTERENYRPIFLMNTDGRILSIILP SQI***MKKIIYHDQVGFIPGMQRWL NVHK\TMHVIHHINKMKGKNYLIIS ADAEKSLGKTYHCFMMKTLNKLGI EGTLNIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPLSPLLFNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEPKDSTKKLLKWWN
4439	9936	A	4735	164	613	NLNMEATGTDEVDKLTCKFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIED\T *LREM*KNFRKDSISRIWLTREEFP QIEGSALTDCGWGCTLRGTQMLL AQGLILHFLGRAWTPDALNIEKLE L
4440	9937	A	4736	40	359	
4441	9938	A	4737	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRRYVYVMVVIDFVLV SNILPKFNHLC\TH\TH\TH\TH\TLFST YLKNDRDKTIMCKLSLIG*LAESEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYE\ARRHPYFYAPELLFF AKRYKAAFECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
4442	9939	A	4738	133	359	LLNFMLLFHRYYALKVSYFKSSSLDR KLELLWNKYWVNTLSSSSSLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK
4443	9940	A	4739	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVR WKKIFAKHTSDKGVES\NIYKELS*I NKASSSSSSSSSS/HSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW
4444	9941	A	4740	1	375	LVPKRA*YWHKNTSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSPMQLIQENTG/IMLQD IGFGKDYLKTSKAQATKQK*TRKH WEMLQDIGFGKDYLKTSKAQATK QK
4445	9942	A	4741	1	296	FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVLSASWDHRSPLPRPA NFFVFLVETGFHVLARMVIS*PCD RPTSGFQSTGNTGVSHRTWPLLL

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4446	9943	A	4742	3	380	FLEEYNPPKVSQEEITSSSSSSSSSSSS SSSLSSDIES/VIKNTSSNNKKNP PDGFTAKFYQM*KDELISTLLKHISK/ IFHSNSFCE*QTTR*FAISITWRAKPD KDTPQKEPYRLISLINIHSC
4447	9944	A	4743	3	369	SFTLIKKTCDIRKANYKTMSLRKIA AVILNKILAN*IEH/RJKRIHHNQIRF I/SGTQVWLNI*K*INVTHHINRLKK KNYMIILIYEKTFDKIKHPFM/K/V LSKLGTENFFFLIKHIWRKI
4448	9945	A	4744	70	345	KVWGEKVWYWQKMTPIVQWDRT ESPQIGN*SLTKEIQWRKDSLFNKW *GNHWTAFFSS/RSNLNLKDLTAVT KIKSKWVTDLNVKHKTIKLL
4449	9946	A	4745	3	345	KFNNDDEMDKFADRQKLPYLAQEE RQNLN/*PYLLKNLNVQNLPIKSTSA PDELICKFYETFKNEIILLCSLFQK MELSQHIHDSNLTLTQ/KI*K*YRTE ENYRDISLINTYAK
4450	9947	A	4746	35	355	PHPWPWSLSSSPPSQSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQLCPCCLKGCWARHMPK*G WNGNPFVPVSLNYPWARNRPSLLTH FVMWEARPR
4451	9948	C	4747	27	416	MMKRLGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKSVLGSTGASLKVFQQWG AGPLPGFTEGGHPKKVFQGPCIKA LEPFDE*
4452	9949	B	4748	5	763	MPSSVSWGILLLAGLCCLPVPSLAE DPQGDAAQKTDTSHTDQDHPTFNK ITPNLAEFASFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAFTVNFGDTEE AKKQINANGTRPFEVKDTEEDFP RPGPDHREGAYDEAFRHV*
4453	9950	A	4749	11	368	GLKSLIN*LLAVYPREQTTL EEV MR DPWVNS/GSGVAFDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFRLS
4454	9951	A	4750	175	349	PSVAGRPRRKGGGRQPAQTRAVGI AGTEPPYYLGLWGPVGVDQG*QP ASFPGPQPVPKAPSNTKEA/SPSNA HSSSLGRLPSSPLPPRPASNTGSLS PRQGTMTTL*GATHLPQHSD*EESTRE SPPPTLEQLPPSVQLIRMPCPLPV TQ
4455	9952	A	4751	2	354	ENCQINNLRFHRLRKPCKEEYTKPTA SRRK*IVNIRIERNGIEQKNRNTSSSS SSSSSSSSSSSLTFR*MDGRSSSSSS SSSSSSSSSQ*QRKATRLLIKI*N ERG DITADLTEIK*LLILOQLNNY
4456	9953	A	4752	121	363	WRDFKTKTVIRAK*GYLIITG*NHO

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						EDTTVINMYAPKTAPKKYMKQKL TDWKRAV/DSKTTAGDLNILLIMD KTKQKINRV
4457	9954	A	4753	178	439	GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGKGEKK RRNKGRKEGREERGKGEREEGYIM CIHGIGNRSLAVLGA
4458	9955	A	4754	193	355	GLFSIEEH*HDSTHLGINTL/LISRLFI EK*LLKRVYQVTQACELYAWNPN DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIV
4459	9956	A	4755	3	227	NIKIGKEEVKLSLFAGDVYLEKPKD STKKLLELI/NFSKVAAY*INIQKSV FLYANSE*SEKEIRNIIPFTIAT
4460	9957	A	4756	115	487	CSLCFVAEWSPWCGWTQLIYPW*E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGF\SMLATLVSN
4461	9958	A	4757	2	436	GTEAEQPSYQPGLELPQGDQEEP/G LAGKTGLGPRFPRTTGGSQGTLLV EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPGGICGVSS SVSTQGPMP*CGQQGN*ALESCRGP ATAALSEQSPASPSSRAARA
4462	9959	A	4758	76	194	
4463	9960	A	4759	310	551	SSKQSSAKPPFCLPNPGKVCRRGRS RT*GCNLQKGSPEKGRRFGHPPE WTIFPSVQRQQA*FSDSPPTNGIP GEWKG
4464	9961	A	4760	1	1165	LRWQREEGQKAGVHVGTMTQHLR PQGA AVLPAALAPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPGSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQ/GEPRHSARG*GPESLP LPVTRNSLVGGLSESN*ACPCR*QK ERLSIRGVPERRPFSGPEPGRGPASC SGLPTTGGTEERRKEGKRAAASKA ALPGWARLPDQPGPAATGSK
4465	9962	A	4761	1	389	EETLPLFADDMILYIKKKQKTKKTT KESTKRY*N**MNVFGKVAGYKV NTQKSIN*QYTI*KVKLAS\FSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI
4466	9963	A	4762	1	346	RACL*FQLLGRRLRQGDGLSLGIRGC SGPGWHHHSPA WATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREE KILAYHYLEKSAIYSISFFLT KHILN

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						TPVCWFSSEHIIYF
4467	9964	A	4763	2	468	FPSLPFSRFLFCITVMF*VLDPLS LSYLTILIPHLKIEFNFEK/CVNH/CF LLMLLLFLL\CTY*MCLGPFYFLP CLSFSSVFHFLSLCCIIGNLFRYIFKFI NFELC/CYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFI
4468	9965	A	4764	3	364	RNLKLISEYCKISG*KVNIENQVFL YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*I/GRLNTKTSVLPNLE **ITAIPIKIPASYFVDN
4469	9966	A	4765	1	755	EESILEEVLEALTSAGEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGDFEHKKED LVELSHRLEDIRAELDEAYVYVNM VWSTV*ETRAEGYFISILQHLLLRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVDICVD QAKLKEFEKALELYKKFEKEFTD PQENS*NCAKKEAQIYGPFNPNSK TF
4470	9967	A	4766	12	321	KSCDWAERLVTLV/WN/PYFKNLNS SYKQLSPMGGYLNWAHTLTETWI IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI CQHNY
4471	9968	A	4767	2	375	MSSPLPSPWSPCLLPQAPGPTLPVP PAETLSVPACFLRLPINPSPSQ*APA WRQLTADWGGHSALGLPGCPGPSI TWPSHSASHLLPQRNQGPMLGYA HLPGHLPTNVLPSGHTPALERPK
4472	9969	A	4768	3	338	QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI
4473	9970	A	4769	66	365	LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASPR SRALALPTRCPGPACGPREPRLQAR GVP/R*IPPRGPHGAPSGLP GPVG C
4474	9971	A	4770	3	345	KRGTPLAGEMAEGHCL\CLPLGTEY LTV\NPIVHLFNSEIG*KIRPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSAHM*SCDL ILI\ITLLSYYI
4475	9972	A	4771	2	352	KRGKPLAGEMEEGHCL\CLPLGTEY LSVKPIVHLFNSEIGKIRPVAGGR HVYSNTASLFFTPLRCLGGEKHKSG LRARPGIVLSLELNHGIDSAHM*FV DILLIITLLSYYIPFR
4476	9973	A	4772	1	296	QRSVKISISENGNSHMEIVSFSLIFCQ FLLHVFCSTIHYDCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF

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4477	9974	A	4773	2	859	GRWPTQPTSLQGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR PWGPLSVTT*NRSWSCYCWRLRV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCHFSQPQRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHPAAPQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRLLCGVPP/CGPLLMLCPLPVPEV GLGPFLRELLNTKKLNCVFNKQKV PNKPACHLGDGSPSLPHQIC
4478	9975	A	4774	158	517	RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSLQPLPPRFN*FS CIILLSSWDYRCMPCLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK
4479	9976	A	4775	1	165	GSLLPLLFIILEVLAKAIRQEKSIGN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT
4480	9977	A	4776	2	516	QNPCISERQYCCEKLPLERSSRPQDS AGQPVTHAHCSSLSTVDLCPPLLAT HRISCWH*QDEVQGGRD/SVDKGD LVALSLPAGHGD TDGPISLDVPDGA PDPQRTKAAIDHLHQKILKITEQIKI EQEARDDNVAEYLKLANADKQQ VSRIKQVVQKKNPEAAQTIGQLD
4481	9978	A	4777	154	406	CTDIQGYPGSRVAQAGVQWHNL/ CLSLPSSWDYRRPLRPANFLYF*ER RGFTVLARMVISIS*PCDPPASASQG AGITGVSHRT
4482	9979	A	4778	1	429	ARLETNSRSVAHGGVQCHDLSSQQ PPPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVISIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA\RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRCVPD
4483	9980	A	4779	1381	1787	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4484	9981	A	4780	1147	1553	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4485	9982	A	4781	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4486	9983	A	4782	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D

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						SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4487	9984	A	4783	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4488	9985	A	4784	2583	3580	DRVSLLLPRLECNAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIQVSHHTWPQEVFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPP HPANFFVFLVETGF/TVLARRVLIS* PRDLPASASQSAGITGVSHHT/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGLCCPGWS* TPELK
4489	9986	A	4785	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4490	9987	A	4786	3	305	FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCSLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVVIS* PCDPPASASQSAGITGISHRAQPIKY
4491	9988	A	4787	1172	1688	VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTHS*VCEAPSPFYVFSH LFSLQSPSHLVCLFCSF*DGVSCLR QAGVQWRSLGSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVSISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR
4492	9989	A	4788	641	1074	VLNLVEFVTRELAFTNVFFCFFVFF FCFFLRSL/DSVTQAGVHWDLGS LQAPPPRFTPFSCSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVVIS* PCDPPASASQSAGITGVSHRAPTN VNKAITNGLFTYFFNEE
4493	9990	A	4789	7273	7925	IVSLFLFILLVFWWWCFFFFFETE SCSVAVAQAGVQWHNLGSL/QAPP PGFTH/LFSCSLPSSWDYRRPPRP VNFFFFFFHF**RRGFTMLARMVLIS *PQVICPASASQSAGITGLSHVRQ GPHNLLTNQVNKFFFFFFLETESHSIV TQAGVQ*HDLGSLQSPPPGLKRFSC LSLLSS*DYRLPPHPPTHF/CVFLVE NGNSPCWPGWS*TPDLR

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4494	9991	A	4790	156	391	IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFKKKTDELILTFI*KGKES VLDKPILKKKNNIVGLKICDFETYY
4495	9992	A	4791	365	506	GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRLRPGP
4496	9993	A	4792	2	503	LTHPAGARPVLLTTPEFEGPCFGTP HGQSLSQSAFSRGHSLGDTVGVGTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREPVPPP *QR\GPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFLPD
4497	9994	A	4793	3	389	FQDLIKR*KATIIKTLWY*HKNNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTCK
4498	9995	A	4794	27	285	VFFFFFFFFLRRLSLALLPRLECSGTIVF LVETGFTMLARMVISIS*PRDLPALA SQSAGITGVSHRAPASFNLTLINLP PLLLWTF
4499	9996	A	4795	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLRTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH
4500	9997	A	4796	74	463	HISQHDSRYLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPSPK*L/SSWDYRRPP PRPANFFCIFIKECFLLARMVISIS WPRDLPASASQSAGITGMSHRARP AQVS
4501	9998	A	4797	1	337	KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRJGKAMWNKIKYGGGL IQ*DLKICHKVRJIEIVWY*LQGRQ/I DQ/WEQ/IQSPEIDPNIYSHLTYDKSP TAIQRKIIYPF
4502	9999	A	4798	3	331	KNYKTLLREI/KEELN*WKDIPRLW LRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFIWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG
4503	10000	A	4799	3	340	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKT TLKKNRVP/PIKFSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER
4504	10001	A	4800	46	195	SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLNKYNWIMRSGDRDHP G
4505	10002	C	4801	353	442	MPLLYVQRLFARTGLCATLFGRRMM SPLYV*
4506	10003	A	4802	1	273	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIVLRNQKG
4507	10004	A	4803	57	231	

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4508	10005	A	4804	2	169	
4509	10006	A	4805	698	1231	
4510	10007	A	4806	58	2674	
4511	10008	A	4807	7	235	
4512	10009	A	4808	1	245	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS
4513	10010	A	4809	175	394	NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSLKFQEVSGAPNKFWSWILPL
4514	10011	A	4810	65	2712	SGSGHCLAEASMGPGWGWKLWRT VALLAAAGTAVGDR CERNEFQCQ DGKCISYKWWCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCP QFWRCQGQVDCDNGSDEQGCPPKT CSQDEFRC HDGKCISRQFVCDSDRD CLDGSNEASCPVLTGCPASFQCNSS TCIPQLWACDNDPDCEDGSDEWPQ RCRGLYVFQGDSSPCSAFEHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCS DGNCIHGS RQCD REYDCKDMSDEVGCVNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQLVAQRRC DIDECQDPDTC SQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIAYLF FTNRHEVRRMTRTRSGYTSFIPNLR NVVALNTEGPSNRIY WSDLSQRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDSVLGTVSVA DTKGVKRKTLFRENGSKPRAIVVDP VHGKHRPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEESIIRCLRVK VWLTYEMQ \DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVL FHNLTQPRG VNW CERTTLSNGGCQYLCLPAPQI NPHSPKFTCACPDGM LLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQHTTTRPV PDT SRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPIVLLVFLCLGVFLLWK NWR LKNINSINFDNPVYQKTTEDEV HICHNQDGYSPSRQMVSLDDVA
4515	10012	A	4811	49	361	STSYPTGSHAFL*PQNVVDAETNS* HINNVLRLKIKLLEENT EKNCHD LGLSTDYY/SVTPKA*ATTTKIDKL ELIKIKNFCTSKDITYKVKRLLIGNNI CK
4516	10013	A	4812	2	346	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCK

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4517	10014	A	4813	2	356	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSFM
4518	10015	A	4814	1	357	VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLGVQIK AGPWVRVKDWVRLEVKIKNRDQV RGEAEVRRIGQQLRTKTRPKLNVHP KRNGSIN*NHITVECYSTIKKQ
4519	10016	A	4815	1	323	PVRGTEQSNKSWASGLQPGWGRAE QLAWGSFNLSKWPSGGGDPQPIILS RVQNMGRRLAR*EAPCQPQQLPSR RSSPVPHQLAPPCHPCGASLSPALA WPPPPPSRS
4520	10017	A	4816	1908	2324	ILASSLRANPGFIRNFHLFFFFFFYFLR RSL/DSVAQAGVQWHDLSLQAPPP GFTPFSCSLSPNSWDYRRPP/RHHAR LISFFLFLVEMGF/TMLARMVSIF*P WDLATSASQNAGITGVSHHHTHRP VIKYLPSPPNLAG
4521	10018	A	4817	1	273	RPRRRYPHSWWFL/QEVAIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHKKW TAPIGVISL*AHPIEHA VSNMLPVD VNLRSIRTVLFHQ
4522	10019	A	4818	3	293	DHVSPGVQDQAGQYSKTPSLQKQ KQKTNRHGSA YLWSELLGSLRQED HLNPGVRGCSELLGHCSPAWAAK *DPVC*KNKTKNLIAGGHPRSFVIQ
4523	10020	A	4819	2	170	KLGFIIKIDFSSVKDNVKGMRRA DW/DFIKIDFSSVKDNVKGMRRA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4524	10021	A	4820	52	228	WASGHVRPYRVLNNFISNQKVMDF KEDLSGIAEMFKTPVKELLIVL*TCL IVAFKSDNS
4525	10022	A	4821	22	376	TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFHWRASSSSSS SSSSSSSSSSS/PSSSSSSSSSSSSSS SSSSSSSFIQNTGINLTDGFLGNVF LDMTPKAQAKE
4526	10023	A	4822	151	379	SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH
4527	10024	A	4823	3	479	RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGLILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHDLSLQPPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV
4528	10025	A	4824	1	57	GKRYTRSDQLRLRAHTGVEKKLV CPECSQRSMRSDRLTGHIRSHQNK GIH*SDELQRLRAHTG
4529	10026	A	4825	3	602	VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRFHFNFNTFKIF*KLGD SMLT AVSVARDCGMILPQDKVIIAEALPP

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						KDGKVAKINWHYADSLTQCSHPSA IDPEAIPVRL/CP**LRGSSNDSLSFC NEWIILSDTGGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQLIEALQNVE
4530	10027	A	4826	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4531	10028	A	4827	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4532	10029	A	4828	2	321	KAVLRRKFIATNT*KK*TSQIKNLL KKLQEKNKFKPKVSRRKTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSS SSSSSSQREDLNQIGNEREDITTGTT EIQ
4533	10030	A	4829	132	290	LVTSE***YQIFFFSPEMESHVSQA GVRWSNLASSLHPLPPGFKRFSCFSL
4534	10031	A	4830	645	1201	GGRDLLRTHSVGPSTPQTIPVLTTPG *CACTQDVSPSPHS/PPMKELWPGA PQGSPGRLSPQPPH*RSPHSPCTLW PAL/PGLASTEGWGAIALYILEKNW GREGLNLPPA*PFCPPQSPHGSVLF PSKASREAPTSNPCLQPQIPRLPSR PKAQAPATHLGGAATHRSAGVAR VCAGAFGGQA
4535	10032	A	4832	115	454	TMMTSWINCFRKG*DDVEHHAH NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKLKLSKL STQWLLKPLHPDQL*TRAELLG*ES LDKYDQDPEALIR
4536	10033	A	4833	1	638	ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRLPLIFHFENPRALKNCAYS TLSVLCQWNNKAWMSAHLFTGW LTKYFKLTIETYCSEKTTFFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMPLPLASSFNSYYLRNRIHRTF VVVAQSWLQCPTTAISDIQIGPVAM GLLLIPSAFVLCWLSIQQVSKLKHF HSHHSYFLRFWRLTA
4537	10034	A	4834	2	6053	KEILQEYLEISSLVQDEVVAIHREM AAAAARIQPEAEYQGFLRQYGSAP DVPPCVTFDESLLLEEPELEPGELQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQQELLQTK LEHLGPGEPPPVLQLQDDRSTSSSE QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQKQE YVLSVLWDGLPRHFIIQSLDGSRL RMEAADPGSPALQNLRLLEGEGFPS IPLLDHLLSTQQPLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRVFQ RGNSNSQRAWVRGPNTGAPHPGVGS RMGRKRRREL RDWEGRGRSPRPFQ GNFGEVFSGRLRADNTLVAVKSCR

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						ETLPPDLKAKFLQEARILKQYSHPN VRLIGVCTQKQPIYIVMELVQGGDF LTFLRTEGARLRVKTLQMVGDA AGMEYLESKCCIHRLAARNCLVT EKNVLKISDFGMSREEADGVYAAS GGLRQVPVKWTAPEALNYGRYSSE SDVWSFGILLWETFSLGASYPNLS NQQTREFVEKGGRLPCPELCPDAVF RLMEQCWAYEPGQRPSFSTIYQELQ SIRKRHRPRCSSSAAPAHMLTALHS PGLLPASTLPAGCSAVSSLCPCCCQ GFLFRAETIKPLVPTESWHVHSSG RQVSEGTSAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPE PASEAGGPARGRRTERSGCPGAQL GPRQRPPEQGATGERAPAFACVAA CTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYLMLDRVQHD PTRHQNGGNFPRSQISVLQNRIEQLE QLLEENHEIISHIKDSVLELTANAEG PPAMLPYYTVNGSWVVPPEPRPSFF SISPQDCQFALGGRGQKPELQMLTV SEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVPHSHNDPGWI KTFDKYYTEQTQHILNSMVSKLQE DPRRRFLWAEVSFFAKWLVGNGQL EATGGWVMPDEANSHYFALIDQLI EGHQWLERNLGATPRSGWAVDPFG YSSTMPYLLRRANLTSMLIQRVHY AIKKHFAATHSLEFMWRQTWSDS STDIFCHMMPFYSYDVPHTCGDPK ICCQFDFKRLPGGRINCPWKVPPRAI TEANVAERAALLDQYRKKSQFLR SNVLLVPLGDDFRYDKPQEWDAQF FNYQRLFDFFNSRPNLHVQAQFGL SDYFDALYKRTGVEPGARPPGFPVL SGDFFSYADREDHYWTGYTSPRF YKSLDRVLEAHLRGAEVLYSLAAA HARRSGLAGRYPLSDFTLLTEARRT LGLFQHDAITGTAKEAVVVDYGV RLRLSVNLKQVIIHAAHYLVLDK ETYHFDPEAPFLQVVGWEEAEPMM VLPFRLTEFQDDTRLSDALPERTVI QLDSSPRFVVLNPLEQERFSMVFL LVNSPRVRVLSEEGQPLAVQISAHW SSATEAVPDVYQVSVVRLPALGLG VLQLQLGLDGHRITLSSVRIYLHGR QLSVSRHEAFPLRVIDSGTSDFALSN RYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAY LFLPDGEA/SPTSPRSPPCCVSLKALS SQRWERTMSTFTRRSFTICQGWR GCLWTYHPWWTSGTTSTRSWPCTS IQTSTAR/VIFFTDLNGFQVQPRYL KKLPLQANFYMPVMAYIQDAQKR LTLHTAALGVSSSLKDGQLEVILDR RLMQDDNRGLGQGLKDNKRTCNR FRLLLERRTVGSEPDDFSKLAAMFR

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						GLIFHSSRSGNREVQDSHSTSYPSLL SHLTSMYLNAPALPVARMLPG PGLRSFHPPLASSLPDCFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4538	10035	A	4835	1	6606	MGFSSEL CSPQGHGV LQQMQEAE L RLLEGMRKWMAQRVKS DREYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKTYSEQWQQ LQQELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRS LWKLF AHHNRYVLGVRAA QLHHQH HHQLLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDES LLEEGEPELP GELQLNELTVESVQHTLTSVTDELA VATEMVFRQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEALQG LQVALCSQAKLQAQQELLQTKLEH LGPGEPPVLLLQDDRHSTSSSEQR EGGRTPTLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQ GKQEYV LSVLWDGLPRHFIIQSLDGSRLRM EAADPGSPALQNL YRLEGE GFPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLN HEDLV LGEQIGRV PQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRREL RDWEGRGRSPRPFQGN FGEVFSGRLRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYVME LVQGGDFLT FLRTEGARLRVKTL LQMVGDAAG MEYLESKCCIHRDLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSES D VWSFGILLWETFSLGASYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFSTIYQELQSI RKRRHRKHRA GTERKGRGMRCTD RRQHFPFARGAQRQRPKATWAGAG FRGWRTRAEP AQRSAPAARGPAGE LQQRAEQGATGGRAPAFACVA ACT RAAVPGRVCVEASMKLKKQVTVC GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAMLPYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNGQLEIA

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						TGGWVMPDEANSHYFALIDQLIEG HQLERNLGGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWSDSDSTD IFCHMMPFYSYDVPHTCGPDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLFDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSGLAGRYPLSDFTLLTEARRTLG LFQHDAITGTAKEAVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSDALPERTVIQL DSSPRFVVLFPNLEQERFSMVFLLV NSPRVRVLSEEGQPLAVQISAHWSS ATEAVPDVYQVSVVRLPALGLGV LQLQLGLDGHRTLPSVRIYLHGRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTRTSKDKSGAYL FLPDGEA\SPSPRSPCCVSLKALSS QRWLRTMSTFTRRSGFTICQGWG CLWYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFTDLNGFQVQPRRYLK KLPLQANFYMPVMAYIQDAQKRL TLHTAALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNR RLLERRTVGSEPDFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMLPGP GLRSFHPASSLPDCFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLW ALSVIQEDTLPSAETALILHRKGFD GLEAKNLGFNCTTSQKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4539	10036	B	4836	114	255	VQPRRYLKKLPLQANFYMPVMAY IQDAQKRLTLHTAALGVSSLKDX*
4540	10037	A	4837	1	452	LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/NRYMQVWFSGLTGLLKS RRVDERHEQQVHMQLVYGTRTS KDKSGAYLFMPDGEAKPTSPRSP CCVSLKALSSQRWLRTMSTFTRSG FTICQGWGCLWYHPWWTSGTTS TRSLHFSFN
4541	10038	A	4838	3	3543	QLGRLGPERRGGRALTVCVEASMK LKKQVTVCGAAIFCVAVFSLYLML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVVP EPRPSFFSISPQDCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWAEDLQVFVVPVSHN DPGWIKTFDKYYTEQTQHILNSMVS

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						KLQEDPRRRFLWAEVSFFAKWWD NINVQKRAAVRRLVGNGQLEIATG GWVMPDEANSHYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK HFAATHSLEFMWRQTWSDSDSDI FCHMMPFYSDVPHTCGPDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSQIFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFDFNSRPNLHVQAQFGTLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSLAGRYPLSDFTLLTEARRTL LFQHHDAITGTAKEAVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVDDTRLSDALPER TVIQLDSSPRFVVLFPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSPVRLPAL GLGVLQLQLGLDGHRTLPSVRIYL HGRQLSVSRHEAFPLRVIDSGTSDF ALSNRYMQVWFSGLTGLLKGSGLC FLA\SIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEA\SPTSPR SPPSCVSLKALSSQRWLRTMTFTTR RSGFTICQGWRGCLWTYHPWWT GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYMP VMAYIQDAQKRLTLHTAALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLERRTVGSE VQDSHSTSYPSLLSHLTSMYLNAPA LALPVARMQPLPGPLRSFHPASSL PCDFHLLNLRTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G
4542	10039	A	4839	2	438	FVPAKVAGAAEPDEDGGRSLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVASDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRNAELCEI
4543	10040	A	4840	1	1608	
4544	10041	A	4841	1	3117	MAPEWRPGTTASLPSGPGARSVCSL RSPEAGSASVFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPVSVPQDLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIFNLKLPCPSTMKNPASLLFSL FEGEWAI AEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKSMSC SLTGSLALQPDQQDHETDSSPAS AYQRIWEAFANQSRERAERDAFLQDT FPEGFLWGASTGAFNVEGGWAVG

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						GRGVQPKHVKEAFRLLNKSIIRVET PDVNLDQEEIQMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASLRLGFSEYCRISNLIVLHLRKVEE EEDSALKRSELVNWYLKEIESEIDS EELINKKRIIEKVIHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRRLKALKTARLQP MVILHHQTLPASTRRTEAFADLFA DYATFAFHSFGDLVGIWFTFSDLEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQQLQGHQC TAGPPPPPGGGMVMMQLSVNNPQ SCAHSPPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSLNCTDPVVCVP SSFFVIGDSGIPLEVIAGSVSADELVT RIHKVRQMHLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAELA CEIPPTSDTKSDTATGGESAGHATFL FREPSGCSDQRPADLNIRVERLTK KLEERREEKRKEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLLE RNREKAEDRAARERIKQQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFPSDAPLEEARQFAAQT SVRVTSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM
4545	10042	A	4842	3	790	GARGTPFLSPASVESSVLLCLLVPHF VLSRGPPASPPSSYHPSLGPGG/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSGPAGSLMEA*GNKRDA PPPPGDPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPGPMAPGRVL HQQGPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKPPG TQFPFRFPDPSGTPCPGYLEIFLLDP IPPRNWLAPLAAAQ**/PWGRWE MPMALPRGGLPLYT
4546	10043	A	4843	1	1026	
4547	10044	A	4844	1	722	MALEQRLKGGSGAALRSKAFPAEG TAGAKALQESDWSIGGAVSKPVF VQSVRELVADPCASNPCHHGNCSSS SSSSSDGYLCICNEGYEGPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*Q/QSCLALRQR*HCLPGSRKQG\ KSCRNEMGSSGGDPYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHRIPVLPHRWTKC DPPSGFRGTGPPGGDARLGE
4548	10045	A	4845	2	2028	CSPAAPRRPVRSCCPRWPCCCCSSE RGPEAAPWPTRCPPRPCL/LPGCAA QPCRNGGVCTSRPEPDQHPAPAGE PGYSCTCPAGISGANQLVADPCAS NPCHHGNCSSSSSSSDGYLCICNEG

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						YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPAISLGNNGDT AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHRIP VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVND\SVTKS\NCGFA LNSGGE\VSTCVPGESHANDLECSG KKGCTTKPSEATFSCTCEEQYVGT CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGY\NGELCQSKID YCILDPCRNGATCISSLSGFTQCPE GYFGSACEEKVDPCASSP\CQNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGTSYKCLCD PGYHGLYCEEEYNECLSAPCLNAA TCRDLVNGYECVCLAELYKGTCEL YKDPKA\KSACLNATCDSGDLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGG\SCLGDQPNGY\TCHCPHW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEFPLRGPFHPYADHP DRGDLPHQPH
4549	10046	A	4846	1	703	TISCPA VRSRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMEKPYNKNEGNLENGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPQGEKGPASQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRITFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA
4550	10047	A	4847	180	866	GAYVHGGRGGLCVQSLFQGVSSSDF CPPITLVPTLRPRAPCLWCTQDPA PPCQSQRRLGPGFQGAAGLKPSGGL PNILLPESPSKRFNHGQLPVPQTVFG GGGSRGPPLLVPPLPLFVFPFCGCF LSQPRGHRSPSSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTSQSLLFYGKDLVPK
4551	10048	A	4848	112	679	KI*NMWCYSDTGQFNVVKLSVLL*I IYIFNKILSSFLVKTGKLSLKS VN/NK QQRITKTSKENKRGGFMR*DIKTF YVFAVIKSVLYMQI*ID*WKIESSET DLHISSHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF*IAT/ENIFVTFSNVGND FLKYQLKSKIKKLKMRMVVYQMV P
4552	10049	A	4849	33	394	GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSHPAACAACPRLPGL CSCAPGSAPLPRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPPAPAAPKAE* LLQGGEFFSDPQPLAPEPRQLR
4553	10050	A	4850	2	269	LSGVCTVHIRGVCVWAGGNPSGTE LPGLPPRPSASPPHPPQG*GVALP\

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						PVLCFLVLPHPPTPNLIYPPCTVPFS PLPAPFAFFCW
4554	10051	A	4851	1	543	LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTTPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRP/PQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDFLWLGTPSSSTKIKWTRPPAV EPLLVLHPTPTLPLPVPIVTQRVE YQGRFF
4555	10052	A	4852	831	1301	FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLIE KLVINFLKKKFPTTRASP*PNQSTSR SSPFSYPGRRVPPLQTSSVPELRTPY WTGAPPLNGSSGYVSPTLPPPLMH
4556	10053	A	4853	1	1222	
4557	10054	A	4854	2	563	AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQ\TPPLTPVGGSN PQPIPAQSHPTSSSSSDGLRDNVPW LKVKNSPLKQSPGYQTELVIQLVW VGGEPPQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKSQPSGAGLC DISEGLVPSKA
4558	10055	A	4855	648	1377	EYLHGGWEHLQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHPLAPN QACGVGLIDWRPRWTRGGTAAAG ARTPNLNPGAALT/GRHSCSVKK GSELELSRRR/TLPVVSPGGGGCE MLRPDPASSP\SSQTP*PVPGAEAQT LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGSTPKVSSFPLPF GGPLHSP*Y*PGPENWEGGGDEGPL SHPARVPAAQSETECVPTESPFQ
4559	10056	A	4856	3	394	SQAPS/GVAAHTPPLS*AWTQPWNS IHMASTRPNMPLRSGPA\CMPLQ QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTDSDDLQLYKEQGE GQGDR
4560	10057	A	4857	3	666	SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFTP ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLRNSGFFPSLNP RWGPFPSLWERF*NCSQPFRLRN PPVPL*GVLASNPWPPHPHHPH NMPPAPPRVRLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR
4561	10058	A	4858	3	361	FFFFRKWVNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF
4562	10059	A	4859	3	397	DQPTDIILDEQ*LELFHLRTGIRRG PVSSLPFN/IRAIRQEK*IKGIQLGKEI

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						KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPFTVAIKKLKYLKI HLAKE
4563	10060	A	4860	2	328	AHIDAVNEAMRLEHGFHAPTMSW PVSGLTMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK
4564	10061	A	4861	13	410	NKMRRQATDRDKMLAKDTDFDKGT LEIYNQFLKFNNKKMSIPIK*WAKN L/NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFFPALHLFYQ LTFRKSISH
4565	10062	A	4862	3	293	DKGLKGRGFPTFTSFGQPTWGLGL LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGERGPPGPPGLGV*ALKGK RADKKGGASFPGF*KFPVGLP
4566	10063	A	4863	125	366	GIPGERRLEPPG/PKGPPLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQQ GS/GNPGPKPIFPPGPPKGRKYRVGP MAPPLQ
4567	10064	A	4864	79	336	HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDDDALLWQPHGSIRDMDR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCEC\HRRVFIYRQAPAMST VFYNRKDCLO/TVDRMLIHKVASLK TNDPILSIQAPK
4568	10065	A	4865	2	512	KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGPLSPRVLG LQA*ATVSGLTGKFYKTCKEEIIPIL TILFQKTEKGTLO\SS*EETSTILIPNQ EGKKNFQNGCLSMDPGTGKVPLTK ILVNQIQQSVIHKDNISI
4569	10066	A	4866	466	1451	EVCGLKKARISLFFF*DGVSLLCCPG WSAVAQSRLTATSASRV\K*FSCLSL LSSWDYKRPPRPANFLHF**RQGF TMLARLVISIS/WIS*SVPPWPPKYLE L*AKAGDSLEPGSSRLQ
4570	10067	A	4867	3	379	NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLSRSP*CE\GRSDR LG*PP*GGQGGGGHGAPSTPGPGG\ GPGDFHSPKPPPSLVPRPTEARGSP GP
4571	10068	A	4868	2	1718	SEGAPRRGAWGGPPARSHTLAPT PLPP/GPLSLCFACLKWLGVDRD AG*LGSQKAGGRGHGPMGQGGKT PPAHAW*PTGWCTGKP*KLGFLCPF HIPPVSLACFLLSAASDFSVLTWQ LWGP*EPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPRGLPLLNGF/QRPNL TPYGPAPALALS*PPQRWEELAEGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGPQPPVASKGPFSS*PKVLREPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*IGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRLVLSFCFPLLPGS* GTRASGRGHSPSLKPGPRAGRQ\G ETRGS\GSPGE*GCWSQNWDGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEQADQNPSA FGPKEWEAAFLPNLPCQGGQQRGPSP PPPPGCRNGDPSQGLGAGAEYSLGP LPYT
4572	10069	A	4869	253	451	RWKAWFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGTG GGK/YKGNNPRWKRGGGKHGTGGK K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGGKL/SNNPR WKRAGGKHGSGGKFKEIIPDGSVK VESMER
4573	10070	A	4870	2	269	EGGLGLNRFPPPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEPPRGGE/R GNWPGGMEGEGGIDAPAS
4574	10071	A	4871	20	312	SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPT* PVPTSPPPAPTARPGSRAPSSPGLA PTLTGPGG\PLRPPPPPAEEP
4575	10072	A	4872	299	472	KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS
4576	10073	A	4873	1	3454	MKHTLIPRIKNACLMSSSLAVPVNS LVCLGKILEYLDKWLVDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKLG ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLSEHKTLEQLHI MQEQQKSLDIGNQMNVSEETKVTN IGNQQIDKVFISHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQPKVSMNQLSQKPN QWLNQFVPPQVSPATGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSL EEQLPQYRLKVDTLFLYENQDWTQ SPHQQRHASDALSPVLAETFRYMI LGTDREVMKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNVHLSE QNESLEEQLGQAFDQVNQLQHELC KKDELLRIVSIASEESETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLEKE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETNAQMSRMTEEL SGKSDILIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHLYFSQSYGAFT

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						GESLAAEIEGTMRKKLSLDEESSLF KQKAQQKRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLLNQGSSEEVAGSSQK MGQPGSGSDSLATALHRLSLRRQ NYLSEKQFFAEWQRKIQVLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDDEEGITF QVQQPLEVEEKLSTSKPVTGIFLPPI TSAGGPVTVATANPGKICLSCTNST F/TLFTTCR/IYLHPSDITQVTPSSGV PFHLSCGSSGSSFHSNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSP\SENPL QPLPK\SLAIPSTPPNSPSHSPCPSPL PFEPRVHLSNFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLDRLK RLGIARVVKNPGAQENGRCQEAIEIG PQKPDSAVYLNSSGSSLLGGLRRNQ LPVIMGSFAAPVCTSSPKMGVLKED
4577	10074	A	4875	1	638	LAWGGKKGKASSDSGGLVDSISTL TTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAETP*PQMGE *TDVCGSQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIV\NSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*WLVWKTGGSRKKDSES WVNLTRTPIATAVPDMTTDSLGIQ SIPGHPVLQPIDPGESL
4578	10075	A	4876	31	448	PKSLLSLVKINYGYPK*QATKAK LDNWDYIKLQSFCTTKIMNRVRRQ PAE*ENIFANQTSKGLISKIYKELK QLNSKKANLIKWNSSDLNR/HFSN EDIQMASRYMKK\STSQIREMQIK TTMRYHFMPIRMTT
4579	10076	A	4877	3	286	KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDNCS*IGKLSI AKNIYVSNPG*FDAIPKIPARFFYA FGLYCRNSVSLSPRLN
4580	10077	A	4878	3	236	ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTPLVCQLDQHSFLHS/FLV IPTCPVPLLG*GILTKLSASLTIPRLQ P
4581	10078	C	4879	206	262	MVAIGTGYRRPGLRTFLN*
4582	10079	A	4880	2	756	LTSSRGARAPLARAP/LDPAFRAN PLRSYGSGLPTFPYLHCNMPKAC SPWRPAADMGTTPGARFTPSPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENSRRRTSPG SRRVTDGTGRLAGAPCSATPDSGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWNPSVVRPSKV LRLNICYYTP\SHAPAAAPGPADFQ GPARAHRTPEPRRFRHGPLSRGE P
4583	10080	A	4881	3	322	MGSVTGPLYSGYKEEVVCCTLVEV

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						FPSLLQVSRNPRMPFDLGLILIFCLG GQGFPRATTVSGHWPE*LSQSSSSP KLRPPTL*SKPAHPGAAEALKA VPR TSAGAR
4584	10081	C	4882	240	500	MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKLSSRCRAPLRRRAA RTRSXSQXWRRXTT*
4585	10082	A	4883	22	696	CTFGSFPFGLSAWSFRASLPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPPCNLSKEDLLQNPYFSKLLNLNLS QHVDESGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIQELLVDYYV KIQDTNVTSEDKKFHETLEQRLLVT ELMRLSPSQEREIPPLGLEKADLL E
4586	10083	A	4884	1	594	AVVHFRLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QSPAENVLTALRAPAAPG/LQVCF KGSAGGASGRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPSEHLKCLGPC SSVNTSECRVENRSLNCPFTPCNL
4587	10084	A	4885	2	326	VKTAEFVNKWKQNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMCDWNTSDFCVTPQYNE TEH*WKKVKRHLGREENLTL*IVK LKEQDFEASQ
4588	10085	A	4886	2	373	VLLTPEERTVVIALWRKVNVALC R*GAWA**L*AYPWTHRFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQSELHCDKL HVDPENFKLLGNVLVCVLARNFGK EF
4589	10086	A	4887	3	332	HLSIINLVNQLNSPLKAYTLPVWIP SSRGPTICCLQEIHFASKNTYKLKV KELSSSFQANEKEKHADKTGFK\PK L*REKNHGYIMIKRSVQKENIYIYM FLIADPDIC
4590	10087	A	4889	1	304	HSCSSMRMPPLPTPPP/IVLCPHPSP LIKALVSSKPP*VPSAETWPVAAL GA*VPAVLGWPLHTENVLPVPLPL EMPRIQWHFMLCSFPQRSRADEST
4591	10088	A	4890	1	254	RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSS SSSSS*LPVNIRQ/EKVI*GMQIVKEE LNLSL
4592	10089	A	4891	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGFTVSARMVISIS *PRDPPASASQSAGDTGVSQAPV
4593	10090	A	4892	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS

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						GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR/YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCLSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLYFYFHRDEGSLCCPGWS* TPELK
4594	10091	C	4893	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIILILSTISFHQLLH*
4595	10092	C	4894	4827	5060	MWIFYFWTLNSVPVIYMSTLMSIPHY FDYCCFIVSDIMLPEITFTFILLMV ALAIRGPLHFRRHFRINLSIATKNA*
4596	10093	A	4895	2	311	FILHVCDKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPATH NPILTTHTSTPPPTLTINLTSSP
4597	10094	A	4896	2	374	DLTPKV*SRKGKIGKLDFTRTKTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTAKDVKEHFTEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF
4598	10095	A	4897	1	684	
4599	10096	A	4898	1	1349	
4600	10097	A	4899	1	821	MLQTSWGYDNPRVTQKVPPFQLNC LPMTVVLLILYAEMATDWNVRVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKTENKAWPKMLKGKKA KGKKVAPAPAVVKKQEAKKVNP LFEERPKNFGIGQDIQPKRDLTRFVK WPRYIRLQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAKHYRPE TSKRRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI
4601	10098	A	4900	1	868	GTRPKMPKGKKAAGKKVAPAPAV VKKQEG\LAKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR QRAILYKRLKVPPAINQFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKAAPKGTFTPKRP PVPSKQ*G*TTVTTLGGGPRKASAG WWIAHDVDFLELGLSFLAALCRK NGGSPYCIHKGKQDWGRIVNKK TCTTGRLSHR*TSSED/NKALLKLVE AIRTNYNDRYDEIRRHWWGNNVLP KSVARIAKLEKAKAKELATKLG
4602	10099	A	4901	145	745	RRRGTSQCNLITIVNHISEITVIMFIE CSLCIKVIRLFHILILLDFSSKPAPPPP

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						PCGAPGL*TATLLSRLRTARDLGTRL*ASPASPLCAVPSPAAAFL/SLPLPLCPSSSSARELSPTPGLSGQPAPAA SPGPG/PAG/PPPPPLAVRPRFAPHL QLCPPPFSSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS
4603	10100	A	4902	94	432	TFLFLLIFSSEYWKFKKQYSLEKSL FVAYNHKDG*THFLKGNNQFIFSLA/ LFTLGDIIYCKDIFGRLLGLQP/TDISSS DSPFLSFSSSIYILTWGQARWLTPI PAFWEAKAG
4604	10101	A	4903	109	422	FFEDGVLRSVAQAGVQWRNLSS LQPLPPRFK*FSCFSLRSRWDYRHA PPCPAFFVFLVETGVTLARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS
4605	10102	A	4904	3	364	HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FOISGIRQGCLLSSFLFIILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITTRANK
4606	10103	A	4905	50	394	LSYSWHSIHLMLKIISWHFDGQFSA LVIL*LSVAVDADYSHFLETASLL DFETVLSWFSSYLT/DMFLFTLVFS L/PFSIQLLNIGISQGSVLSPLLYAS ASGYMSLNIMYRH
4607	10104	A	4906	49	366	SGSSLAAVFWGPKGPAQAPGPWAP WASPSGPDLPRLHPADPQRQLST VPLPLSRPPALSLIAPMALSHSCSNIP P*TPPPASLRPELTPARS/PPTR*SHS PPP
4608	10105	A	4907	119	246	FCFHHLNLPFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPFSLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR
4609	10106	A	4908	1	280	ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCSLPSSWNYRCAPPCPASFFV FLVE/QGFTMLARLVLS*PQ/CDPP TSASQSAGITGMSHCTWP
4610	10107	A	4909	406	661	SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDGLSLQPLPPQFK WFSC/PASPKCWDYRREPPCANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPFLLL LFFSFFFTGSHCVAQAGLK/PLKLR RSSCLGLRKCDYRREPLRLAPSW TFRM
4611	10108	A	4910	3	459	ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQLINVIKVELDGRKMGDAQP EMFDKVLVDAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ
4612	10109	A	4911	1	95	TPKVHASWQK/MAD*SGQCPVLQIP

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						LSSLMMQ
4613	10110	A	4912	253	1531	SWKLAEKVWEAQLPGFSPPPQCSV RCGRGQSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTG WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLRPPALQPCQGQ ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSSTF APWVGTPGPGFCVLP LLTQPPVCRSL RTCPGSGLPRIIPPERGPGHLHGFLCH HRSPIGLGPLWNPLGSSSLFPGLQQ GMSSR*TEGVGKVNGTQSDFSGT GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRLHRTLEG TRPVFLEDFS
4614	10111	A	4913	131	355	STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTG/TGAPPHTTPS RPLNTRGPTEEFSPRPPPQHRPSSC
4615	10112	A	4914	3	420	QQPPTRLD*GPKQLMPHSPHNPHIT* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACLPL*RSTRPGTLKPKAT PAAPPPTTVHKPVASLRSHLRADGPG APPHTTPSRPLNTRGPTEEFSPRPPP QHRPSPPPTK
4616	10113	A	4915	11	375	
4617	10114	A	4916	3	260	
4618	10115	A	4917	3	208	
4619	10116	A	4918	1	422	
4620	10117	A	4919	127	4348	GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVNRPKSKTKKAPI KITITKAAPAAPPVPAANEIATNPKI TWQALNLPVITQISQALPTTEVTNT QASSVTAQPKKANKMKRVTA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIASATEVSLAA TATHTATTQGQITNETASIHHTAASI RTKKASKARKTIKVINTDTEHIEA LNVTDAAATRQIEASVVAIRPKKSKG KKAASRGPNVSEISEAPLATQIVTN QALAATLRVKRGSARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLKVQDKTIPIKRSMDLRDV IQEYDEYFPEIIERASYTLEKMFVRN LKEIDKQSSLEVLISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGLRPGVRHSLFGEV RKLITDEFVKQKYLEYKRVPNRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVQ AAAVAVAEAEARAEARQMIGIEE

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						AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASFS NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSSSEASISFGGMPCTSASFS GGVSSSFSGPLSTSATFSGGASSGFG GTLSTTAGFSGVLSTSTSFSGSAPPTS TVFSSALSTSTGFGGILSTSVCFGGG PSSSGSFGGTLSTICFGGSPCTSTGF GGTLSTSVSFGGSSSTSANFGGTLST SICFDGSPSTGAGFGGALNTSASFGS VLNTSTGFGGAMSTSADFGGTLSTS VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTSVCFGGSPST SAGFGGALNTNASFGCAVSTSASFS GAVSTSACFSGAPITNPGFGGAFSTS AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPSTS LCFGSASNTNLCFGGPPSTSACFSG ATSPSFCDPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTIIFGSGSNTSTGFTGEPSTSTGF SSGPSSIIVGFSGGPSTGVGFCSPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAGFGSGAA\SLGACGFSYG
4621	10118	A	4920	3	1380	NMLGKYL*VKDQTKIPIKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDPRIASVWWSGGT GWGAGLGRGPRVLTCDVDDGQMV KLSAVSLLNVLCF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLIT\DEFVKQKYL\EYKRVPNRSP P\EY\EFFWGLALPTTETSKM\KVLK FACRVQKKDPKDWAVQYREAVEM EVQAAAVAVAEAEARAEWFQHQH WLYLANPAPSNAGASSGPKFYCW PAVDPSTGVGFCGPKHQVASSGGP STGAGFGGGP\NTGAGFGGGPEHQ WLWQVEPPVLPVAF
4622	10119	A	4921	1	412	TRMGLPDASRRRTCRMDPEGWQE AMSSA*GRITLQRLSTGPEGQGGRE KVGPEGGSENPPQPKAAGVLSKHL PGAPAQPPQRPPSSPPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPVPPVPPWPP
4623	10120	A	4922	117	295	
4624	10121	A	4923	1	3564	
4625	10122	A	4924	1	355	LPGIEVLWQGPVVSKVIPVESIEEV

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						CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCIPQLV
4626	10123	A	4925	3	3145	AAAEGELGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSP MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCEREGERGRGRSRRG AHLELKPSPLRAGAPTDRGRGGP AEVAAAGGRRMVQESQATLEERE SELSSNPAASAGASLEPPAAPAGE DNPAGAGGA AVAGAAGGARRFLC GVVEGFYGRP WVMEQRKELFRRLQ KWELNTYLYAPKDDYKHRMFWRE MYSVEEAEQLMTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGE PET FLFCPT EYCGTFCYPNV SQSPYLRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIIKRAPVIWDNIHANDYD QKRLFLGPYKGRSTELIPRLKGVLT NPNCEFEANYVAIHTLATWYKSNM NG\VRKDVVMTDSEDSTVSIQIKLE NEGSDEDIETDVL YSPQMALKLALT EWLQEFVGP HQYSSRQVAHSGAKA SVVDGTPLVAAPSLNATTVVTTVY QEPIMSQGAALS GEPTTLTKEEEKK QPDEEPM DMVVEKQEETDHKNDN QILSEIVEAKMAEELKPM DTDKESI AESKSP ESMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPV TLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKSFVQWLGCRSHSSAQFLIGDQ EPWAFRGGLAGEFQRLLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPD LIG DKLVGGLLSLSDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEAEKIMLSFHEE QEVLPETFLANFP SLIKMDIHKV T DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFY SKLGC FEIAK MEGF PKDVVILGRSL
4627	10124	A	4926	3	251	HERHELQMLVDAPCSDLAQELRQS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQLYLLALYNEVSLLS*QDIF NVALDVCMCRS
4628	10125	A	4927	1	408	GTSLNSLSKTKAKDLFIGDVIHNAG PHRDKKLKYIPEVVYSGLYPPYAG GG\GLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSC EEPHL MSFRSYFHG
4629	10126	A	4928	187	378	LCQKTM SLFTHSFCFSVGRNMEGV

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						LMDVDCESVYPIV*ASN*GLASAEV GGSFEPRLRPAAWAT
4630	10127	A	4929	26	121	PDRTMGGVREQRQSPGAQRTFFQLL LSFFVES
4631	10128	A	4930	3	867	
4632	10129	A	4931	1	558	EVRVKCVKALKGALYGIPDLTACL KLFTGRFKDWMVSMIMDREYSVA VEAVRLILILKINMEGVLMVDVCE SVYPIV*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLLLASFFVESKSHFVTQGGSGQF SAHRNLCLPGSGNFHVSASRVAGIA GAPPHTWLIYVFFS
4633	10130	B	4932	1	1617	MKNGVQWAEAGHDYVLDLVS ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFVNSWDSDEDMSTRPQPQE HMPKVLDSDGYSSHNQDGTNGETE AQRGTATHQQOPTMAAVSESDSLG EPAVPHKGLDCYLDLDFVLSYGD ADLEKPTAIAYRMKGGGQPGGGSS SGTEDTPRRPPEPKPIPLDASTLAL QQAFIHKQAVLLAREMTLQATALQ QQPLSAALRSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPAAPVLAQDQASPETSL HRDAATVTQMHLTGQGRLLSLD DSSLHLWEIVHHNGCAHLEALSFO LPSRPGFDGASAPLSLRTVTVLLV AAGDIAALGTEGSSVFFLDVTTTL LEGQTLAPGEVLRSPDDYRCGKA LGPVESLQGHLDPTKILIGYSRGLL VIWNQASQCVDHIFLGNQQLES LCWGRDSSTVVSSSHSDGSYAVWSVDA GSFPTLQPTVATTPYGRACTPVAHD HIDELVRGAVFSEKHFCIEDL*
4634	10131	A	4933	1	811	HASAGAGCWHLPGLIEGAAQKGR GRQVIAVARTADVIMMLDATKGE VQRSLLKELESVGIRLNKHKPNIFY KPKKGGGISFNSTVTLTQCSEKL VQ LILHEYKIFNAEVLFREDCSP DEFID VIVG\NRVYMPCLYVYN KIDQISME EVDRL\ARKPNSV GSSSCG\MKLN\ DYLL\EMLW EYL\ALT\CILHQGRR RDRR ARFSQDAILRKGASVEHVCH RIHR\SLASQFQVTPWVWGAP PSY SPQAGGALTH\TMEHED VIQIVKK
4635	10132	A	4934	1	431	QRFPAAFGVPGARRDAPPHSPPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLPSRPATGTESARRC ISGDTQSQFLRLARPCRQPGPS* DRC RPGVVSCLDREEKNAGHWL SMAFS LLWVLATQHCLHPEESLTM
4636	10133	A	4935	56	252	GAQERGCPREKHGNAELAEGVLIL RGRGKPPSASLAGRE*I*SRGPEWK VTVNQTAKAKERTGP
4637	10134	A	4936	81	896	CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQELNTIRKALSQNLGGG

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						LAQAA YPAQVVSLISDVAGDPVE VIASGPTVASSHNVDCLHILNRYG LRAALPRSVKTVLSRADSDPHGPH CGHVLNVIIGSNVLALEAPAAAGRG TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLQGQGMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S
4638	10135	A	4937	100	332	NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIIKLLEENIK*YLSDL GVTK*KLTKFNFLKIKHFCSPSSC
4639	10136	A	4938	692	900	NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGE\TWSLLKIQKL AGHGWPAPGSPSCLAGLRQE
4640	10137	A	4939	87	322	ARLVQNTGAQLKEVQYKLFGLF FE*/QSHSVAQAGYSAVIIHCNLSL LGSSDPFFSAS*VAGTTGMCQHA W LIFDR
4641	10138	A	4940	91	356	GHAFLFGGYSSSHWPSTYPPHAPV PPPPPSPPYPSLPPFHSLPPIKPFPLPP /SPSPSPSL*SPPTPPPTLLIPSPSPPP ASPPLQ
4642	10139	A	4941	2	332	CGGPPGSPDTRGGS LIPQGV*AA\GP MEQVPLVAPSSAIPAVPGSLSGTPSH QPVLGTHTPSCPGLTYIPPESEL DCPAPGRQRPCPGQTP LTPCPPSFI FSKQ PRA
4643	10140	A	4942	637	1560	VWQLDKSMRAAQWPAPAGGAAGS EWAGLKR\RPLGWSSFSAAAQSPL ELLGHPQSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTERRHSSSC *GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMGK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLTPTWAPPMCK RIL*KCTCNSLPQKPSMALQCI*NEI NKTSTTSPTCLAPH*APATLACSPF LQPAELLPISGTLHVIFHPRTLPK RTGSFLSSPQVSV
4644	10141	A	4943	2	335	ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKCLEESIR/VKLCDLRLSK ISWILKAQSIEEQTDTWDLKT*NNY SSNGTVKRIKRQVED\WHKVFARRI SDTGLVSRISC
4645	10142	A	4944	2	345	FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIFVFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLFFFFG DKSFRFCCPGWSTMV
4646	10143	A	4945	178	388	RREPLHPANLLFFFFFFEMESP SVAQAGVQWRDLSSLQAPPPG SCHSPTSLS*VAGRLRNKNCLNPDAW
4647	10144	A	4946	546	850	FSVLFYFFESESCSVLQAGVQWRDL GSLQPPPPGSSHSPTSAS*VAGTTGT CHHTQLIFIFLVETGFHHIGQASLKL

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						LTS*FAHLGLPKFWDYRCEPPHPA
4648	10145	A	4947	169	358	GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSCLTLLKPWDSGTFPTFSFN FFIYLAEKGFNG
4649	10146	A	4948	1	145	ANSAAMP SLGCSASSGLVFWPQGL YLLGVVSVSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQHVA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSL SLLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVSVSPLPPTPTTVTFPEQI
4650	10147	A	4949	1	295	GTSSRLRLHRTDELTA PSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHL PKIQKPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTA PSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHL PKIQKPLPPTTERHDWSR RLAGKKPPVPKHGWVP
4651	10148	A	4950	119	1036	HASCLKTQALQECSVGVGGGLPVS PAGPPRCFCPALPAAALALQGTTPA TGG*A WGLSSPDWTFSTKKLVMS ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSEL RHRARGPAQICST RTRPAPWWT*SLPPPGHSRAVGF RCGPASP\GVPVNA AVALPPSTCGE ESRLPQEEGGI HMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS S\GPPAAQGERADSRALGTAPPGE LALRPTPGGIGTPPAGGSEDISREVD PAKRHGLGA
4652	10149	A	4951	2	1262	GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQQYK PDSTAAPDQRAPVFLVVMFWTMM LNGPFSRFSADSEHPTLQASACDAL SSILPEAFSNLPNDRQMLCITVLLGL NDSKNRLVKAATSRALGVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAA WSLGNLTD TLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVD AINKWTAPWT SQAYNALTSVVTSCNFKVRIRSA ALSVP GKREYQGSVDQYARIWNAL VTA\ LQKSED TIDFLEFNTVSSLRTQ ICQ\ALIHLLKLG/RSASDLPLMKET LELSGNMVQSYILQSLKRSRIGR
4653	10150	A	4952	52	730	KSACDALSSILPEAFRNLPNDRQML CITVLLGLNDSKNRLVKAATSRAL GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLNVRAKAA WSLGNLTD TLIVNMETPDPSFQGRVLWSPAENG YDQALEASKDKDKVKRHA VRA GNLLHFLQPSH/GKTPHLQKFI*GSL SRALN FLLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA

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						LTSVVTS
4654	10151	A	4953	3	363	HELEFEIKNTIPFILAP/N/NIKYLGIT/LTKYVLYLN/DLYAENYKTLMK*IRDLNGDPLSCKVKNLIKINKYMKIEILCSRIGKDSNIV*VSLLPQLACRLNAIPIKIPANHFVEVN*LILKFI
4655	10152	A	4954	179	438	ENIMSKTSTENCTKQCHFVHVN*YSIFFFFLRQSL/DSVTQAGVQWRHLGSLQAPPPGFTPFSSRFLSPSSWDYRCPPTSLANFFCILVETGF\TVLARMVSI*PRAPPASAS*SARCKLHLPGSHRSPASASPVAGTTGARQQA\WLIFVF
4656	10153	A	4955	1	264	QFPKPSRGP/TPTKSLFHILSPPNQ*I SPPP*QLPPSLYQIPPTIRLSPLPLAESPSPLSVGLGGPLGWVGQLCLSFPGGPKHVEV
4657	10154	A	4956	3	369	HERHELVKEFNKVSGYKINAHKSVALLYTN/DDQAENQIKSSTPFTIAAKSVK/YLGIYLTKEVKDLYKENYKTLKEIVDNTNKRKHIP*P*MGRINIVKMTTLPKAIYKFNSMPIKISPSHFV
4658	10155	A	4957	2	338	GCWDN*ISTCKRMKLDCSLMLHMKINSM/WIKDVNIKSSSYEK\NIGVNLPDNVLGNGFINMMPKAQASKEKIINWDSAKLK/IRK*RQLTEWEKLCANPIYSHLIPVLCYLYLV
4659	10156	A	4958	42	447	IELVTVLQFYRAFYLFERYAGFLFYYYFLFFVEIRFHYIFQAGLS/ELLGSSDPPTSGLPKCWDYRR\DHRTWPDMDQDFLMFHIFPKLFSFPDMCFLASE*P SANTWLLL\VVQSSFLLSHTYHPPGKASTLWFS
4660	10157	A	4959	377	1220	FRKVVPLAESH\PAVPG\GKVRTSRSPKSPPRALPT*/PGLFNPGCQRETSPSLG/PPGQHP/VPGQLNSKRKQIPHNE LVEQTLRSGLTSAQPAHPTGGYSCSKLRPGPLPNPNGLCRCSDGRIPGDERPLALSRT*IHLRACTGPDAAAQVLPGLLPCPPHLPPLSGMFD\SWLAPP LPDPCQRPTPPQAPSSEANNQRSQAPGCGPHSLRDSELQGQCPGPAQAFCRGSGLFQLTQLTGPLHGTR*RLSPKNSQALKPHM*AVGRILHWPPAARP GNSGRYPDD
4661	10158	A	4960	3	353	HEVPAKGPRPHLTD\CPPTQDFLPGFSPRPASGPPPPSLSLRLFQPG*TVWSPGPPCPVVPDCTSASGQVPFLPPAF RFKNVF*PSRPSPGTRGGP/PP*VCTS R/PLP*TSEPQPG
4662	10159	A	4961	301	343	TRMAHFS*STKPSPMGPIQWSHMPGAFSE\SSSCHSHSAFLPPYFSHGPSNRPPIRALCRNLPLPLPNKPRAPSAADEDNSLNVEWYVPYITRPQA*AALIKINQDGTFLVRDSSKK
4663	10160	A	4962	2	319	ARGPGPSGKSGARSLGNTPRRGAGLGRVPWSLCY*EGVESGRPEGAGPGTSPGVGFIGAYHGRGVTKVGG

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						LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP
4664	10161	C	4963	109	372	MQAWINIRKSVYVIHCVNLIKXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XKLRLPQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS*
4665	10162	A	4964	3	990	RTLRECYK/HI*ANELNNLDEM SKL KDA/TLLQLTQEEIETLKYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFQ EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPKDKDITRPVSLMIIGAKIFK QNI*HTQVYAHIHRIYVYHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKT KT QERTF/FILLKGIY/NKPMADIPNGKK LKA\PLRSGTTRVPDRFWKWQ/CP LPLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQT
4666	10163	A	4965	3	314	HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAVGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNRGQGRPPWKAGKLGKCQEV LFRFAAF
4667	10164	A	4966	2	329	ARGECCRKAFCIYDCVIHE/CEECR KAFCIYDCVIHERIHNGEKLYEC*E CETSLSSNSVLIQHQRHTAEKPYEC NECGKAFHRTSVFLQHQRFTGEQ LYKCNECWKTFRCSSRFIVHQRHN G*KPYECNECGKAFHRTSVFLQH RFHTGEQLYKCNECWKTFRCSSRFI VHQRHNG
4668	10165	A	4967	61	533	WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKQRRALPTAS*FQGQSHAA PETPSYVGQDQSPSPGG*RPSTSPEG DSCFP
4669	10166	A	4968	22	482	GKGPGGPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRPLDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRA WT LDLPQLGWGFWDCMALALESRSSG ESPSLL
4670	10167	A	4969	146	1299	GAPGPWPTGTTWLPGAAGAVPDGP FLLPSSAALSRTAS*FSQPPVPPAL TVPWPRCGC*TSCPAVPQSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSGWPLPTTLPLPWG L/PRLQSREHKPALSAATWQGLVVD PSPHPLLAFFLLSSAQVHF*PGLRSW VGPFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPISYFNLTVDLNRNDYHSASS SSSSSSSSSSSSSRRLSWSPKHHPL

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						LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALPVRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK
4671	10168	A	4970	298	954	QVQGHEDFLGARNTTLCSSFSCPGP GILGAEILETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPNLAGAGP ESKPWWVEAKQKP*SGLLLPLVVS VPRS*NCEPGVGERSGRGVHLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQKQSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPPSPHHPQTPPKQVPYL
4672	10169	A	4971	4	410	PIERPHELKHRLLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG
4673	10170	A	4972	148	268	LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL
4674	10171	A	4973	397	1449	RSHPSGTGRRTSRLESWFLGVSCCK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCPIPS*LS*QRSQG SPSSCLIGHLLALWAAFGLGVTSPL QYTGIRSSSPTA*ATVQGDSDGHKGG TGGTGLGRGRNTQPDAAACGRGHR SPTR/RPHGNPNGNTGCAEGGQARS LLPKLAPKLPGWPVSVPAVAV\PGD FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG\ GRGAEAPPSPTLAQRGSPPGVAIFP PACGIPP
4675	10172	A	4974	2	637	ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKRKRVRRL TLNFKTYFYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWIPTCERM KLAPYIIYKKIK\WIKDLNIRAITVKL IKENIGPGARL
4676	10173	A	4975	254	590	KARYILPDLMIGLDDFFFLGETKFP FAPQPGHQDGLG*LKLTPPRDFP/C LTPPRSGNYRLGPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA
4677	10174	A	4976	103	378	CFLYSICRGADTQRRFKLSDSLINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRNNAKQPVN*YHR CTETFSLTRMELLVSV
4678	10175	A	4977	2	327	RQCLALWPRLECSGVIIAHSLSLHL GSSDPPTSAS*VAGTTGMHHHAQLI/ LFWVLIDTG*CYVAQTGLEPLNSGH

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						PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF
4679	10176	A	4978	19	1009	KTTQQQQNLFFSSAHETFTNTDHL GHETSFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNNVTLS NTKIINFLDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVVLNLPNTKTYW*TLKF/EE MIPIVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISLVDAKIPSK NLSNYICSRLNNAHPQRSTDPNLQ NF
4680	10177	A	4979	3	358	STSNAYHSNSLHQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNITIPY* YFAFLP*KLRTQSRLLSFLNIVLK NPANVTVISINIKRK
4681	10178	A	4980	3	341	FFETESNSVAQAGVQWHDGLSLQP PSPGSSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFETESLSVAQA TGVQWVRSWAYCNLRLPGSGRFLC LCLPSSWGLQGVR
4682	10179	A	4981	658	1001	LILSARPPKGEKGSFLLAEFSSYFHS GLFSSARSFFFFFFFETESHCAQA GVQWDLGSLQPPPG\SSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS
4683	10180	A	4982	53	394	PQQSGFWFIYFSKQGCFFVNILNIC SFVLFFFETESCSVAQAGVQWHDL GSLQPPPG\SSDSPASASRVAGITG ACHQTWLIFVFLVDMGFRHVGQAS LKLLTSGFKKWVT
4684	10181	A	4983	66	516	HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVLLYFIFVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHSVTQAGVQSHNLSSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS
4685	10182	A	4984	3	324	HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAK'KMNQCQGYLWVFMALSA* ISKRKRLINYL SFYLSKLEK*EPTK PKASSRKVV
4686	10183	A	4985	108	277	ARVIRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLPKCWDYP*AT APGQHPYS
4687	10184	A	4986	29	454	
4688	10185	A	4987	116	424	
4689	10186	A	4988	1	1217	PPTTCTPACQGLSGAAMKSLVLLC LAQLWGWHSAPHGGLIYRQPNCD DPETEEAALVAIDYINQNLPGYK HTLNQIDEVKVWPQQPSGELFEI IDTLETTCHVLDPTVARCSVRQLKEH

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						AVEGDCDFQLKLKGKFSVVYAKC DASSQDSAEDVRKVCQDCPLLAPLN DTRVAHAEKAALAAFNAQNNGSIN FQLEEISRAQLVPLPPSVTYVEFTV SGTDCVAKIATEAAKCNLLAEKA IMAFVKATLK*ESLGGGRRLQLTCT VFQTQPCDLHSPNPEGANEAVPTP VVADPADAPSPPLGAPGLPPAGSP PELPCFYWAAPPQVHQLHRAHYD LRHTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCCCLGPVVP SIVPGRIRHFKVLG
4690	10187	A	4989	1	443	KKFVIPDFEFTGHVGRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSVGH TKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAI VVS SLIKMDCNKA EKDFVLQHLNKK
4691	10188	A	4990	3	217	ATKRKKMKDKDKA\KLEAMGTS KTNEEDKRRGLDKRTPDQA AFKEM QEK RDFSRLDTL TEHYDIPKVHH
4692	10189	A	4991	3	475	AASTESGMVAYYQVQKGPLKLG VAKLGVTK/RVRPEGPRDSVFIPKLP FLGTPGDPPTRRLLMFFSRKKKKK DKDKA\KLEAMGT\SKKN EEEKR RGL\DKRTPAQAAFEKMQEKRHME RILMKA\SKTHKQ RVEDFNRHLGTL \TEHYDIPKV\TWTK
4693	10190	A	4992	783	5158	PDKSGRRRDVEGGVCCFLSLRNSR YLLSTHILERGKKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLHLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPMTL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NITLWCRSPSRJSSKFLLLKDKTQMT WIRPSHKTFQVSFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWIAETPALPGCNVNILCH GWLQDLVFMLFKEGYAEPVDYQV PTGTMAIFSIDNLTPEDGVYICRTH IQILPVLWSEPSNPLKLVVAGLYPK PTLTAHPGPIMAPGESLNLRCQGPIY GMTFALMRVEDLEKSFYHKKTIKN EANFFFQSLKIQDTGHYLCFYDAS YRGSLLSDVLKIWVTDTFPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNVTYSDTGIYSCHYLLTW KTSIRMPSHNTVELMVVDKPPKPSL SAWPSTVFKLGKAITLQCRVSHPL EFSLEWEERETFQRFSVNGDFIISNV DGKGTGTYSYRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVVLWIRWKCRRL RIREAWLLGTAQGV TMLFIVTALLC CGLCNGVLIETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE

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						FVLLKDG TGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWL AGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPSEPLE LVIKEMYKPPFFKTWASPVVTPGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLIISVGIGDGG NYSCRYYDFSIWSEPSDPVELVTE FYPKPTLLAQPGPVVFPKSVILRC QGTFFQGMRFALLQEGAHVPLQFRS VSGNSADFLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLFAEPSSVVP MGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFFITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRP SGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHSDSLEIWVTDKPPKPSLS AWPSTMFKLGKDITLQCRGPLGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LJVVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQEGEPG TPANSPSSTSQRISVELPVP
4694	10191	A	4993	1	369	GTFQLPKPIFWIEAETPALPGCNVNI LC\HGWLQDLVFMLFKEGYAKPVD YQVPTG\TMAIFSIDNLTPE\DEGVYI CRTHIQMLPTLW\SEPSNPL\KL VVA GGCGLWLLASGNCCPRYHGWS
4695	10192	A	4994	183	429	ISIKSMKLISDYKYCIYIYRYHRDVI RLGIIDIYSVLHPTSAQYTFSSLHGT LTTRDNILGHKTLNKF KRIEIRQYL FSDQ
4696	10193	A	4995	2	270	TSGCLQGSCC\TGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPPCCSPSSAGCRCSL GCF RRCPLRSSRRSRF
4697	10194	A	4996	1	428	NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLPSVDLCPLLLAT HRISCWHCQDEVQGGTDSADTGD LEALSLLAGHGD TDGHIILDVPDGA PYPQRTKAGIDHLHQKILKIEQITIE HEARD DNAPDYPKLANN
4698	10195	A	4997	131	412	RKWLKLLPCSFSSKNIYAETFSPCV CIRVCIHVCVYTCVYTCVCIHVCSC PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTDQSHFI
4699	10196	A	4998	2	175	KFTWKHKGPRIARNILKRKIKVEGF TLPNFKTYKAAVTETVWYWHKD SGLDHFVLL
4700	10197	A	4999	2	175	KFTWNHKGPRRIARNNLEKENKVEG FTLPNFKSYKAAVTETVWYWHK DSGLDHFVLL

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4701	10198	A	5000	1	909	MVLEVSVSDRDAVWRLWRAPIGES QQRSLGFWSKVLPYSADNYFPFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SIIKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDGGKQRFVLT GVDTYSGYWFAYPAHNASAKTSIY GFTECLIHCHGIPHSIASDQGTLFTA KEVWQWAHAHGIHWSYHIPHPHPIA AGLIEWWNGLLKSQQLCQLGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQSRVEVEVAPLTITLSD PLAKFFFLLP
4702	10199	A	5001	1	1014	
4703	10200	A	5002	349	718	AGPEGTTTAECP//CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTLIS WKWQSASAKTTIHGLTKCLIHHDIP HSIASD*GTCFMAKEVWQWYCFSH SQDSRVQESRGGIGSCTTHHPCSF PN
4704	10201	A	5003	1	558	
4705	10202	A	5004	1	2205	MGAVFEALWQYSPPELPAKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTSGH CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGKISRTALK EPTVHKVTASLSPVATSPQPMLP SDFPPLSEEINPMLPEATVIASPKAIA RQDNVDSPQEPPTTPQFSSRPITRLK SQWAPRGPECVIGIDILSSWQNPFIG SLTGRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNSPIWVPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPK/KAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDAIWSLWNAAGESQRR PLGFWSKALLSSADNYSPPERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIKLLK WYIHDWVRAGPEGTTTTSVITQWAH EQSGHGGRDGGHAWAQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLISATSTSLEVT VPEGEMLPDRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSYSTYEGIDGWPDEAPTAT KPPVMPAPALPPDTRSGSKAPTVP PYPQMEHHQVQLASNNSNTEALGH LSPQSSWVQTPGQNSGPAIPNHLGK DMISPPQMAPAGVKWESQKY
4706	10203	A	5005	155	531	GNLWSVDLRPGTPLRQNFRTIRQQ HSRFTKNHCSQTPLLIPRQTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQYTFVLPR LTWLQPC*VPNLPAETNTEPSNGT
4707	10204	A	5006	1	518	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP

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						VHKAQQKQFAFSWQQQQYTFTVLP QWYINSPALCHNLIRDLDCFSLPL DITLVHYIDIMLIGSTIKWVVHSS/ DSIIKWKWYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G
4708	10205	A	5007	1	2592	MVRKAKWKPLQLPLPRKIVNQKH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYS PFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP HKVGHAAQHSIIKLKWIYCDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQEHLSFTKADLATGIVEPICQ QQRPTLSPRYGTIPQGGTFILTGIN YSIYGFAYPAHNASAKITIRGLTECL IHGHGIPHS/IVSD*GTHFTAKDVET RIHRPRNQGEVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLEGGT LPPGDPTTIPLNWKRLRPRGHFGLPL PLSQQAKKGVSVLAVTDLQDE FSLLLHNRVTAAPFSLHSSFAILD NMIEKANKCHVEGVHDVSDPAQRR ECDRHTGSSCHLLRGPPQLQSQLVS GPRSPKSDSGESCLAWPTFKAQEV PLAQGSPRNSVQEPSRGTGSPKSLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDASR KGVTERV
4709	10206	A	5008	1	942	MVGKAKWKPLELPLPRKIVNQKH HIPEGIAEIAATIKDLKDAGVVIPTT PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAAVDPDVVSFLIEINTSL GTWYAAIDLNAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDFALLQDITLVHYI DDIMLIGSNDHKVGAQQHSIIKWK LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQHGLPLTK ADLATTAECPVCQQQRPTLSPRYG TIPSLPLTKALTLQLKKCSSGPMLM EFTGLAMFPIHLKQLD
4710	10207	A	5009	1	1795	MRKCGKPQFKLGQTNKANSRIQEE LIHSKSLIEQEGEKPVQFSAFHRMW QPADSQCDIIDSADIWADPLVRHREI

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						ITGSGGINRRRTRGGRGRGGEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAAINHQRRQ GHSYCKGQKQNSNQNSVTHVEL WHWLNHSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLDGTGSELMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVGSNGTHPVVIYPVPECIIGILSS WQNPHIGSLTSRKTDGSRMTVHY HKLNQMVTPIAAAIPDVVSLLEQVN TSPGSWYAAIDLANAFFIPVHKAH QKQFAFSWQGGQYTFTVLPQGETL VNFSLPQDITLFHYIDDIMQIGSSDQ EVANTDLLPRKSTTPSG/LYGFWR QHIS/HLGILLTPY*VTQKAA/SFEW GLEQEKALQQVQATVQASLPLGVY DPADPMVIEM/SLSDPSSHKVGCAQ QHSIIKWKRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTDMG LPILHAMLLWIHLWIHGLPYPSWY STQQCL
4711	10208	A	5010	3	169	DFQPFTRVTVHWGKGNQDQTFRGLL DTGSELTLPIDPKHHYGPVKVG\ AYGAQLL
4712	10209	A	5011	1	562	
4713	10210	A	5012	3	591	DPADPMVLEVSEADRDA\VPISQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLMGHQVTMRPE LPIINCVLSDPCSHKVGHAQQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQPAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKWT VALQPLSGTSLQDSSEKSSQWTEI
4714	10211	A	5013	2	586	
4715	10212	A	5014	3	514	
4716	10213	A	5015	1	994	MVRKAKWKPLQLPLPRKIVNQKH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYS PFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP SRHKVGHAAQQHSIIKWKWYICDQARA VPEGTC*LNKEVAQMPM
4717	10214	A	5016	1	643	MVGKAKWKPLELPLPRKIVNQKH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAVVPDVVSLFLEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDFLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSIIKWK

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						LYIHDQAQTGPEGT
4718	10215	A	5017	3	1074	VTASLSPVVATSPQPMLPSDFPPLS EEINPMLPEATVIASPKFIARQDNVD SPQEPPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNP HIGSLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSRWMTV DYCKLNQVVTPIAAAAPDV/VSLLE QINTSPGTWFEWSPK\KALQQVQAA VQAALPFGPYDPADPMVLEVSAD RDAIWSLWNAAGESQRRPLGFWS KALLSSADNYSPPERQLLASWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWYIH DWVRAGPEGT
4719	10216	A	5018	1	1482	MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDTGSSA CRWPIVGLHSVILLDKVTKEKDEL RDSNSWLQKQILSLKFSKTALSES LI SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMITLFRGYWTEPTLIPED PKHHCSPPVKV RAYEDGSWKMTV DYHKLNQVMIPVTAAVPDVVSLLE KINTSPALFHNLVQRNLDCFSLPQDI TLVHYVDDIMLIGSSEQEVANTLDL LVRRLLCAKGWEINLTKIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRRNGGYTW AQQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIP\RGDQPATWWQ VDYVGPLPSWKGGQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHISIADQGSHTAKEVQQW AHAHGIHWSYHVPYYPEATGLIEW
4720	10217	A	5019	1	1494	
4721	10218	A	5020	101	304	
4722	10219	A	5021	1	1912	MTVDYCKLNQVVIPIAAA VSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQQKQFAFSWQQGQYTFTVLP QWYINSPALCHNLIRRLDCFSPLPL DITLVHYIDDIMLIGPRQLLACY/W ALVETEHLTISHQVTRPELPIMNW VLFDPSSHKVGC AQQHSIIKWKWY VHDWARAGPEGTTTPVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLTGIDTYSYGFAYPACNAS AKTAICGLTECLIHHDIPHISIADQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQLQC QLGDNTWQGWGKVLQKVYYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFPATLQSAGLE VLVPEEGTLP PGDTMIPLNWKLRLP PRHFGLLLPLNQAKKGVTVLAGV

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						TLDYKDEITLLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLOQL KPEALVPKGVVFPPGDTTMLSLSW KLRLPSGHVGLLMPLSQVQKGV VLAGVIDPGHTSAASLVLRSCVWS GSDTIVSPGSQDFRLGINDTTGFPV PD
4723	10220	A	5022	3	835	DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLPGYPKRHCCPPVKVR VYGGQTDGSRMTVGYHKLNVV TPIAAAVPDVVSLLLEQINTPPSTWY GQVAAFAPPTTKKEAQLVGLFDF GGNTLLIWVYSGPLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKLGRMRMDLSE LGKNREEYWYPVQQAQKGVKVL VVIDQTIKMKSVYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK
4724	10221	A	5023	2	1300	DLWPFTRVTLHRGKRNDQTFQGL DTGSELMIPEDTKHHCGPPVKVEA YGGQVINGVLAQIQLTVGPVSGT HPVVIYPVECIIGILSSWQNP SLTSRKTGSRMTVHYHKLNV VTPIAAIPDVVSLLLEQVNTSPGSW YAAIDLANAFFIPVHKAHQKQFAF SWQGQYTFVLHQGYNSPALYH NLIWRDLDRFSLPDITLIHYIDDMT LIGSEQDVANTLDLL/SDLSRGGF* *SSG*DDPFCGHHSASFSPHPCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGH*VPNLPAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERAVERP/TWSTCLLWIWVCLSCT QCFCQDYHLWTHGMPYPLSRYS AQHCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI
4725	10222	A	5024	2	790	PRGRNRRRKTFQERRMTLNESPEKI GKWIECYGHPPASKLVEIYHTV FVEDKLSICIRSFNKKADGSRMTVD YCKLNQVVTAAIAAIPDVVSLL EQINTSPDTWYAAIDLANALFSIPV HKGYNLSALCHNVIWRELDL CFSLPRDTLVHYIDIMLIGSSVQ EVENKLDL LVKDKLLHLAPPTTKEE VQHMVGLFGFWRQHPLGLVHLHQ PIRVIRKA A/SFEWGPEQEKALQ QVQA AVGGKQSENNLGHQRSPGLWFS
4726	10223	A	5025	281	1461	VRVLSPEKELKLWKNTHKLLSYP TVGA AVTQLQNLAMGVIGSHGAR GQVVALNRQRQGDLPFTRVTVH WGKG/NMQIFGGLDGTGSELTLP GDPKHHCPPVKVGAYGGQVINGVL AQVQITVGPQTHPVVISPVPECIIGID ILSSWQNPFIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFFTSLFNSPIWPV QKTDGSRMTVGYRRLNQVVTPIA

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						AAVPDVVSLLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAF TVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSDLAIKWVM HSSIASSSGSGICVIRLKKVLAQA
4727	10224	A	5026	1	3179	MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREYGG NYAHSIIISHQVPPTTCGNYGSTIQD EIWVGDSHGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVGQSARMISKPA DSQDVHEL VLSKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVTGII ATIKGSNEEDTDTPLFIGKVRTLEFP FVNGSAEIMLMPSNQKHKTDEKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPIIKLMILPDPEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWIIESVLNSWRKGCNKLNRQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLPDGPKHHCAPPVKVGA YGGQVINGVLAHPLIWL VQKTDGS /WRMTVDYCKLNQVVIPIAAVSD VVSLEQINTSPGTWYAAIDLANAF FSIPVHKAQQKQFAFSWQGGQYTF TVLPQWYINSPALCHNLIRRDLCF SLPLDITLVHYIDDIMLIGSSEQEVA NTLDLFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQL\QLLACY/ WALVETEHLTISHQVTMRPELPIMN WVLFDPSSHKVGCAQQHSIWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLVL PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSESASNI WYCFSHSQDSQVQESRARS GTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAA TRRHNDSEIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMERYRSI RASLNITMPYD*GQWETTAAQARSS
4728	10225	A	5027	2	1284	CHCGPP/VKVEAYGSQVLKGVLQA VQLTVGPVGPRTHPVVFVPECHGI DMLSSRQNPHTGSLTGRVWTIMVR KAKWKPLELPLPRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSRMTVGYCKLNQ VVTPIAAAVPDVVSLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTF TVLPQGRWEINMT

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						KIQGPSTSVKFLGVQWCGACQDIPS KVKDKLLHLVPPTIKKEAQCLVGLF GFWRQHPIHLGMPLQPIYRVQTMA ASFEWGS\EQEKALQQAG\QAAVQA ALPLGP/HKDPADPLVLEVS\SDRD AVWRLWQASI/GHKVGHAAQQHSIIK WKWYIRDWARADPEGTTKGQQR RWWQLAERQDSRDREA AIGERQET AVGKTARDGEAVCD
4729	10226	A	5028	422	1252	TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMAIHQFYLD RKQSKSKIHAARSLSEIANDLTRTRT LENSKLANMGSKGKIISGSSGSLSS GSGARRHCILLPGSQESDSSQSACK DMLAALKSRQE\ALETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGP\AFKLDEQKILPKGEEA ELERLEREFAIQSQITEADRRLASDP NVSKKLKKQRKTKYINAVKKLQVY
4730	10227	A	5029	1	400	RHEERTTGILTSEGLASDTSLICVIED FFDTALISRSSESGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKSRDELV HKWFDDEVIAEAFKEIKDREFETDS RRFLN
4731	10228	A	5030	1	612	
4732	10229	A	5031	64	323	LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEKL\STSPD EPVPRSHHVVSLLKSTCLYFTSG\T TGMIQFFWKA
4733	10230	A	5032	287	508	YYSIFLIYYYYYFLR\WSFALVAQAV VQWCDLGSLLQPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL
4734	10231	A	5033	1	3627	
4735	10232	A	5034	3	3613	
4736	10233	A	5035	353	406	MLHLQGIILMIVLYSCCRELIHSFLK DSKSMPCNWGESDGPVTGARHPSW EEEEEDGGVWNTTGSQGSASHNSA SWGQGGKKQMK/CSLKKE
4737	10234	A	5036	1	514	ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKAFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEEPFTCTVCRKSFRNSSC LNKHNHIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK
4738	10235	A	5037	1	3222	
4739	10236	A	5038	1	4267	MGPWAWKLRWTVALLLAAAGTA VGDR CERNEFQCQDGK CISYKWVC DGS AECQDGSDESQETCLSVTCKSG DFSCGGRVNR CIPQFWRC DGQVDC DNGSDEQGCPPKTC SQDEF RCHDG KCISRQFVCDS DRDCLDGSDEASCP VLTCPASFCQNSSTCIPQLWACDN DPDCEDGSDEWPQR CRGLYVFQGD SSPCSAFEFHCLSGECIHSSWRCDG

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						GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGCSHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKQCCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDREYTSILIPNLRNVVALDTEVA SNRIYWSDLSQRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTDVLGTVSVADTKGVKRKTLF RENGSKPRAIVVDPVHGFMYWTD WGTPAKIKKGGNGVDIYSLVTENI QWPNGITLDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDEKRLAHPFSL AVFEDKVFWTDIINEAIFSANRLTGS DVNLLAENLLSPEDMVL FHNLTQP RGVNWCERTTSLNNGGCQYLCLPAP QINPHSPKFTCACPDGMLLARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFFQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVAFVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMGGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSAAGFLKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLPVLAEN YNKSDNCEDTPEAGYFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKL\CMGSGNLCE PMNKRGDTTGYTGAFRCLVEKGD V AFC*KHQTVP TGT LGGEKNPD PW A\KDLNEKDY\ELLCLGWVPGKPV E EYAN\CHLARAPNHR CGSHGKDK EACVHK\ILRSTASHLFG\SNVTD\CS GNFWLVRS\ETKDLL\FRDDTVCLW AKLHDRNTYEKYLGE EYVKA VGN LRK CSTSSLLEACTFRRP
4740	10237	A	5039	2	342	LSRVVL SAAATAAPSLRNAA/FLGP GVLQATRTFHTGQPHLVPVPPLPEY GGK VRYGLIPEEFFQFLYPKTGV TG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF
4741	10238	A	5040	53	940	DCYLDVSLTMLS RVVLSAAATAPT IIMKNAAFLGPGVLQATRTFHTGQP HLC PMY\PIPEY G\GK VRYG\LIPE\

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						FFQFLY/PLKTGVNTDPNVPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQNAIDYGRSLYQALVQKRH YLFADVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDAVRN GTTNSLLNW\VEKHVRAKLFPPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW
4742	10239	A	5041	2	205	APVTSW/IQPKDGSCPFSESTKTISLY ISSEQQFHLPRPSEDDFIEDTADML\ VSFSGYSSAPKNQEQ
4743	10240	A	5042	1	360	SPCLSERQFCCEKLPQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGGRDSVDKGD LEALSPLAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHHKILKSTE
4744	10241	A	5043	106	396	
4745	10242	A	5044	77	4026	
4746	10243	A	5045	1	344	LDFIQTMLQVVGVVSVAVPV/IPWI AIPLVPLGIIFILRRYFLETSRDVVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLLFLA
4747	10244	A	5047	3	378	ERDGA TLPLTPGLSPPPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHCFYKGYVNTNSEHTAVISLCSG MLGTFRSHDGDYFIEPLQSMDEQE
4748	10245	A	5049	2	278	FVNHGCSQ/TLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS
4749	10246	A	5050	1	1539	MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFPCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQRLAQGPKPGPPAATV ARQTSRVSPAPPCSLRPGLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQQHEEFEEG\CK AA\CN\GPIYDG\KWSKT\VG/YLGP EDDHFAELTYNYG\VG DYKLGND FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVFET\EAPGGYKFY\LNRS PQSDPVLK\VTLA\VDLQK\SLNYWC NLLGMKIYEKDEEKQRA\LLGYAGL TSV\LELQGV\KGGVDHAA\AFGR\I AFSCPQKE\LPDL\EDLMKRENQKIL TPLVSLDTPGKATVQV\VLADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWF\AKHNKPKASG
4750	10247	A	5051	21	223	HPGSRGCSEPRSGHCTPAWGTVKVK T/SRLNKNKTKQKKEVKDCMSSTPL

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						AHPPGVWCEWRGLIPSSSP
4751	10248	B	5052	64	543	RGWKRDRDKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMYYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFPLISLIAGFQRVQALTT NLNLILPPLKDSTE*
4752	10249	A	5053	1	567	AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPG\HKARGPGGPF GGEPPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRPPLLPKGN PWTKKPPQHLSPDTTGPPPPPLETLE AEFGSLKIIKAGKLKTKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ
4753	10250	A	5054	3	763	SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GNSRGSFRGRGRGRGRGRGRGRG NPRLNFDYSSC
4754	10251	A	5055	1	372	RHEQGIFLETSTFMTDQLVDALT TWQNKTKVGLLWSA\AHIRFKPTLS QQKSPEQHETVLDGNLIIRYDVDR AISGGSIQTREALIKILDDLIPRDQFN LIVFSTEATQWRPSLVPASAEN
4755	10252	A	5056	1	1021	AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELYEE LLKRRLGVYELLLKVRPQQLVKHL QMDIHIFEPQGISFLETSTFMTNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQQETVLDGNLIIRYDVDR AISGGSIQENGYFVHYFAPEGLTMPK NVVFVIDKSGSMSGRKIQQTREALI KILDDLSPRDQFNLIVFSTEATQWR PSLVPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSVSLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSFLCLGFGFDVS YAFLEKLALDNGGLGRG
4756	10253	A	5057	570	831	HGNYRNVICLLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAGK AADTTIILSDEYFMEVVLGKLDQPK AFFSGRLKAEG
4757	10254	A	5058	1	2229	MGSPLRFDGRVVLVTGAGAGLGRA YALAFARGALVVVNDLGGDFKG VGKGSAAADKVVEEIRRRGGKAVA NYDSVEEGEKVVKTALDAFGRIDV VVNNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAAK LGLLGLANSLAIEGRKSNIHCNTIAP

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						NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESCEENGGLFEVGAG WIGKLRWERTLGAIVRQKNHPMT EAVKANWKKICDFENASKPQSIQES TGSIIIEVLISKIDSEGGV SANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGV GASIKDPKDLKFIYEGS SDFSCLP TFGVIIGQKSMGGGLAEI PGLSINFAKVLHGEQYLELYKPLPR AGKLKCEAVVADVL DKGSGVVIIM DVYSYSEKELICHNQFSLFLVSGG FGGKRTSDKVKVAVAIPNRPPDAV LTDTTSLNQAALYRLSGDWNPLHID PNFASLAGFDKPIHLGLCTFGFSARR VLQQFADNDVSRFKAIFAKPV YPGQTLQTEMWKEGNRIHFQTK\V QETGDIVISNAYVDLAPTSQTQAKT PSEGGK\QITFVFEEIGPRLKDIGP VVVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGPAKGAADT TIH/ILSDEDF/LWEVVLGQA*PSRKA FFSGRLEGQEGNIMLS\QKLQMIL\K DYAKL
4758	10255	A	5059	1	7449	
4759	10256	A	5060	1	7458	MTDSKPITKSKSEANLIPSQEFPFAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQR\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTQGL EATDTNGLSSSARPQGGQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFGIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCP LRPQQA AAVQRPSMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNIA AVKCMRSIRRWAYEMFRNERAIRF VVMVTPEDLKANA EYIKMADHYV PVPGGPNNNNYANVELIVDIKRIP VQAVWAGWGHASENPKLPELLCK NGVAFLGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSLTVEWTE DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHLELNPRLOVEH PCTEMIADVNLPAALQGFKPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCFSWGENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNIDITGWLDYLIAEKVQA EKPDIMLGVVCGALNVADAMFRTC MTDFLHSLERGQVLPADSLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLLSYNG

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						NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLTQYTVEDG GHVEAGSSYAEMEVMKMIMTLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQQT PILGEKLHQVFHSLNLTNVMSGF CLPEPVFSIKLKEWVQKLMMLTRH PSLPLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQA TILDCHAATLQRKADREVFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLDICFISH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSEHCKVALRAR QILIASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVLP TFFYHANKVVCMALEVVYVRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVSQ CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQEFAEDRIYRHLE PALAFQLELNRMRNFDLTAVPCAN HKMHLYLGAALKVKEGVEVTDHFR FIRAIIRHSDLITKEASFEYLQNEGER LLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRLQAQEVKINIRQTTTG SAVPIRLFITNESGYLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGM LIN TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPAQAQTRVHVHNVQA LFLKLGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPGEDLLYLRASEMARAEGIPKIY VAANS GARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRISSLN SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGMIAGESSLAYEEIV TISLVT CRAIGIGAYLVR LGQRVIQV ENSHILTGASALNKVVEPCTVQDIA NHVVSQVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLG GIPVGVI AVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMYDQVLKFGAYIV DGLRQYKQPILYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVEIKFRKKDLIKSMRRIDPAY

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						KKLMEQLGEPDLSKDRKDLEGRL KAREDLLLPYHQVAVQFADFHTP GRMLEKGVISDILEWKTARTFLYW RLRRLLLEDQVKQEILQASGELSHV HIQSMRLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST
4760	10257	A	5061	6	906	EQPALLPRYRSGIRGYMKTVVLDLL RRYL RVE\TIFSKARDADANTSGMV GGVRSLSFTSVWVLSPPAHYDKCV INLREQFKPDMSQVLD CIFSQAQVA KKNQVLIMLIDELCGDPDPSLDELISI LNELTQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMA SLEVYVRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLRRHSTELFMD GFSPLCQRMGAMVAFRRFEDFT
4761	10258	A	5062	2	560	APRLDVSFSQIIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDI WALGCMIIEMATGNPYLP SSSDLDLLHKIVLKVGNLSPHLQNI SKSPIFAGVVL PQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISSS DLLHHEYFTRDGF I*KFMPELKA*L LQEAKSQF
4762	10259	A	5063	1	573	
4763	10260	A	5064	2	791	NLVN LIEVFRQKKKIHLVFEFIDHTV LDELQHYCHGLESKRRLKYLFOILR AIDYLHSNNTVVDI WALGCMIIEMA TGNPYLPSSSDLDLLHKIVLKVGNL SPHLQNI FSKSPIFAGVVL PQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVKGGRGDISEPKKKE YEGGLGQDANENVHPTSPDTKL V TIEPPNPINPSTNCNGLKENPHCGGS VTMP PINLTNSNLMAANLSSNLFSP QCEVSCNREEP
4764	10261	A	5065	3	524	TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHVVIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLQ/NNLHRRTMME RLHLFPDEYIPEDILKNLVEELPQPR KIPKRLDEYTQEEIDAFRLWTPPED YRL
4765	10262	A	5066	1	250	YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLPKNLHRRTMMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL
4766	10263	A	5067	129	796	MGKCSHLANFAAIASIRLQGLHKPV \YHAPE*L/CGDHVVIMNTRHICIF/H GNKWGTSILFRILAYPGWSLDKVT SLAFAFTLRRSQW/CNL*NLAIYGIP AKKTFTRRTIDWKGHLHLPDELYS

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						RKIFLKKFS*EELPSTTEKYLNLVDE YTTRRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLLSFSNLQDGVKQ LLQFEHLFLCAESLWGKVRKV
4767	10264	A	5068	15	350	GPGSAITVGPQPL/RAQRNHRLPVPS PGLSIVMGLRPVPSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ
4768	10265	A	5069	1	2175	
4769	10266	A	5070	3	86	KNYRGTMS/KTKNGITCQKWSSTSP RRPR
4770	10267	A	5071	2	583	LLLLFLKSGHGEPLDYVYAQGA SLFSVTNKHLAGAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLFEK*MYLSECQTG NGKNYRGTMSKTKNGITCSKMGVP LPHRPRFSPATHPSEGLARNPDNDA QGPWCYTDDPEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL
4771	10268	A	5072	844	4515	TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLPLCPSFPLCPEECM HCSGENYDGKISKTMGLECQAWD SQSPHAHGYIPSKFPNKNLKNYCR NPDRELRPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVA VTVSGHTCQHWSAQTPHTHN RTPENFPCKNLDENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDPNKRWELCDIP SGTEASVVAPPVLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPRAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIECAAKCEEVEEFTC RAFQYHSKEQQCVIMAENRKSSIII RMRDVVLFEKKVYLSECKTGNGK NYRGTMSKTKNGITCQKWSSTSPH RPRFSPATHPSEGLEENYCRNPDND PQGPWCYTDDPEKRYDYCDILAE *RRECMFAFVGGKLLTGKIFPRTMS WDWECQAWGLFRSPHGHGYIPSK FPNKNLKNYCRNPDRELRPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRGNVA VTVSGHTCQ HWSAQTPHTHNRTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNPADKGPWCFTTDP SVRWEYCNLKKCSGTEASVVAPP VLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS

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						IFTPETNPRAGLEKNYCRNPDGDVG GPWCYTTNPRKLYDYCDVPQCAAP SFDCGKPQVEPKKCPGRVVGCV HPHWPWQVSLRTRFGMHFCGGTL ISPEWVLTAHCKLEKSPRPSYKVL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALLLSSPAVITDKVIPACLP PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVIENTVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDG GPLVCFEKDKYLQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N
4772	10269	A	5073	9	141	FYRLSLGFKCDWFTMEKRV\KLEER YRDMAEENLKKDISISLKL
4773	10270	A	5074	3	360	QTKPKESRKRIIMFRTIEFNETENRI ESSSSSSSS\SSSSSSSYKCLARLT/ RKK/EKIQIIVRSERKEIITNYRIKRIT KGYIELLYANQLYHLMKCPKFLER HKLLKLQEETKSGV
4774	10271	A	5076	1	245	AAAYYYYTAARRRQKGERRKKRK EER\KEEKKKKRKKKEKKKRRRRG GRRTKKEEKKKEKKRRTKKEKKK KKKKKKKVSM
4775	10272	A	5077	68	246	SMAFLTIEDTALKFIQNHKRPQIA\ KPILSKNRAESITLFSKIHMYPTVI KPLRVST
4776	10273	A	5078	3	364	TSIVAAQMFNVITVMQVRISPQHMT SMWPIMVCELSQTFTQLEEDVKDK VESLRSTNKVNRTKVSVDANGPS VGYIPQSEL\IMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE
4777	10274	A	5079	2	1315	GKDAKILCSNPNTGEVLYELPTNTQ RCFDIQWCPRNPAVLSAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSSFG NLDPFGTGQPLPLQIPQQAQHSIV LPLKKPPKWIRRPVGASFSGGKLV TFENVRMPHQGAEEQQQQHHVFI SQVVTEKEFLSRDQLQQAQVSQGF INYRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTA KPVFIPTDTSSRWALPWRTATSW NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL
4778	10275	A	5080	18	3600	
4779	10276	A	5081	238	480	SIQFYFFSFQDSKGKHSLSVSVIGPQN GWNDPPALNRVPKCKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA\ PVPLS
4780	10277	A	5082	352	4060	DYSRRYILRMKLKEVDRTAMQAW SPAQNHPIYLATGTSAQQLDATFST

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						NASLEIFELDLSDPSLDMKSCATFSS SHRYHKLWGPYKMDSKGDVSGVL IAGGENNIILYDPSKIIAGDKEVVI AQNDKHTGVPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVATQMVLA SEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIAWSMADPELLSCGKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPVLSAASF DGRISVYSIMG GSTDGLRQKQVDKLSSSFGNLD PFG TGQPLPPLQIPQQT AQHSIVLPLKKP PKWIRRPVGASF SFGGKLVT FENVR MPSHQAEQQQQQHVFISQVVTE KEFLSRSDQLQQA VQSQGFINYCQK KIDASQTEFEKNVWSFLKVN FEDDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDS DQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNR MADAIILAAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESCDLKNWREALAAVLT AKPDEFSALCDLLGTRLENEGDSLL QTQACLCYICAGNVEKLVACWTKA QDGSHP LSLQDLIEKV VILRKAVQL TQAMDTSTVG VLLAAKMSQYANL LAAQGSIAAALAF LDPDNTNQPNIMQ LRDRLCRAQGEPVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQYPFGTGG SAMYRPQPQVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSA YALPPGTTGTL AASELPASQRTGPQNGWNDPPALD KVPKKKKMPENF MPPVPITSPIMN RLGDPQS QMLQQQP SAPVPLSSQSS FPQPHLP GG\QFPWGYSKPFGFKQ GMATIFFQSPNIEGAPGAPIGNTFQ HVQS\LP TKKITKKPIPD\ EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DRTFSTITSGLHNI ARSIETRNYSEGLTMHTHIVSTSNFS ETSAFMPVLKV VLTQANKLGV
4781	10278	A	5084	121	419	DLCFTTPKAGRRQEITKIRAE LNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKD\QINTVRNDKGDITTYPT EIQKTLRDYYEHL YACRVENLQ
4782	10279	A	5085	1	279	TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHLCSR\DLRLSHKTS LNKFKKIVIIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4783	10280	A	5086	1	279	TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHLCSR\DLRLSHKTS

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						LNKFKKIVIIPIGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4784	10281	A	5087	1	1915	MAILPLLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCPGAGLL FVPPSLDRRAAELRLADNFIASVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRLHLSNQLAALAA GALDDCAETLEDLDLSYNNLEQLP WEALGRLG\NVNTLGLDHNLLASV PAGAFSP\HLKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLAF GGNPLHCNCELVWLRRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPPLAVPAGRPAALRCRA VGDPPEPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFTCIAA NAAGEATAA VELTVGPPPPQLANS TSCDPP/PGRGLPDALTPPSAASASA KVADTGPPTDRGVQV\TEHGATAA LVQWPDQRPIGIRMYQIQY\NSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLA VYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTAPPAPPAALRAHTVVQLD CRALGARPRTCGTLARRPPL
4785	10282	A	5088	1387	1567	GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPPGSSDSPASVSQ AAETTGTCHH
4786	10283	A	5089	96	408	SPRKTRHSTNPPLECHVGWVMD SRDHGPGTSSVSTSNASPSGAPLA GRYGCTPH\SF PKFQNPSELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT
4787	10284	A	5090	390	665	PLNIHYCFLGGKYL VFGFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT PGTF\IPYCSMAHAQLCFHGHRDAV KFFVAVPGQVIS PQSSSS
4788	10285	A	5091	185	386	WEASKKKPRGAQISNAITTYKYLPK VG\KNYQTEALYKPIQTGKIGHPV FFQKPPLLDGQNYDTPP
4789	10286	A	5093	3	330	GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPVGNMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG
4790	10287	A	5094	2	349	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGENPPNSFYGAIIIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSF GREIHHQDREF IPGIQGGFNIGN
4791	10288	A	5095	2	353	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS

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4792	10289	A	5096	1	262	RGRAGGEPLPATTGAAPPPGRRLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGEE GTGREEWNEKAEFTL
4793	10290	A	5097	116	177	LGEHGVYSGVGTGGRLLSS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV
4794	10291	C	5098	231	347	MGLGPHLKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI*
4795	10292	A	5099	518	931	ATRHSMLSCHYTYIYIKHTHTHVFI YIYTYTYIHTHIYTYTYICHTHIHIYI YIYIHTHFFFFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHA/DSPASTS QAAGTTGAHHHAQ/LIFFFFVFLVET GPHRASQDS
4796	10293	A	5100	2	1109	DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDRLLRGHNQYAY DGKDIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTELVETRPAGD RTFQKWAAVVPSGEEQRYTCHVQ HEGLPKPLTLRWEPSSQSTVPIVGIV AGLAVLVVTVAVVAVVAVMCR KSSGGKGGSYSQAASSDSAQGS SLTA*KA
4797	10294	A	5101	3	1145	SDSPQTPMRVMAPRTLILLLSGAL ALTETWACSHSMRYFYTAVSRPGR GEPRFIAGVGYVDDTQFVRFDSDAAS PRGEPRAPWVEQEGPEYWDRETQ KYKRQAQTDRLSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDRLLRG YDQSAIDGKDIALNEHLRSCTAA DTAAQITQRKWEAARAAEQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTELVET RPAGDGTQFQKWAAVVPSGEEQRY TCHVQHEGLPEPLTLRWEPSSQPTIP IVGIVSGPAVLAVLAVLAVLAVLGA VVAAVIHRKSSGGKGGSCSQAAS SNSAQGSDESLIACKA
4798	10295	A	5102	3	242	GFWAPRVCKDIDKWLSEPEALWF GEGGSPGGCRWGGWLCQGNRA AGGVGAEGACGLLSATGLLWMT GLQEPREPQV
4799	10296	A	5103	1	138	FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL
4800	10297	A	5104	59	337	IPYPALPFTSVEAPNSHVKA VMKTS VLLSWEIPENYNSAMPFKILYDDGK MVEEVDGRATQKLIVILNPEKSYSE ELTYRGNCAGGLELMVT
4801	10298	A	5105	54	226	TKAETENLRPVT/EIKSVI/NSLPTK

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						KSPGLDGFIAKFFQTYKREIPTLLKLLQKLKW
4802	10299	A	5106	2	265	ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLKSFCTVKE TIKMKRQSVWEKILVSHVSDKWFI SKIQGIYITQYQ
4803	10300	A	5107	1	296	GREKEEGESGEDWGRV\GREKEGG EGREEEGEGGREEEGEGGRKEEGE GGREEEGEGGREEEGEGGREEEGE/ GREEEGEGGRQEEGEGGRRREGRG GRS
4804	10301	A	5108	1	253	
4805	10302	A	5109	190	472	
4806	10303	A	5110	1	314	HNVPVPHVFMQLQKEITKKNSTFRVHI KAVFYN/HDIYCMPPLLNYRKTDFV IVIDPPWQSKSVKRSNRYSLSPLOI KQIPKLAAPNCLLVTLTNTQKH LRFIK
4807	10304	A	5111	3	362	FFFFFETESLSPVQAGVQ*HDLSSLQ PP/PPGFTPFSCSLSPSSWDYRCP PPA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARP PPQFFIQLPLYNIHTLEGR
4808	10305	A	5112	3	385	FFFETESRSVAQAGGQWHDLSLQ APTPGFTPFSCSLSPSSWDYRCP PPCANFFVFLVETGFHHVSRDGLDLT SDPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSLFSHKQRSFG F
4809	10306	A	5113	1	390	SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQMSGRDGNITGIQ QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTTITIESEG GSTFAKASFVAGNRTDISLDDPNF WQKWA
4810	10307	A	5114	2	214	GRVDIERAILVQTGQQALEPAVRL RRAPYPCHTSDLFLNNVGFFFLIM MLTWMVSVASMRPLVSQQE
4811	10308	A	5115	30	379	KRSVNSPGRALSELGVSTELGFLRC VSVVCSLSQEYFLFTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLLPVFSF MEGFYWAWCLVFFCL
4812	10309	A	5116	1	304	GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMRKGHVQQ ARALLQTASALSPHMYETDFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH
4813	10310	A	5117	119	264	
4814	10311	A	5118	720	2798	VYWPHSFLGCPSNYPLYLGAETRQ GGRARPPFLPLSFPPRFRPNP SFQN VLETQRISYSFLLADTSNTRATSGH AQQPAPILPLREVAGAEDIIRVHV PFLSLSDLQIAKRLGSFSSDPDTYI KEFKYLTQSYELTWHDLIILSSTLL PEKKERVWLAQAHANDLHRQDPTKPI GAAAVPLEPPWKYQPTDPGRASR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLTFK VFNNREEQIKLDKAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTVLGVQLSPGAQAMTP AQATLINSPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALS PDLSQPFVLYTTKNQGIALGVLGQQ KGNPPSFDPVAYLCKQLDNTVKGQ PTCLKASSAVAVLPLESKKLTFGQS TTIHSPHNLQDLLSSWALSSLSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISSSPPTHSCDILDHLQPFNPIS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPETSSQKA ELALTRALTSKDKQHWLISEPVQ RPPSSVHST
4815	10312	A	5119	2	697	HGRLLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVVVDVLRQASKACV VKREFKKAELIKHAVYLARDHFG SKHPKYSDDLDFYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLVASSKRV KALILEEIAIDCHNKETEQRLLQEAH LDVHLSSLHLASKSYGDLAVVVLVH MSLLKSY
4816	10313	A	5120	3	277	EEEEAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE
4817	10314	A	5121	1	337	GTSSCVREVQAMGKKVVLVKVH LKDKFVIDVDKNISISDVTSSLVVL RNDSTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMTILFSD KLSFTAPQLYIFTG
4818	10315	A	5122	2	302	ARGLPFFTRNDFSVWTIA/RNKC VGLSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQLERMVGLKG ARQEFVMKVMPLACLATQSWGPR HL
4819	10316	A	5123	3	346	HENWKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCARNACTSIS WELRQTLSSVFDLITGQGGKDW S/LR/MFSRSLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP
4820	10317	A	5124	213	425	QNSQGKLFSSGCLPFCGSNTKGILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH
4821	10318	A	5125	1	356	GTSTRIIFYRDGVSEGQRQQGLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLCSDKNHPLGKRGNSPTG SNCGKITHPTFEFDYLRHAGIQG TSRPSYYHVLWDNRFFS
4822	10319	A	5126	1	238	HMHSHHMHSTPHA/HHTHHMHS

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						HHMHSHTTHMHSHHMHSHAPHAL TPHACTHTTHMHSHHMHSHHMA LTPHACTHTPH
4823	10320	A	5127	180	405	IWGEQDTFHSMAKWIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG
4824	10321	A	5128	61	85	PS*NYPP*KGITFGPLNKK
4825	10322	A	5129	3	2004	RRRRRPASPPAGLALAPRSPSASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLLHPPEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPDK ENVTLHWAANNRIDLVKYYISKG AIVDQLGGDLNSTPLHWATRQGH SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDVDM MDQNGMTPLMWAAAYRTHSVDPTR LLTTFNVSVNLGDKYHKNTALHWA VLAGNTTVISLLEAGANVDAQNI KGESAPDLAKQRKIVWINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFWNDLNLFIHLPLANSVALFYN FGKSWKSDPGIHKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRSKH CGVCNRCIAKFDHHCWPVWNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIDF FEFRCCGLFRPVIVDWTRQYTIEYD QISGSGYQLV
4826	10323	A	5130	3	144	HEKYHKNTALHWAVLAGNTTVIS LLEAGANVDAQNIKAILRCHMAL
4827	10324	A	5131	148	325	RQGKECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLPAYYKLNLDLTNAD PCAVRYLLFDQN
4828	10325	A	5132	175	405	NILNSQFSTFLNDYVEFFVVFKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGR*SSNLSLPSSWDYRRVP
4829	10326	A	5133	14	26	YSPHEVGWKGRNREKMFCSEINVV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHSCLYTSK GVE*FTGIIFSS
4830	10327	A	5134	177	454	PLLERAKIGRPEKPMETRQGWGPF SPKVPGQKKFWG*LAPISPGMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNGGPYLQ
4831	10328	A	5135	3	92	NAWRTATEEWWTEDWNEDCSEP* HFTYVI
4832	10329	A	5136	1	442	PLIMNSIKSFSDDHAQCGRÆFDRQED DIHLVTLCVTELNDREENENHFPVI YGIAVNIKTAEIYRASFQDRGPPEQL

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						RAARTLAGGPMISIIYDAETEQLRI\G PYSWTPFFHVDFWLHQDDKQIFEN LSTSPLAEPHFVEHIRSYLD
4833	10330	A	5137	177	566	EPFWSLSYLSLRRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAIEY RASFDQDRGPEEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPFFHVDF WLHQNDKQILKGRVYRLGKS*ISAP WPHL
4834	10331	A	5138	1	981	PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQQVGPQGLLYVQ QRELA V TSPKDGSIILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSHAQCGRLEVHL VGGFSD\DRQLSQST\HHFLIEFDR QEDDIHLVTLCVTELNDREENENH FPVIYGI\AVILLSLTA VNIKTAEIYR\ ASFQSGVREEQA/LRAARKL*AGG PMISIIYDAETETTS**DPYFLGHPPF HVGFWL\HQD\DKQILDES FHRPL AE\PHF\VEHIRSTLMVF*KNTPSPA \NTLFPGNKALLYKKNEDGLWEKIS SPGS
4835	10332	A	5139	1	405	AYVTVCNQCGRESKLLSKFYEEL NIQGHKQLTDCISEFLKEEKL*GDN RYFCENCQSKQNA TRKIRLLSLPCT LNLQLMRFVDRQTGHTKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT
4836	10333	A	5142	2	204	ETGFCHVVQAGLKLGGSDLPASAP QSAGITGMCHCAQPTKVS VASKVF KGSHKD*ILT*GYANKGA
4837	10334	A	5143	1	360	QQLTVLVAHLGVTLMDQRGYHWL LKSLMTQYQGLLYENP*ITL EIVNTL NPGTLLPNESVPGSALHCRVDVVHE MLSIQRDLTDHTLRDSIEYFIDRS FILGGDPLSGVCSSDFGLST
4838	10335	A	5144	36	380	FVALMGHKMSHNKFKIEIIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSLAKLENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK
4839	10336	A	5145	1	362	ELNLPAPELPRKRTENLFLQLAEYV AHS LNVT*YVCEGTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGDFTIPVGR N*LGQKLYKSITGTQGGSPG
4840	10337	A	5146	2	428	MFLLVVINLHILFVF*FKLFSWS*AIF L*FLF*FMSESENIYYAEIGIITIVT LKSLIATYCINPSSHCHYKVYLVLSY LYCIIVNFDIYFLLLCVPFCYFSLJISL SPLFLLIYMIFLYIHFILLFVIFYTFIP FSFY
4841	10338	A	5147	3	361	TLFQL*DLRKQRLEDLSTLIPRIYPG WKCRTHFLMKKSQIVIAGWYRRY AQHKRNQPTKSTVLVLQSYIRGRK ARKILRELKHQKRCTEAVTTIAAY

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						WHGTHALTETERLKEEARRKH
4842	10339	A	5148	1	424	VHLTADDKVIIAGLWSIVNAQDAV GETLGRLLQGVYPWIQRFFGSFGNLS SASAI VVNPKVTAHGKNVLTSLVD AITHLV DLMGTFAQLRELH*DKLYE DPENLHTLGHVLT VLVVIHFGT*FT AEVQASWLMMDTERANAL
4843	10340	A	5149	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
4844	10341	A	5150	38	501	APSPDA\MGHFTTEEDKATITSLWGK \VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAI\MGNPVKVAH GKKVLTSLGDAIKHLD\DLKGTFA QA*SELH\CDK\LVDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW
4845	10342	A	5151	2	198	KVRPPPLKKTFDSDVYRVLSEVD FERFAELPEFRPEDDLSSFS*PFLSP PPCMSTALAHGDFSL
4846	10343	A	5152	1	119	DIMTGPHDEVA AKNIQLTNEIQTLE TE*HEATKEFQVLS
4847	10344	A	5153	3	83	RMVLRMLPLSTDEALCFHAMFQPF LDMIHEAQQAMDIHFHSPDFQHPPT EFIREGDDDRTVLREMHHI*TG*LR VKWRCEEWR*I
4848	10345	A	5154	2	370	GAARLDERTKEGSDDDESG*GARA ELEGNKEGESEGQYKAKGERSAWS KLRTEIRQKAEESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIRQREKKN TAKGEGQERQKNLSHKRHDISC
4849	10346	A	5155	106	344	RPCQQMQINVIHPINRMDKKHVIPI DTSDKI*HPFMIQTLNLTCI**MYLSI IKAIYDPYTADIILTG*TFNAFFSTI
4850	10347	A	5156	198	474	
4851	10348	A	5157	1	131	PQEV PQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA
4852	10349	A	5158	104	440	FSKIYHFLCCCFLSKNCPILLHFL KIYLLALGNINISYFYSYHSKTLATG LKLTDDSQHISHGTSGSRFKCLLS KAVLMSSLPVYS*LLKLLDVREVS NMVHDTLGIL
4853	10350	A	5159	2	393	EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHAALTSSRLYLLM LFVGDPSPSGSNGSPDS*GLLLFRN DQAHIDLVCFSVILSCFFLFLSLCEL LWNAKQAMDQRQEQRRLQEMTK MARRPF
4854	10351	A	5160	2	154	FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLFLWRAIGNIY
4855	10352	A	5161	142	399	HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYYS

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4856	10353	A	5162	3	410	HEG*PTFSSILHPPGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFSVPGPQCLWPR*GPSYTAS LPQALRARPSQMTRVPQAPPPTGPG PVVSPCANTN
4857	10354	A	5163	168	435	IIAQ*N*FLKNNFQ*TI*K*NKTILFTT RSK**I*QKQKKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVTL SKLNYRVNVI
4858	10355	A	5164	2	427	QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVSV W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHSDACQHAFM
4859	10356	A	5165	11	1232	MAGAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRRCRCVCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKKGKFTELRLL DEEEALAKKFIDKNTQLTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPLDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLRMSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTRPASSPSTT
4860	10357	A	5166	115	447	MSSWARLCESPVVWYF*HVLFFVCL HKLRALISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLKCKTPGSGD RVETVEMVGCWVEEDHNGGSPSF LIRIYLFYLF
4861	10358	A	5167	1	423	ADMKAHLLHSGGMGFSCCESTGF VKHS*LIHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRIHRPERPF ACGYCGKGFYKSKLAEHIRVHTKS CPAANELDIKKMLHPLV
4862	10359	A	5168	481	908	EGSQWEAQKALAIQPVPCGAVRVP WTTSSIPASIPKQSVGKGCDCLR*L GDFAPARGEEACEHTEPFRNSRGV GGAWARPGYLVLSLLSLQCPDSAC NQDLLAYLQRIALYCHQLNICKVK AEVQNLGGELVVSGVSIS
4863	10360	A	5169	2	2799	EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDPSSVVKR GNMVRAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKLRNAGN EQDLGNQYKALKPEVDKLNIMAAK

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						RQQLKDVGHRDQMAAARGILQSN VPILYTASQACLQHPDVAAAYKANR DLIYKQLQQA VTGISNAAQATASD DASQHQQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIISGA ALMADSSCTRDDRRERJVAECNAV RQACRTC VSEYMGNAGRKERSDAL NSAIDKMTKKTDRDLRRQLRKAVMD HVSDSFLETNVPLLVLIEAAKNGNE KEVKEYAQV FREHANKLIEVANLA CSISNNEEGVKLV RMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDA VDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPM ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSDFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQ\MCMIMMEMTDFT RGKGPLKNTSDVISAACKIAEAGSR MDKLGR TIADHCPDSACKQGLVA YLQGI ALYCHQLNICKSVKAEVQNL GGELVVSGNCDTCGALQGLKGWPP PLCLATHWVDSAMSLIQA AKNL MN AVVQTVKASYVASTKYQKSQGM SLNLP AVSMKMKAPKKPLVKREK QDETQTKIKRASQKKHVPVQALS EFKAMDSI
4864	10361	A	5170	25	458	
4865	10362	A	5171	3	764	GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKAYFKR YQVKFRRR\RKGKTDYYAR*RLVIQ DKNKYNTPRYRMIVRVTRNDIICQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARRLLNR FGMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS
4866	10363	A	5172	8	400	PLASFDTGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCPLCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVTCPLHMFPCYR LMIRIW
4867	10364	A	5173	2	400	SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCP CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELSNLN NNVPIFVCTMAYPTDPCPLHIFPCY RLMIRIC
4868	10365	A	5174	1	216	AGRTGRPEERAPESKSGSGSESEPSS RGGSLRRGGEACGTS DGGPSPF*GS SVVSFTLLSYLGYYSYLLSTV

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4869	10366	A	5175	301	446	SYFSYIILIIRGNESEGGFFEN*YFCL LINGGSWSGEPPIRRNSHTFNC
4870	10367	A	5176	155	404	AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLTF LRTEGAR
4871	10368	A	5177	172	443	TGMIRGPWTKVGPGAIEKPPVGDGK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFFHANICPLSEKERQF RKQTALVDL*KPKPR
4872	10369	A	5178	3	428	PDQTLCCCAEMGSHCVAQAGLEL LGLSDLPLASQSAAITGVGHACP VLGS*RPSQMLCPFPWLLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFSPPGAGCLSLSCMECSFP AKVLVIPFPSEPPCS
4873	10370	A	5179	2	432	NIVSQNNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVNFVLIIC LFLAAAFSPEAASASVD
4874	10371	A	5180	163	585	VEVRAHPKKRQRKKKEKKKSDRYS SSSSSSSDSSSSSDSEDEDKKKENR RKKKKKNRSHKSSSESSMSETESDSKD SLKKKKKSKDGTKEKEDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSEEREKATEK
4875	10372	A	5181	18	566	AEQSGEAAAGPVGAPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKGSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKRRNLVGSSSDSED EDKKQGRKKKKKNRSHKSSSESSM SETESDSKDSL
4876	10373	A	5182	27	382	SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFRCVTM DYVNNQNL*TNKGPEPDD
4877	10374	A	5183	2	342	GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEL*SQKCGPNPM CCSFVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPPEIGKMMLQV IDERPGSALSRC
4878	10375	A	5184	2	147	AETGFHHASQDGLDLTS*STRGLGL PKCWDRREPQRPADTWFLKSTT
4879	10376	A	5185	8780	9035	LALQVHTMTPSKFFIFLVETGFHH VSQDGLDLLTF*STRGLPKCWDRYR SEPPRPAYFYIFLRRSLSLSPRAGVA VSRDHATAL
4880	10377	A	5186	75	355	SNKNPSISCPRTWGECVCQATSRST WFLYPMPYAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPPLLG VFPKPLLAPLFPEGPGP
4881	10378	A	5187	262	354	VWSPPLTWCLVCQCRYYPGLLM

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						MCFILPT
4882	10379	A	5188	1	104	ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP
4883	10380	A	5189	1	144	RDKVFALSHRLECSGAIHAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT
4884	10381	A	5190	99	241	CFPGA WVR LQLTQASDGPWQCSSS QRLHHAPHVVTLYLCCAFSPCSPVK LRDFESA VNNFEKALERA KL VHNN EAQQA IISALDDANKGIHRELKRTNY VENLKEKSEGEASLYEDRIITREKD MRRVRDEPEKVVKQWDHSEDEKE TDEDDEAFGEALQSPASGKQSV EA GKARSDLGAVAKGLSGELGTRSGE TGRKLLEAGRRESREIYRRPSGELE QRLSGEFSRQEPEELKKLSEVGRRE PEELGKTQFGEIGETKKTGNEMEKE YE*SHR*R*GSSVL VLDGDIAQEHG GKDGA EQLSDASLPGSDYSSHLK LMGP GSARVARGSIMHHTLSHSTC VVPSPLALQ
4885	10382	A	5191	303	427	IVLFEKKIFFFFETGSCSVPKAGVQ WCGHSSLQP*PTGLM
4886	10383	A	5192	82	352	RVPERVLPRIPPASCPVSPASRPL* GTPRAAPETRRRPRTARDPRGLRW QTQPAAPLLASPGPGVAPVASGAPI SRNDFQLCKARMLL
4887	10384	A	5193	1	248	QKLKKLARHGGACACGHKLLGWL RW*DHMSLRGQGCSES*SCRCTPA WTTE*DPVYQHKILSL*DFLI*KASS NRSSVIYEL
4888	10385	A	5194	3	370	AQWRVDS DGAPKRIADSATSPKLL YVDRV VQEILETERTYVQDLKSIV* DYLD CIRDQTKLPLGTEERSALFGNI QDIYHFNSELLQDLENCENDPVAIA ECFVSKSEEFHIYTQYCTNYPR
4889	10386	A	5195	28	183	YDRKRPVGKEKIGKLDCKMT*NFC ASKNTIKEMKRQRTVWEKIFAHYIS ERK
4890	10387	A	5196	1	681	MHPIGIALSKVPVESKEGDIMSHTG GSVPYLDNLNKASVCRGQSCR VFQ VKEMVTQVESEN NQEEQKQVRLPE SRLTPWEVWFIGKEKEERDRLQLK ALEFKEDWKLKRRVTKKSGSVSV SISSQG\NLTVCDCCESFLLTKPVSC KHLIKSHSCPALAVAS/CQRPEGYW SDCGTRSHSDYADEEDSFVSDSSDQ VSSRRTVTHSYAPPQSQPHHRHTQT GTTATYL
4891	10388	A	5197	1	2862	MPGPLGLLCFLALGLLSAGPSGAA PPLCAAPCSCDGD RRVD CSGKGLT AVPEGLSAFTQALDISMNNITQLPE DAFKNFPFLEELQLAGNDLSFIHPK ALSGLKELKVLTLQNNQLKTPVSEA IRGLSALQSLRLDANHITSVPEDSFE GLVQLRHLWLD DNLSTEVPVHPLS NLPTLQALTLALNKISSIPDFAFTNL SSLVVLHLHNNKIRSLSQHCFDGLD

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						NLETLDLNYNNLGEFPQAIKALPSL KELGFHSNSISVIPDGAFDGNPLLR IHLYDNPLSFVGNLSDHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRDL YNNIRDLPSFNGCHALEEISLQRNQI YQIKEGTFQGLISLRILDVSRNLIHEI HSRAFATLGPITNLDVSFNELTSFPT EGLNGLNQLKLVGNFKLKEALAAK DFVNLRLSLVPPYAYQCCAFWGCDS YANLNTENNSLQDHSVAQEKGTAD AANVTSTLENEEHSQIIHCTPSTGA FKPCEYLLGSMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKLFGLIS VSNLFMGIYTGILTFLDAVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFPGETPSLGF TVTLVLLNSLAFLMAVIYTKLYC NLEKEDLSENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISISPEIMK SVTLIFFPLPACLNPVLYVFFNPKFK EDWKLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCES\FLLTKPVSKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEE\DSFVSDSSDQVQACGRIAC FYQ\SRGFPLVRYAYNLPKVKD
4892	10389	A	5198	2	413	VDFFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFSCSLPSSWDYRR PPRPANFFVFFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH
4893	10390	A	5199	1	142	RKMFGNGRARSQVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP
4894	10391	A	5200	1	375	GEATMNPSEAEVVCVPTWVWP VSTR*MGGRE*RKERAEGKRGKGG MEKEGAGERRGKEKNGDSRERGRE GKSVTDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA
4895	10392	A	5201	109	331	PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS
4896	10393	A	5203	2	168	FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG
4897	10394	A	5204	107	357	DLRWYSSFLWMCCIPGAKWHPING SSCVMMGMIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAAYQSIQ
4898	10395	A	5205	3	376	CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFDPPEPSRPGN*GLLGPALCP SDLYAFGPQGIVNQGLPQWRPGW GHPWRLPEPDS*APAIPQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF

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						S
4899	10396	A	5206	1	262	QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIMMNDVYG PMSQILETLNKCPhFRQR*VLLLD EYIVLLGRFILFA
4900	10397	A	5207	2	296	NGTHASYGAFYLEYSLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSVGLGGAVLS SEDRSWGVSLLSRASAPRLPLAHL RC
4901	10398	A	5208	30	280	FYYAFKEEIPVLYSLFQKIETGGILL NSALLIPKST*YRRPYKKGKLNRYR PKSFVNINVKILNRI LANQIKCIKRI TYYS
4902	10399	A	5209	1	277	NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPLKHRRKRVGKGPLR
4903	10400	A	5210	220	585	EILVRSRLRQDPLRSRRGKRHTGRRW DGS GW RATGARE*RRESRGWEME AREAGRKPASERRKGSRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS
4904	10401	A	5211	1	291	SFLETLLPRLGCSDAIMAHCSLELLG YMRCHLSLPS*DYRPTPSRLANSFF LIHGGFTLSWADLQLLGLKQSF RK SWGLTGVSHHAQFPFPYYLY
4905	10402	A	5212	228	379	
4906	10403	A	5213	317	534	ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKV VNPYDKAP VSRIKNLLKLNKNTNNLIVKKK
4907	10404	A	5214	3	366	IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWK VTRKDG NASGT TLLEALDCILPPTPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLKPGM VVT FAPVNV TTEVKS VEMHHEAQK AK
4908	10405	A	5215	1	1254	
4909	10406	A	5216	33	1472	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GFVEFE\AG\SKNGQ TREHALLAYT LG VKQLIVGVNKMDSTEPPYSQKR YEEIVKEGSTYIKKIGYYPDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDG NASG\TTLLEALDCILPPT PTDKALRLPLQDVYKIGGIGTVPVG \RVETGVLKPG\MGVTFAP\VN VYN GK*KSVEMHHE/AL*SEALSWGTVN GLQLSRNVSVKDVRRGNFAGDSK\ NDPPME\AAGFT\AQVIILNHP\SQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSG\KPMCVESFSDYPLGRFAVR DMRQTVAVGVKAVDKKAAGAGK

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						VTKSAQKAQKAK
4910	10407	A	5217	178	566	KGGATCPESPQDRKRRGNLDMKLYSENEGMA SNHGKMENE*QPQDQRKPQVTLYSGRQEVKRGRGKDRKQGQNRNRR*GNV*RIKGKPESEGEAKEGKSEREGESEMEGGSEREGKPEIEGKPESEGEPL
4911	10408	A	5218	27	336	TNPVQQTLVPIWTSTRLPDTHEDKAFSAPQIEDRGTPGLGSRGPALGPSPTPDCAG*VVAAGPGPAESHPRAPKPTAGMSPGVARLSSPGSGSQGSWQNERP
4912	10409	A	5219	2	454	HFNM RDPLTDCPYNKVYKNLKEFSQNGENFCKQVTSVLQQRANLEISYAKGLQKLASKLSKALQNTRKSCVSSAWAWASEGMKSTADLHQKLGKAIIELEAIKPTYQVLNVQEKKRKS LDNEVEKTANLVISNWNQIQAKKKLMVSTQET*STADLHQKLGKAIIELEAIKPTYQVLNVQEKKRKS LDNEVEKTANLVISNWNQIQAKKKLMVSTQET
4913	10410	A	5220	26	130	TTWKYQYKNLERNQKEITELKSTIAEINITRGI*R*FEQTK*INELEDKIMEIFKDKR*KKGEKSLRGLWPPSRDKEACMPWKLQTEKKKGAERLSEEMAESFSNLLADMNINS*ELKSTIAEINITRGI
4914	10411	A	5221	48	394	SPSMCGSLDPPTLPQTWLVQVPSMLTHPCPPPPHPCPLAHPSSLLPSTHIYH**HLSPPYPNPGTQEGHSGVRLRATDVASPSVLGQFPSYSISVPREGHAATVAAKGPLECRA
4915	10412	A	5222	3	726	EQEVDYDPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLH/EKTPVSDRVTKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKKHPEAKRMPCAEDYLSRGPEPVMCVA
4916	10413	A	5223	4274	5256	HTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEVDVMCTAFHDNGETFLKK*VIRCL*FKIKKHGVTP*ANTL*KLP*QKYFQH*DLEVLL**FFKEVVFDTT

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						KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNILPKFNHLC TH TH TH TH L TLFST YLKND RDKTIMCKLSLIG*LESLEF GGSGENV DYN YFCNIVCYRK/ADCF SFLKFRYL YEIARRHPYFYAPELLFF AKRYKAAFTCECCQAADKAAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
4917	10414	A	5224	1	332	RMPCAEDYLSVVL TQLCVLHDKTP VSDIVAKCCSESLVNSQACLSDL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF
4918	10415	A	5225	7	564	TTRAAGREALSPGQGAGGGEGGAE PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHPA TAGGRKVRPAWPAAAGEAGGHS TGRAGAAGGA AVGTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAA TRNRIMPKTT
4919	10416	A	5226	132	917	PGLFYL GEEQPGPQAGGPAAGQG ATAGAE EAGCPGGAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGPQAGGPAAGQGATAGAE EAAGCPGGAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEP RHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPGLLWLATAGGRKVRP AGPAAAGEAGGHS GTGRAGAAGG AAVGTGGCQQRWIR
4920	10417	A	5227	3	1245	AWEFVWHPGGFDRSCPGPQGGE EGGEGT*EGSGSLALRPRPLSCPR GPGPGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGPQAGGP AAGQGAAGAEAAAGCPGGAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEP RHTATGHAAGREGRGGR ADQG*SLSQTDLW TSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAEG RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGASP GLLWLATAGGRKVRPAGPAAAGE AGGHS GTGRAGAAGGA AVGTGGG AAGPGGLPM
4921	10418	A	5228	612	795	PGFISAIGGLVGLSSYDFYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICSISS
4922	10419	A	5229	1	345	SSWSFTLVTQAGVQWHDLSLQPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSEFKRFSCSLSPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSTQKI
4923	10420	A	5230	1	1212	MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISR GDSDDSRVNSVLLFTILNPIYSITTP TRLNVFKNDQDTWDYTNPNSLGQG DPGSNPNKRQRQPPLLDHHPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEEWLADGYAV DRAITHLNNFMFGQKLNVCVGA QAREGSRGTGERKGGEGWGPAAEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESRRNRFST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSKG SERSSSGLLEWESKSDALETGLFLN HYQMKNPSINLVT
4924	10421	A	5231	1	421	FDPPGCFFTPIGNPFGPFQGNFHRK NGVQAMVEFDSVQSRQAASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNSLGQGDPSNPN KRQRGTVISQD*PSLLKNYCTCDF FSCSYICAAHVLCGTFQ
4925	10422	A	5232	2	1883	DEQRRRSGAMVKMAAAGGGGGG GRYGGGGSEGGRAPKRLKTDNAG DQHGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPAFVNYSTSQKISRIDE*ND YR\SVNSVLLFTIVNTINWITTDVLY TMCNCPGPVQRIVIFRKNQVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNPNSLGQGDPSNPNKRQRQP LLGDHHPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPEYGPADSP VLMVYGLDQSKMNGDRVFNVFCL YGNVEKVVKFMKSKPGAAMVEMA DGYAVDRAITHLNNFMFGQKLNVC VSKQPAIMPGQSYGLEDGSCSYK DFSESRRNRFSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSKGSRSSSGLLEWE SKSDALETGLFLNHYQMKNPNPGPY PYTLKLCFSPAQAHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKARVEEGFPPP
4926	10423	A	5233	2	337	DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNEANN SGVNDPFTGWLEK*FSKWKGIIASIL TSLAAMGVLLVRCVCLQRLM QRLIKMALTQTS

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4927	10424	A	5234	62	343	RQLNRNDPNRNKGKKVGKQCLRF WNNFILTCLIGVSEIEKKNGAE*IF EEIMSKNFPKLIKYPNQIQEA**TPS KINTEKTTFRH*IIGKR
4928	10425	A	5235	1	359	TDDDLNWLDSHRTFREQGVDETET CLLRRKFSYSDQNVDSDRPVQLNLL YVQARDDILNGSHPVSFKEACEFGG FQAQIQFGPHVEHKHKPGFLE*MTF CFSFFSFLSSFSFSLFLS
4929	10426	A	5236	2	264	SYYPGEISVPPFNICHFFLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSFLK*FFYL*FFPESVISF GSFSNSD
4930	10427	A	5237	3	246	LIPRGQGSTVVLPPYNPATSI FGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN
4931	10428	A	5238	78	411	VLNSPICNCLYPILCSFLFLIYFVVC FYTFIPVFYLVYHQEIVI*SLTLVFFV CVVKINTRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS
4932	10429	A	5239	2	175	TKLDFIGIKGFSSVKDNVKGMRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4933	10430	A	5240	1	335	VTIRGAGIPDES RNVNYS LASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTICNHEHYIPLNLP MAFAKPKLQRV*DSBLEYSLSDEY CKHHFLGGLL
4934	10431	A	5241	139	354	SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIQARNHKD NLTSIAVSQTHIKVATCENNLP
4935	10432	A	5242	2	332	ILAGAI*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLGLI NEFSRASG*KINVQKFLYTNNVQS KNEIKEPSLCTKASKRIGYLGHLTK EV*DLYSERTKPH*KKNRILRNTFN KRSVRLVQ
4936	10433	A	5243	137	290	GSSDINQTKHVRS*VNRQICSRTTQ QSPEDCDFKKDGLVKRCMGTQTRQ SL
4937	10434	A	5244	1	363	LTCSGDKEQIKDKSHVLKKGKNFE RETS*KKK*SLPPFDDNVEPNLYV EENICKSDSERPRSSSSSRSSSFT PSQTRQQGPLKSMMDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR
4938	10435	A	5245	2	376	VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR
4939	10436	A	5246	60	185	
4940	10437	A	5247	1	146	RWRDLGSPQAGFR*FCCLSLSSW DYRHAPLF*QFYLFILLFCKKYF
4941	10438	A	5248	2	298	TFFTPFPVAKPNPRGPKTPAPYFSPQ

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						GPQKIYPPKFLGPPFNFPPLLGGKVF RAPNPRV*LPPGARPSSSSLLPGF* KIPKPLFY*KKIFPTPQKTKK
4942	10439	A	5249	77	370	EYS*SVVFLDLMRQEELRRMEELH NQE
4943	10440	A	5250	83	467	YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQORQLREGROGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV
4944	10441	A	5251	1	359	KYTL SRLATVPPTLNPAEYNISPDR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTMDMRNQKLIREGKLDQ
4945	10442	A	5252	3	349	SSLATVPANLNPAEYSISPDRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ
4946	10443	A	5254	1	415	NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTSVEEMIASTAYLEL FLRSISEPALLRTLRLRLLHRHDTH TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLPCNHV MLSQKPAVRDVL
4947	10444	A	5255	34	394	YRHYTICCIIGFLNTITMMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDESYGHIKPIISKVMEM YQPIAVVLQCDAYSLEYGDSLDCFNL TIIRHSTRLYLI*SYHFTS
4948	10445	A	5256	178	417	ILVPPAGGKGNLI*WNP GPPGARG FPGLTPPRGGKKGRAQPPENLVF* EKTGFPIVQRGGLKPPPGPPKGGE*R GGPP
4949	10446	A	5257	749	1049	DGSSLLGPRPGGKGNQTKGNPRPP G*RESPPHPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHDPKPG GKKRGEPPEPTTGPSKRGKKQGF
4950	10447	A	5258	1	359	LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD
4951	10448	A	5259	1	441	FFFLNRVLTLTQAGVQWCDHGSQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFYNKFTSWG HPNSQYYSGISWGQSTNILLGY
4952	10449	A	5260	1	553	FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMPLGTAFILFQMKTLVLV RRGINQDN*HWRQEDPLIPISPGFPS RIPPLKSEMSLPLSTDGSETRTQSP FDEIYMAHDASGLRLPDSPPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE

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						RESRKEERQRSKPGEAAALGGVAC TFHLKSRS
4953	10450	A	5261	1486	1695	GKSCRPNYIFILFSSFLRRSFALVA QAGVQWCDLGSLOPPPPGFK*FSCL SLPSSWDYRYPPPLCPANFC
4954	10451	A	5262	1	334	RRFVSQETGNLYIAKVE*SDVGNVT CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVPTIWRADGKPIA RKARRHEGCEM
4955	10452	A	5263	78	313	KVTYIQKNVYSKCTAGWVFTQRRAR VGSREPFPAAPSPGPHGGDPPSPQL G*PLSPLPQPAPVRLPSPVMMSERIL PF
4956	10453	A	5264	3	320	IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLNEIVDQIK TSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFGLKILE KEKG
4957	10454	A	5265	3	941	APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFTVDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSENPP\SFTITVTSEAG\ENDES IHIKLLSCVLA VQTTLKFTYSEKYPD EAPLYEIFLPGKILEDN\DVSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NV\LDHIITRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKA/RSF DAELLEIKKKRMKEEEHAGLDKK\S GKQLFETDHNLDTSDIQFLEDAGNN VEVDESLFQEMDDLEDEDDDDPD YNPADPESDSAD
4958	10455	A	5266	1	332	LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSRFRPGKKV*G*PKGFQR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPVAKIPI
4959	10456	A	5267	3	375	SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSPNIGAPLISSMG TTMDGSAPSTQVSPSVQTOQHQM LSSSSSSSSSQMQMQQQQLQQHQ MHQQIQQMQQQHFQHHMQ*HLQ Q
4960	10457	A	5268	1	360	KGAPKHGQAPLGDPPRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKND SGKARP*ILDPKSVSC IPAPSSHRPLSPTPNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA
4961	10458	A	5269	1	181	KKKPQTWEKLV*GLF*KKRNPWG QRVPPVTPPLWGVKKRGGVFFRGL KPPLKPRENPFF
4962	10459	A	5270	10	108	SHINVPMNQPVVSLGPGQVTKGW DQGLLMCE
4963	10460	A	5271	1	336	EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWGSQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSR EKMAIGVLIQMVGPWPRPVAYLSK

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						ELDGVSKARSEGCE
4964	10461	A	5272	1	118	TEVRHGKLDSSKWIPIRGN*NIYNP HCLSYKLEHGSDQEIPSDWYPFATV QFSVPDLC
4965	10462	A	5274	2	327	SCLVLVLLCVEYLFYPYLFHQSIQCVFT GEVSFLQAAYSWVMGFFVFLFILIH SYFL*LLWGLFISLHLWLSLTCEDLF LLFFSRCLIIYICFVLLFMSFLILWR LLVF
4966	10463	A	5275	171	331	LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPVSGE*LSNL*YVQTMECYS VLK
4967	10464	B	5276	83	332	MGKRDNRVAYMNPAMARSRGPIQ SSGPTIQDYLNRPRTWEEVKEQLE KKKKGSKALAEFEKMNENWKKE LEKHREKLLSGX*
4968	10465	A	5277	76	138	
4969	10466	A	5278	1	1050	
4970	10467	C	5279	146	433	MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGGF*
4971	10468	A	5280	27	264	NPNHQSLLCRAFCGVLILPVLALL TRLSFGELTYNNHFIYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G
4972	10469	A	5281	135	358	VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCCKGIHRLPHTIQVGQN
4973	10470	A	5282	15	196	KGKIVKLDIFI*NFSSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKLNLKKF
4974	10471	A	5283	307	383	YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNLRPLFELPTVISAVVQ TKISLGR
4975	10472	A	5284	3	267	TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPSTTLKAFK STMEQLVEKACFRDYHRLGL*TLSG SCCRS*P*SRRVQ
4976	10473	A	5285	1	260	TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESTASASRLGT/TISSHP VSHKCSFHKSG
4977	10474	A	5286	60	292	VTNFLIFHMRJISKYISIFLTVFFVFSQ IVLLFKHSYFSYLELWKMQRKDSK NAT*KRAL*RFHEKSFHEGCMCIKS
4978	10475	A	5287	738	1152	KGRVWSWCSRKRTFCFSFGSFSSDA LTSYITTAIPTATAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFGQYTNQPGTGNMGKKQPRIT LCPLNKRKVVAVKPN
4979	10476	A	5288	3	555	RKRTFCFSFGSFSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVVTSAQQKAGRTITARITGR CDFASKNRISSSLAIMGVSPPHLSC

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						CGKTSSQSTVQTHSLKQLPAKYPRTHSIPESSTLSLPRSLGTQISSHPVSHKCSFP
4980	10477	A	5289	94	323	VIGYRNIRCTILTSTITSSLSIL*LNH*PETRLSE*AGV*DKGLVVAQMMWLMDHIFKYTNFGIVSLVHGDFIRQ
4981	10478	A	5290	2	319	MVLVTLDDKYAVAALWGKVKVDEVDGEALGRLMVVYPWTQRFWES*GDLSPPDADMGPNPKVKVHGNKVLGAVSNGQAHVDNLKGTFTATVSEMHCCKLHVAQEPEVL
4982	10479	A	5291	1	159	RDLQHFPSVAM*DQTQNDIASTSNHESILQGIKQSQL*EEVQLME*APVDC
4983	10480	A	5292	187	282	LRSY*CLLLMISFTRNANLFR LHGTHTDTFKCLEYEKCFNCNSDLIVHHRINMDHNPHTSA*DSGLLLGMHF
4984	10481	A	5293	1	156	SGGVDEQMMREKEELMLWLQDYEKIKKAEREL*EQIKREMCKKNQKRKREKK
4985	10482	A	5294	179	322	NKVGGLTLPNCKTYKATIKTWYWRKKRQIGQ*NRIESPEIDPHKY
4986	10483	A	5295	2	395	RDRESDRDQRRERERRTRKWSRSRSHYRSPSRCRTKSKSSSFGRIDRDSYSPR*KGRWANDGWRCPRGNDYRKNDPEKQENARKEKNDIHLADDPNSADKHRNDCPNWITEPINCGRPRTNPEKL
4987	10484	A	5296	3	228	HELPHPLGLKRGCVVLEVAEHVVLGKALLILLPYRFKRNILAMDDKTGMTRNPHFSHNNWIPTFFSTQYFWIIFKVRWPRLKDTTDLRILAPNCLADRLSRHRCNIWQFMQGIPLVLNFGSCT*PSFQPQQLYTNLFQHPVFLDHL
4988	10485	A	5297	61	360	YVSNKCSNHRK*SLSSSSSSSERESSFVPQVELHGRDLG*LQLWLPFGFKFPGLTPLRNGDDGPRPQPPANLGLLVKTGFSPVAHLGVNLGTLGDCPALP
4989	10486	A	5298	124	351	EREFRFVPQVELHDDRDLGSLHPGTPGLRKFSGLTLPRSGDNGPGPPPVNLGFLEETGFSHVAHFGLNFGT*GDCP
4990	10487	A	5300	3	388	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQRQLHLNGTFPNTSDADMEPCVDGWVHDIISFSSTIVTE*DLVCDSSQLTSVAKCAFMTG*TADGFLGAHLSHRVRASSNVCMMGGSIVC
4991	10488	C	5301	47	269	MPPLIQSGMSSRTKTRTSSPCWNVHPAPEQYEAPDKDFMIVALDCSAAPRAWVVTWSSWCPQQHHDIAVPVHA*
4992	10489	A	5302	1	253	MYTQ/HPEQYEAPDKDFMIVAL/DL LSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPILGTNLNPEF/ISVCCNNATWAIGEICMQW

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4993	10490	A	5304	229	2984	PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQLLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGILKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTIASKGELQMWPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELLDSDALNRPLNIMIPKFLQFF KHCSPKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLLEVRIDRLIPHMHSIIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRVTLPHEAERPDGSED AEDDDDDDALSDWNLRKCSAAAL DVLANVFREELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLPPELPHLIQCLSDKKALVRSIA CWTLRSYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPLLIQKWNLKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQKATLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLA GLGGHVEQLVARSNIMTLLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMVL NNLVEIINRPNTPKTLLTENTGRLTSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNPGGVVQDFILFCDAVASW VSPKDDLDMFYKILHGFKDQVGE DNWQQFSEQFPPLKERLAAFYGV
4994	10491	A	5305	47	411	
4995	10492	A	5306	20	1020	LSLTSRMEEAELVKGRQLQAITDKRK IQEEISQKR\RKLGEDKPKA\QPLKT KAL\REKWLPRWNPASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAEQISTKEEAILKCLKS IERTTEDIIRSVKVEREERAEESEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSSIPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAAYNGTDGLAPVEV EELLRQALERNKSPTEYHEPVYAN PFYRPTTPQRETVPGPNFQERITIK TNGLGIGVNESIHNMGNLSEERGN NFNHISPI
4996	10493	A	5307	1	95	GTRTFLRITYLSEIARRHPEFYAPELL *FAKR
4997	10494	A	5308	1	338	GTSLSA*GLNIDGQLGLGHTEDIPY YTPCRSLFG*PIQQVACGWVHTIML TEHGQALLCGCNSIVQLAGPHGHL RRVGT*TIELRRENAVHIGAALMPH

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						VALTTSRSIFQCR
4998	10495	A	5309	3	472	VTEFAKTCVADESAENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPRLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGRAF KA\VARLSQRFP
4999	10496	A	5310	12835	13995	TIPIESDIFPSIFYLYLSSLAYADTYE ALSRFY*KKKLINLLSLN*ATHFPK IMPVVQVELKAKFN*LFRKCFLPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFF*DGVSLLCCPGWSAVVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQT
5000	10497	A	5311	1	349	GTSKKLANKVVYNVGLCICLFDITK LEDAYVFPDGDGASHTKVHFRCEVC HPFLHEILTGKIKGCSPEGAHHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY
5001	10498	A	5312	1	410	IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFPP*SLQIMFETFTNP AMYVAIQAVLSLYASGRTTGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL
5002	10499	A	5313	216	390	GSADARAPPVLSPVIFCPS*FLTGRP LQGMVMGMGQKDSYVGDEAQSQR GILTLKYPIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLN KANREKMTQVRLGRRPCSSRPFPSH FLPILISDGSSPAGRHHGGHGPGLLR GRRGPEQAWHPDPEVPH
5003	10500	A	5314	4	1254	HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\PRA\VFPSIVGRPRHQG VMVG\MGQK\DSYVGDEAQSQRGI LTLKYPIEHGIVTNWDDMEKIWHH TFYNELRVAPEEHPVLLTEAPLEP QGQTRKMTQ\IMFETFTNPAMYR GPSRAVLSL*ASGR\TTGHCHGTLG DGVTHTVPIYGGPLPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRD\KEKLCYVALDFEQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHET TFNSIMKCDVDIRKDLYANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KIIAPPERKYSVWIGGSILASLSTFQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QMWISKQEYDESGPSIVHRKCF
5004	10501	A	5315	279	418	VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH
5005	10502	C	5316	274	530	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV*
5006	10503	A	5317	2	736	RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLKQNCSELF QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCSELF FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLS
5007	10504	B	5318	120	1070	MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLKQNC SELFQGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQL*
5008	10505	A	5319	2	668	
5009	10506	C	5320	246	365	MDDFAAFXXXCCXXDXKGDLLXR RKVKNLQLQVQLPLGF*
5010	10507	C	5321	261	656	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCKGDXKGELL XRRVXNLL*
5011	10508	C	5322	158	607	MLCQSVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCKGDXKGELLXRRVX NLL*
5012	10509	C	5323	158	532	MLCQSVPCAEDYLSVVLNQLCVLH EKTVPVSDRVTKCCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCKKAD XKG*
5013	10510	A	5324	2	740	PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLKQNCSELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCCCTESLVNRR

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						PCFSALEVDETYVPKEFNAETFTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY
5014	10511	A	5325	1	588	
5015	10512	A	5326	364	1356	TGDHAFQLWKSMTHTFQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVVLRLAKT YETTLKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEQLGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQL*TS *SKKNAL\SEDYLSVVLNQLCVLHE KTPVSDRVTKCTESLV\KGDHAFQ LWKSMTHTFPKSL/YAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEQLGEYKFQNALLVRYTKK VPQVSTPTLVE/VLKKPRKSGQQL* TS*SKKNALCRRSIPWS*TSYVCC MRKRQ*VTESPIRNLGKVGSKCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCTESLVNRRPCF SALEVDETYVPKEFNAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEQLGEYKFQNALLVRYTKK VPQVSTPTLVEVSRNLGKVGSKCK HPEAKRMPCAEDYLSRGPEPVMC V A
5016	10513	A	5327	1468	1946	LHISWEGEPIDYSVVLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCLEQLGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLKVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKQ*VTES PNA AQNPW*TGDHAFQLWKSMTHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLLEKSHCIAEVENDEMPAD LPSLAADFVESKDVCKNYAEAKDV

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						FLGMFLYEYARRHPDYSVVLRL AKTYETTLEKCCAAADPHECYAKV FDEFKPLVEEPQNLIKQNCLEFQ GEYKFQNALLVRYTKKVPQVSTPT LVEVSRN/LRKSGQLR*I*TSCGRAS EFNQTKL*AF*AAWRVQIPECAISS HQESTPSVNSNSCRGLKKPRKSGQH TKKVPQVSTPTLVESRNLGKVG KCKKHPEAKRMPCAEYDLSVVLNQ LCVLHE\KTPVSDRVTCKCTESLGG TGRPCFSSSGKSMETYVPKGFNAE TFTFGSFCT/LSWEGEPIDYSVVL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCLEF EQLEGEYKFQNALLVRYTKKVPQVS TPTLVESRNLGKVGSKCKHPEA KRMPCAEYDLSVVLNQLCVLHEKT PVSDRVTCKCTESLVNRRPVC
5017	10514	A	5328	1	2063	MKKVKERDSFIMEDLGAEGLKSSA YSRGVFRRDAHSEVAHRFKDLGE ENFKALVLIAFAQYLQCCPFEDHVK LVNEVTEFAKTCVADESAENCCKS LHTLFGDKLCTVATLRETYGEMAD CCAKQEPERNECFLOHKDDNPPLP RLVRPEVDVMCTAFHDNEETFLKK YLYEIARRHPYFYAPELLFFAKRYK AAFTCCQAADKAACLLPKLDEL DEGKASSAKQRLKCASLQKFGERA FKAWAVARLSQRFPAEFAEVSKL VTDLT KVHTECCHGDLLECADDRA DLAKYICENQDSISSKLKECCEKPLL EKSHCIAEVENDEMPADLPSLAADF VESKDVCKNYAEAKDVFLGMFLYE YARRHPDYSVVLRLAKTYETTLE KCCAAADPHECYAKVFDEFKPLVE EPQNLIKQNCLEFQLEGGYKFQNA AISSVTPKKVPQVSTQLLTPTLVEVS K/NTLGKVGSKCKHPESKKKCPVA ENYLS\SVVLNQLC\LLHEKT\PVSDR VTKIAAQEPL\VNRRP\CFSALEVR* NIPFPKEVNA\ETFTFHADICTLSEK ERQ\RKQTALVELVETQAPRQKE QLKA/VLWDDFAAFVKIAAKA\DD KETCFAEETISGNGAKKAIFLVNDE FILMSLTLIQNHRTYSSLPPCLYDSK KLLFHLYASIYFPVPPQDACKGVSE L
5018	10515	A	5329	1	339	RRRRKKNEKRKRQRKIKDEKSRKN SLRVEMRETWRQREKQKEEDREKR KGQKEKERRKREIEEKEST*CEQME IGKTKKVNIHCRWQTQLKLFHLFS LFSIKMSLSSFSTRA
5019	10516	A	5330	2	189	ARGGDAGDAFDGFGFGDDPSD*LS SCHIDVHRYLFSALCDCYTFYFVHI RVFLLSMRLADTA
5020	10517	A	5331	3	346	HELETFP*CHNMPLLFYRDRLSASD MLQVRKVMHDVYESIITLNNESQST SSSNNEHPGGQERSLARA

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5021	10518	A	5332	2	442	VFMDADTLVLANIDDLFDREELSA APDPGWPCFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPPFIYNLSSISIYSYLP AIS* EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPR
5022	10519	A	5333	1	292	VLANIDDLTREEMSAAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPPFIYNLSSISIYSYLPVLP
5023	10520	A	5334	81	1163	VTNLRPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDGSDAHLTLMKRPGLG VTLTKLHCWSLTQYSKCVFMDAD TL\VLANIDDLFDRE\ELSAAP\DPG G\PCFNSGV\FVYQPSV\ETYNQLL HLAS\EQGSFDGG\DGILNTFF*QL GQQDIRKHLAFIYNLSSISIYSYLP AFKVFASAKVVHFLG\RVKPWNY TY\DPKTKSVK\SEAHDPNMTHPEFL ILWVGTSFTTNVPLL\QQFGPWSK DT\CSYVN\VGRCLQGAISHLSLGEI PA\MAQPFV\SEERKERWEQQQAD YMGADSFNKRKLDITYLQ
5024	10521	A	5335	1	241	GTSNSEHALDDRSTAQCRVQMQUV QQL*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTLKSKAL EAYALELT
5025	10522	A	5336	13	229	ACPRSPPPDPRLGCCFPPPPAVC*AP AGPHPDGTTSELECTPAPHPSCPEVS VQKPEPSALYGTGFPFGLQS
5026	10523	A	5337	1	341	GLGSGTSSSVKSSISPKRVARWSFS SRVCPVCPSALSV*DSRSP*ASKSS SNASGSPFCRVKKLLSCELQSKADS FSSSAVSRDRLSSSSMLSRGQL*Q ETSKEAQMPR
5027	10524	A	5338	3	168	
5028	10525	B	5339	978	1502	MSNLTLCISTKHTPGISRakeKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QOKFRSETITEELVGLMNKFVEDT KKGVHQKEGWPSAYGVTKIGVTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHQFVSEKRVEQ W*
5029	10526	A	5340	3	239	HEAKSSPNLVKAILLQIQEATQIPRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT
5030	10527	A	5341	3	322	HEAKSSPNLVKAILLQIQEATQIPRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLSSETMEAR KKWHNYQMIEKNCQPTILHPAKLS FK
5031	10528	A	5342	4	351	VGRGRQSHLSHSHPTDPKGQQASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQQTSAGHLLSMSHEALTW

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						VDRATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA
5032	10529	A	5343	3	163	HEEQPEGLSPNLDRLGDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL
5033	10530	A	5344	112	362	EREQRFTGLNDVHYLPIMYIVVGCA IFIT*V*RGWSSPTKCRSTDTYCVNP STRLHAYMAPRHKLSHSCAERDPD QFTLLRHC
5034	10531	B	5345	85	206	XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX*
5035	10532	A	5346	142	653	GFWHQRILGASDQAHLLLPKQDG SADGARRVLACARGQGDRLRLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPSSPRGPRTLHR VEKV\PGAPVTPLPVAFSCNPDHGIE DPAFP*PAAGPR*LQEGPCGGSRAS RAPPTSTRSCCTECLRNSLILIC
5036	10533	A	5347	261	538	GSRSRLLFSPRGPRTPYPAWKSTGA PVTSPIAFSCNPDHGIEDPAFP*PAA GPR*LQEGPCGGSRASRAPPTSTRS CCTKCLRNFILIC
5037	10534	A	5348	7	264	FQKISALPQRSDYTHNTPHTDPARV SYKHAGANHHTIHTPMTNVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN
5038	10535	A	5349	208	713	SVKMOVRYSLDPENPTKCKSRGS\N LRVHFKNTRETAQAIGMHIRKAT\ KYLKDVTLQKQCVPFRRYNGGIGR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNAKPMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEE VAQKKKISQKKLKKQKLMARE
5039	10536	C	5350	286	591	MVRLFNLNPEKRQRKSWQIRGFQS SCFTLGTLVKLAQAIGMHIRKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGGPKKECLN FLLHML*
5040	10537	A	5351	1	305	GTSIYNVLYEVPLPPGRSLKFSGVY GPIICQRPSTNELPLDFPVKEVFELL GVDNVYQLFTWALLQKYILLYVQR *CNVTKALELSNLLLFHICDIKLV
5041	10538	A	5352	15	234	LSCPDQVPHSLVPYPEPRRATASV PETSGPPFPHRRPYATTPALGHNP HA*LSSSFAGSRYKLGEMLHI
5042	10539	A	5353	3	257	HEVKYKNPAQ*QWHRLGPDHVP EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI
5043	10540	A	5354	3	334	IIKFIWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTLFNKWCWERWIAIC RRIKLDLV
5044	10541	A	5355	1	119	QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM
5045	10542	A	5356	3	349	HEPANADFAFRFYLIASETPGKNIF

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						FSPPRFPAA YAMLSLGACSHSRSQIL EGLGFNLTESESDARRRCRQ*VGT LDLTQHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR
5046	10543	A	5357	1	499	
5047	10544	B	5358	66	641	MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNPQTSVRTPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIKKP EMFETAIKESTSSKSPRKINSSPNV NTTASGVEDLNIIQ*
5048	10545	A	5359	2	306	ARGVCGGCRCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVVFVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL
5049	10546	A	5360	3	120	HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC
5050	10547	A	5361	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFFLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
5051	10548	A	5362	1	108	
5052	10549	A	5363	2	536	ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGERLLKMQ NQRGGRA\LFQDIKKPAEDEWGKTP DAMKVAAMALEKKLNQALLDLHAL GSARTDPHL\CDFLEPHFIDEEVKLI KKMGDHLSNLHRAGWPRRLGLGE YLFERLTLKHD
5053	10550	A	5364	3	331	HEQYPGSISISLTDLGCPDMPVIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSMKIY ADIIGSEDTTNEYRSIALYFEREMR YLQAAKF
5054	10551	A	5365	3	52	HEQSWKAENEAF TLADLKQLPEN PPVLMPRGNVGTPLRVFLELIRACR LPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT
5055	10552	A	5366	3	323	STFFFFLQRSLALVAQAGLRTQW RNLGSLQAPPGFTPFSCSLPSSWD YRRPPRLA\NFFFFFFVFLAETGFH CVLARMVSIS*PRDQPASASQSAGIT GVSD
5056	10553	A	5367	3	337	HERHEDTLTLKERNRGNKGILDDID DHNIIHYHLPDA*SEEYEFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSVDVKVENPQHNDFMKLITML ITHMHDLQDV
5057	10554	A	5368	16	313	SHSVTQAGVQCWHLHAQLIFLYF LVETGFHRSVDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFKCS PRPQAILDFAFTSHELCLGSMRLKLS

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5058	10555	A	5369	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5059	10556	A	5370	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5060	10557	A	5371	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5061	10558	A	5372	1173	1295	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5062	10559	A	5373	1027	1149	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5063	10560	A	5374	2250	2372	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5064	10561	A	5375	934	1092	FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPRIYILTR SR
5065	10562	A	5376	2588	2824	VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVVFQRTSAPVMADLT PTVS
5066	10563	A	5377	935	1138	RRGFTMFHHVSQGGDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQGLKVSVVLH
5067	10564	B	5378	79	1551	MSEVTKNSLEKILPQLKCHFTWNLF KEDSVSRDLEDRCNQIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQEHADQAEIRSLVTWGN YAWVYYHLGRLSAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNPE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALEKSPCQTDVLR SAAKFYRRKGDLDKAIELFQRVLES TPNNGYL YHQGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNGKSEDTAVQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNAP NYWYLQGLIHKQNGDLLQAAKCY EKELGRLLRDAPSGIGSIFLSASELE DGSEEMGQGA VSSSPRELLSNSEQL N*
5068	10565	A	5379	925	1127	FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDLILNDTIMPNIK
5069	10566	A	5380	438	815	TRPSFSFNPLTLFFFLRRSLALSPRL ECGSAISAHCKLRLLGSSHSPTSASR VAGTTSARHHA WLMFFVFLVETG FHLVSQDSL DLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLSYT
5070	10567	A	5381	7944	10115	KQCNYGHNLKTC SNFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTPFS CLSLPSSWDYRRSPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF
5071	10568	A	5382	1	211	LKTSEKWRNRQDKSNKGSKKAERK

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						RATHADRNREAARJRRKTYTNERK HYEHHRTAGKDQDERATEDSRE* RE
5072	10569	A	5383	2	373	ARECHHLCKINYMDLVKEFMLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLISLIKSTASNFDPIKLFS
5073	10570	A	5384	112	913	DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSLRRQFSYCF YGMVLVPFSPHPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTOARDTPPQLP ERPPEG*ALFPPFPYSMAAPPSQLKPT LKITAVRS*ASGGATGLGGWSPLGL P*EQGLRPTATLTQTSGIALNPRSLT PAPQLRLSCPPHFALTTRAVPGGPQ PLAWGPEPGTPPAQPRPSPDSAQSH TVYRRESILFFIL
5074	10571	A	5385	2	345	SFWLLCGSSCDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPCSQVS VLTCTAAQATNLSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPPTTPPPPT PAPPHLPSTPPP
5075	10572	B	5386	36	340	MFLDEYARRHPDYSVVLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEFQGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI*
5076	10573	A	5387	3	182	
5077	10574	C	5388	602	877	METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFGMRYLVSFTPKE YPKCSNFPTLCRRVFKET*
5078	10575	A	5389	1	404	GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLKET
5079	10576	A	5390	110	424	LSLLQREREGHLNGSPSFMKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAYFYIC YIYYCYIF*FILLCFYTLMTIFFGLI
5080	10577	A	5391	2	361	ARETVKRIQYPIPLEGRLGLKPLIES LI*DGLLELCMSPTYTPILLVK*SDW *Y*LVEDLQAINQTVQTTHPVVPNP YTILSKIPYDHWFTSIDLKDAFWA CPLAEDS*DIFTFEWARA
5081	10578	A	5392	3	335	QSQSWWRQKGVSRAGAPIHPQGL LFGFS*GDLGPLGLTGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY
5082	10579	A	5393	61	497	
5083	10580	A	5394	16	951	RRPKIRDKFWGSV/KKLAHSEASPMI SGASKRAKKQINVYVGKGS/QGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MVVVWKLLDRDTVFALVNYIFFKG KWERPFVVKDTEEDFHVDQATT KVPMMKRLGMFNIQHCKKLSSWV LLMKYLGNAIAIFFLPDEGKLQHLE NELTHDIVTKFLE\NEDRRSASLHL PKLSITGTYDLK\TVLGQLGITKVFS NGAD\LSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEK WVNPTPKITGLSLLNPSP PSLGPLPGMTLKKGLSWK
5084	10581	A	5395	2	306	GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPA YILKISFITL PFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIY
5085	10582	A	5396	1	375	
5086	10583	A	5397	162	426	
5087	10584	A	5398	140	426	
5088	10585	A	5399	158	705	PSEKNKNLLLGVVYVRHLPNLLD ETQIFS YFSQFG\PVTRFRLSR\NKRT GN\SKGYAFLEFESEDVCQNSCLKQ WNNYLFGGKTLG/QCHFMPPEKVH K\NSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKKKERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT
5089	10586	A	5400	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVQGASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVQGAGLELLAPS DPPA
5090	10587	C	5401	197	415	MLLYVGLPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5091	10588	A	5402	671	986	KGVLFFFFFKTES\HSVAQAGV\QW CTLGS LQPP/PSRGSSDPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5092	10589	A	5403	65	921	
5093	10590	A	5404	213	442	
5094	10591	A	5405	1	1506	
5095	10592	A	5406	1	286	DRLIYIPFPDEKSLVPILKANLGKSP\ VPKDL DLEFLDLPWGCGRLPRRG NQGCAHSLHSPAGHACYSLT LDR GFLQKSKPKAVKLPRFSFG
5096	10593	A	5407	2	158	
5097	10594	A	5408	1	9064	MLARAARGTGALLLRGSLASGRA PRRASSGLPRNTVVLFPQQA WV VERMGRFHRILEPGLNIPVLDRI YVQSLKEIVINVEQSAVTLDNVTL QIDGVLYLRIMDPYKASYGVEDPEY AVTQLAQTTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKK

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						QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSFAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGT DAS LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEV PADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARJPLRLRSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPGPGSLPW GSQKPGACWMASRFSRVVLVLID ALRFDFAQPQSHVPREPPVSLPFL GKLSSLQRILEIQPHHARLYRSQVDP PTTTMRQLKALTTGSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVM GDDTWKDLFPGAFSKAFFFPSFNVR DLDTVDNGILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGHHPPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMMTTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLGLPIPGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASCFCILLASQW AISPGFPFCPLLLTPVAWGLVGAIA YAGLLGTIELKLDLVLLGAVAAVSSF LPFLWKA WAGWGSKRPLATLFP GPVLLLLLFR LAVFFSDSFVVAEAR ATPFLGSFILLVVQLHWEGQLLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETP VCHSSPWLSPLAS MVGGRAKNLW YGACVAALVALLAAVRLWLRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPPRLRVLVSGAS MVLPRAVAGLAASGLALLWKPVT VLKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQE EFRGRLE RTKSQGPLTVAA YQLGSVYSAAMV TALTLAFLPLLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTTGKYLSSD SLKDNSDSQGLRKRQPPGNEADA RVRPEEEEEPLMEMRLRDAPQH FY AALLQLGLKYLFI LGIQLACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRLRSALVSSYRFLET PSAGA ELFRPASATMSRQTTSVGSSCLDLW REKNDR LVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFILRASLAQGFT EQA QDIQRS LERVLETQEQQGPRLE QGLRELWDSVLRASCLLP ELLSALH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLLKTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPDLASP LHCGTQSQTKHILASRCLQTGRAGD AAHYLDLLALLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLLPKMSRLWEDARKGTKE LPYCPLWVSATHLLQGQAWVQLG AQKVAISEFSRCLELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPLPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVSLSQPKMDELQLFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVIHCEGEP IKREDEEESLNEVGYYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESESNLKRA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSQLLTMDGLKQRAH VIVMAATNRPN SIDPALRRFGRFDR EVDIGIPDATGRLEILQIHTKNMKLA DDVDLEQVANETHGHVGADLAAL CSEAALQAIKKMDLIDLEDETIDA EVMNSLAVTMDDFRVRTTPVPQW ALSQSNPSALRETVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPFGCGKTLL AKAIANECQANFISIKPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADRVIN QILTEM DGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAKAGARSWADV D LGVPGLKMTNGFSGS*P*QEILPACF AKLAIRESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVPEIRARD SLL KEAQSFCAFLFSDNDIRKY\EMFA QTLSQ/ESRGFGSFRFP SGNQGGAGP SQGSGGGTGGSVYTEDNDDDLYG
5098	10595	A	5409	96	299	
5099	10596	A	5410	174	324	
5100	10597	A	5411	74	242	

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5101	10598	A	5412	129	899	AAPGLGRGGGAAAGGGAVCPGTE RPCAMAYAYLFKYIIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\ITRSYYRGAAGALLVYDITR\ *DTFNHLTTWLEDARQHSNSNM/V IMLIGNKSD\LESRREVKKE/EKGEA FA\REHGLIFMETS AKTGFCRKEG ILFNTAKEILLKKFPRKGVFLTFN*W RANGH/IKLGPQPAAYPIATHAGQS G\GQQAGGGCC
5102	10599	A	5413	1	408	MQLKRANPGPRRAPVRETVMLLLC WGVPPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANRWGAPTAN WLANASVINPGAIYRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNG WLGVTLSRQPGENG
5103	10600	C	5414	1	1026	MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSLSAPNLEPLLKKKTNP TFLKSLSGGLNLFNFPFVETYTVEE VKVHPRNNTGGYNPEEEEDETASE NCFPWNVDGDLMEVASEVHIRRVQ KKEYVEENKIPRNPTYKGCEGPLQE NYKPLLNKIKEDTNKWKNI PCSWIG RTD TVKMAILPKHDRVAEQRVVGA LVKQRASQCPCRGRGSGPPGTAT ASPSGRRPFGAVIAPRFPSHALSSW YAGCNAEKSEVNAPGTQGMRFIS AASYKDWVQVLQKQDVS RNMGTK ARM MPLGSSGGCHTIRTEVTQDSE GQLAAVTTTGYTVVGLLEPPKVS D*
5104	10601	A	5415	1	681	
5105	10602	A	5416	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAE EK VPETTTTFWAPGVEAPGDDAERRR REASGPATRHSP LPTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCHIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
5106	10603	A	5417	1	1274	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPLGLLG RPGMPPQPQGPAPLRPDSSDDRYV MTKHATIPTEEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRA LKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSC VEPKMQVTITLTSP IREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCV IIR ILRDL CQRVPATWSDFPSWAMELLV EKAISSASISPGSDAL\RRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFALRLLA F\

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						RQIHKVLGMDPLPQMS\QRFNIHNN QDR\RRDSGDVDGFEEAGKKDKKD YDNF
5107	10604	A	5418	144	522	VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLSTMDLIEH YGKLA FNLDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP
5108	10605	A	5419	1	2437	MAVPGEAEEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAEAG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQAQRLIRMYSGRR WLD SHGTWLPGRCLIRRLRLPTEAS GLGSFPFKTRKELQSWKAENEAF TL ADLKQLPELNPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEEESHDEDDDRGEWE RHEALHEDVTGQERTTEQLFEEIE LKWEKGGSGLVFYTD AQFWQEEE GDFDEQTADDWDVDM SVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEGQGLGCRC SGVPEALDS DG QHPRCKRGLGYHGEKLQPFQGLKR PRRNLGLISTIYDEPLPQDQTESLL RRQPPTSMKFRTDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANEGLPYECAVDV GELVGLGDV MDALRLGPNGGLLYCMEYLEANL DWLRAKLDPLRGHYFLDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVDSHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNLDYYTEVLDLSYLL*PGLLTLS SATTPASIEEA/MCKLIEDY/NLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHFS STLGIQEKYLAPSNQSV EQEAMQL
5109	10606	A	5420	2	78	
5110	10607	A	5421	94	253	
5111	10608	A	5422	2	318	
5112	10609	A	5423	460	672	
5113	10610	A	5424	357	795	
5114	10611	A	5425	310	478	
5115	10612	A	5426	1	399	
5116	10613	A	5427	2	390	
5117	10614	A	5428	3	392	GGKIIVGDATEKDASKKSDSNP\LTE ILKCPTKVLLRN MVGAGEVDEDL EVETKEECEK\YGKVGKCV\FEIPG APDDEAVRIFLEFERVESAIKAVVD LNGRYFGGRVVKACFYNLDFRVL DLAEQV
5118	10615	A	5429	837	1005	

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5119	10616	A	5430	174	247	
5120	10617	A	5431	1	360	
5121	10618	A	5432	1	382	
5122	10619	A	5433	338	442	
5123	10620	A	5434	1	140	
5124	10621	A	5435	3	339	PINFESVGPTYRGSSCLAVVVPEFLG MSVAFVPDWLRGKAEVNQETIQRLL LE*NDQLIRCINLEYQNKARGNECVQ YQHVLRNLIYLA TIADAQSQPALS KAMGIIFQKQ
5125	10622	A	5437	157	371	
5126	10623	A	5438	150	284	
5127	10624	A	5439	84	901	ARKSVRMASRRMTRRDPLTNKVAL VTASTDGIGFAIARRLAQDRAHVVV SSRKQQNVQAVATLQGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLDI\NVKGPKP*MTKAVV PEMEKRGSGSVVIVSSIAAFSPSPG FSPYNVSKTALLGLAQTLPIELAPR NIRVNCLAPGLIKTSF\SRMLWMD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCEDASYITGETVVVG\GGTPS RL
5128	10625	A	5440	2	468	
5129	10626	A	5441	63	219	
5130	10627	A	5442	3	558	
5131	10628	A	5443	7	909	DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKAAVLTAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTFASKLREQL GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLH ELQEKLSPGGEEMRDRARAHVDAL RTHLAPYSGELRQLGARL GALRE NGGARMGQYHAQATEHLSTLSEK AKPALEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ
5132	10629	A	5444	3	195	
5133	10630	A	5445	189	263	PPGSHLGHPANAPSH*GPYPGLHS
5134	10631	A	5446	1905	2052	
5135	10632	A	5447	1903	2050	
5136	10633	A	5448	1	115	
5137	10634	A	5449	1	402	GKTSKLEFSIYLAPHSTTAAIEPYNSI LTHTTTLEHYDWAFMAYNGAIYDI CRRNL DIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVPYPR IHFLATYAPVISA EKAYHEQLSVA EITNAC
5138	10635	B	5450	81	319	XVVEPYNSILTHTTTLEHSDCAFMV DNEAIYDICRRNLDIERPTYTNLNL IGQIVSSITASLRFDGALNVDLTEFQ TNL*
5139	10636	A	5451	1	422	GKSKLEFSIYPAPQVSTAVVEPYN SILTHTTTLEHSDCAFMVDNEAIYDI

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						CRRNLDIERATYTNLNRJIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICA EK/AYHETAFV QKTTCLG*PSQQMW
5140	10637	A	5452	771	1640	ALQLHPHHPHPWSTLIVPFMVND EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGALNVDLTEF QTNPGAPTPIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPWHGVNYMGLL AWLYRGDVGFPKIDNGWPLPTIKN QAQHSSFVDW/CGPTGLSRFGHSTY QPSTVVPGLT WAKVQRAVCMLA SNTTAIAEVA*ARLDHKFDLMYAKR AFVHWYVVGEGMKEGEFSEAREDM AALEKDYEEVGVDSVEGEGEEGE EY
5141	10638	A	5453	89	435	
5142	10639	A	5454	2	287	TNEIEPEEN*HTKARNFRFVTAINN TPRNIREG/DHLLHHWIALADCP TAHMYEDVALIKDHTL DNSLIRELQ TLQEFNITLETALVKGIDI
5143	10640	B	5455	218	3940	MSGGGGGGGSAPSRFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIIT REDGSRFTGFALT FYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQA VTSPPPPPLESYIYNVL YEVPLPPPGRSLKFSGVYGPIICRP STNELPLDFPVKEVFEL LGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPFQWQHVVYPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLRLRASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QM QNFDKASFLSDQPEPYLPFLSRF LETQMFAFIDNKIMCHDDDDKDP VLRVFSRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWTKR NAPAQWRR KDRQKQTHELRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WKFVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERIWSHGLQVKQGSALWS HLLHYQDNQRKLTSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAVVRLSME

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						KKLLSRHLKQLLSDHELTKKLYKR YAFLRCDDKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLKGMDGSLERILVGELL TSQPEVDERPCRTPLQQSPSVIRRL VTISPNNKPKLNTGQIQESIGEAVNG IVKHFKPEKERGSLTLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYETLEKNEVPEENWH TRARNFCRFVTAINNTPRNIGQGWQ VSDAGVLGEPEITSYTTGICPAG*
5144	10641	A	5456	238	406	
5145	10642	A	5457	2	204	
5146	10643	A	5458	1	431	
5147	10644	A	5459	1	225	
5148	10645	A	5460	3	321	
5149	10646	A	5461	1	1257	MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSFPPKDDPSKPVHLTAFLGY KAGMTHIVREVDPRGSKVKNKEVV EAVTIVETPPMVVVGIVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKK\AHLMGDQVERGALWPE KADWAARERLEQQVPVNQVF\GQD EMIDVIG\VTQGQKAYKGV\TSRWH TQESCPRKDPTTEGLRK\ACIRAWH PARVAFSVARA\G\KGYHHRTEIN K\KIYKIGQGYLIKGG\KLIKNNAST DYDL\SLDKSINPSGWAFVHLW*K* PNDFVML\KG\CVVGTKK\RVLTLR KSFAGCRRKRRGFGEELTLSSIDTTS KF\GHGRFQTMEEKKAFMG\PLKKD RIAKEEGA
5150	10647	A	5462	114	456	
5151	10648	A	5463	3	76	
5152	10649	A	5464	2	951	CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIFLKFHAPP EINEGFNDVRLLLNNDNLLREGAA HAFAYNLDQFTPLKIEG\YEDQVLI TEHGRLGEMGKFLDPKN\RICFKF* SL*GRRATDPKDPCAEV\ENAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTHIACINESHQFQAKNF WNGRWRSEWKFTITPSTTQVVG\IL KIQVHY\YEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSD\TTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA
5153	10650	A	5465	3	553	
5154	10651	B	5466	26	384	MHHEALSEALPGDNVGFNVKNVSV KDVRRGNVAGDSKNDPPMEAAAGF TAQVILNHPGQISAGYALYWIAIVD MVPGKPMC\VESFSDYPLGRFAVR

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						DMRQTVAVGVIAVDKKAAGLAS*
5155	10652	A	5467	1	1254	
5156	10653	A	5468	1	1386	
5157	10654	A	5469	33	1653	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GVGEFEAGVSKNGQTREHALLAYT LGVKQLIVGVNKM DSTEP PYSQK RYEEIVKEVSTYIKKIGYYPDTLAF EPISGWNGDDMLEPSANMPWFKG WKVTRKDG\NAS\GTTLLEAL\DC\IL PPTRPT\DKPLR\LPLQ\DVYKIGGIG\ TVPVG\RVETGVLPKG\MGVTF\APS QRLQREV KICPKMHHEAFE*SSFLG DNVGFNVKNVSCQGC SVRGV*H GDSK\NDPPMEA\SLGFTAQVIILNH PGPNKAPG*CPWYWDCHTAHIAC KVCLSLKEKI*F\DRSW*KSLEDGP*I LGS LGDAGHWLIWVPGQAPCVFEK LLKTIP\LGRFA\VRDNEDRQLCGW VSIKSSWTKKAAGSWAKVTK\SAQ KSSERLKNIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S
5158	10655	A	5470	2	4966	
5159	10656	A	5471	2	4821	RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLEDFSDDETNT NLYGTSPSTPRQMKRMSTKHQRN NVGRPASRNLKEKMNA PNQPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDVLNKP YLSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLKLT SVSKKKDREQRGQ ENTSGFWLNRSNELIWLELQAWHA GRTINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQKL RIMGTVLGIKNLSDI GWPVFEIPSPRPSKGNEPEYEGDDT EGELKELESSTDESEEEQISDPRVPEI ROPIDNSFDIQSRDCISKKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHLK MDGSLQRARIALVKND RPVEFSEFP DPMWGS DYVQLSRTPPSSEKCSA VSWEELKAMDLPSEFAFLVLCRVL LNVIHECLKRLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPCDNIDAFEEDLHKM LMVYFDYMRSWIQMLQQLPQASHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGMLLKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLLDVLKS KQYVKVQIPGLENLQMFVPTDLAE EKSILQLLNAAAGKDCSKSDSDVL IDAYLLLTKHGDRAEDSEDSWGTW EAQPVKVVVPQVETVDTLRSMQVDN LLLVMQSAHLTIQRKAFQSSIEGL MTLCQEQTSSQPVIKALQQLKND ALELCNRISNAIDRVDMFTSEFDA EVDESESVTLQYYREAMIQGYNF GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTCKESGRGTRPR WATQGFDFLQAIAPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGVYTCISVDTGEL MAMKEIRFQPNHKTIKETADELKI FEGIKHPNLVRYFGVELHREEMYIF MEYCDEGTLEEVSRGLQEHVIRLY SKQITIAINVLEHGIVHRDIKANIF LTSSGLIKLGDGFCSVKLKNNAQTM PGEVNSTLGTAAYMAPEVITRAKG EGHGRAADIWSLGCVVIVMTGKR PWHEYEHNFQIMYKVGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE
5160	10657	A	5472	3	425	
5161	10658	A	5473	1	234	
5162	10659	A	5474	3	260	
5163	10660	A	5475	3255	3467	LNKNLGLIFFFFFFFFETASRSVTR LEYSGSILAHCELRLPGSRHSPVVS TWEAEAGELPEPRRQRLR
5164	10661	A	5476	1	4497	
5165	10662	A	5477	2	891	
5166	10663	A	5478	1	9786	
5167	10664	A	5479	27	13959	VPFSVAAAEPAQPARAARPRPGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLAGARAEEMLENVSLVCPK DATRFKHLRKYTYNYEAESSSGVP GTADSRSATRINCKVELEVPQLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEEFAAAMSRVELKLAIEGKQV FLYPEKDEPTYILNIKRGIIISALLVP ETEEAKQVFLDVTYVGNCSHTFTV KTRKGNVATEISTERDLGQCDRFKP IRTGISPLALIKGMTRPLSTLISSQS CQYTLDAKRKHVAEAICKEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTQVQLKLTISEQNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRANLFNKLVTLELRGLSDEAVTSL POLIEVSSPITLQALVQCGQPQCSTH ILQWLKRVHANPLLDVVITYLVALI PEPSAQLREIFNMARDQSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGQTMEQLTPELKSSILKCVQST KPSLMIQKAAIQALRKMEPKDKDQ EVLLQTFLLDASPDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KSVSIPSLDPASAKIEGNLIFDPNNY LPKESMLKTTLTAFGFASADLIEIGL EGKGFEPTLEALFGKQGFPPDSVVK ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIPQMI GEVIRKGSKNDFLHYIFMENAFEL PTGAGLQLQISSSGVIAPGAKAGVK LEVANMQAELVAKPSVSVEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKLFHPSKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTDSA SYYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLKFVTQAE GAKQTEATMTFKYNRQSMTLSSSEV QIPDFDVLGTILRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENFLKSDGRV KYTLNKNLSLKIEIPLPFGGKSSRDLK MLETVRTPALHFKSVMGFHLPSTREFQ VPTFTIPKLYQLQVPLLGVLDSLSTN VYSNLYNWSASVSGGNTSTDHFS RARYHMKADSVVDLLSYNVQSGS ETTYDHKNFTLSCDGLSRHKFLDS NIKFSHVEKLGNNPVSKGLLIFDASS SWGPQMSASVHLDSSKKQHLFVKE VKIDGQFRVSSFYAKGTYGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQI TGRYEDGTLSTSTSDLQSGIHKNTA SLKYENYELTLKSDTNGKYKNFAT SNKMDMTFSKQNALLRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTNNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDDHT NSLNIAGLSLDFSSKLDNIYSSDKFY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGLRLEPLKLHVAGNLK GAYQNNEIKHIYAISAAALSASYKA DTVAKVQGVESHRLNTDIAGLAS AIDMSTNYSNDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALEHKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDAEMRDAVEKPQ EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNRQTIIVLENVQRNLKH INIDQFVRKYRAALGKLPPQANDY LNSFNWERQVSHAKEKLTALTCKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIEKLSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWQNVD TKYQIRIQIEKLQQLKRHIQNIDIQ HLAGKCLKHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFVNLIGDFEV AEKINAFRAKVHELIERVEVDQQIQ VLMDKLVELAHQYKLKETIQKLSN VLQQVKIKDYFEKLVGFIDDAVKK LNELSFKTFIEDVNKFLDMLIKKLKS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESLQDTKITLIINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVTYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNDFQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDN TKYFHKLNIPKLDSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHRLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGNLKVRFPL RLTGKIDFLNNYALFLSPAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTHITPPLKDFSLWEKTGLKEFLK TTKQSFDSLVAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFEKNRN NALDFVTKSYNETKIKFDKYKAES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; * =Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion)
						KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNGKLRLEPLKLVAGNLK GAYQNNNEIKHIYAISAAALSASYKA DTVAKVQGVFEFSHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALHKKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDAEMRDAVEKPQ EFTIVAFVKYDKNQDVHSINLPFFET LQYFERNRQTIIVVLENVQRNLKH INIDQFVRKYRAALGKLPPQANDY LNSFNWERQVSHAKEKLTALTCKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLLSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWQNV TKYQIRIQIEKLQQLKRHIQNDIQ HLAGKLKQHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFNILIGDFEV AEKINAFRAKVHELIEREYVDQIQ VLMDKLVELAHQYKLETKIQKLSN VLQQVKIKDYFEKLVGFIIDAVKK LNELSFKTFIEDVKNFLDMLIKKLS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESQDQKITLINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGGVYSTLVITYISD WWTAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPFLTDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDSN TKYFHKLNIPKLDSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHVLTAKGMALFGE GKAFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGNLKVRFPL RLTGKIDFLNNYALFLSPAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTIITTPPLKDFSLWEKTGLKEFLK TTKQSFDSLVAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFEKNRN NALDFVTKSYNETKIKFDKYKAEKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HDELPRTFQIPGYTPVNVNVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTTLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMFEKYDFNSSM LYSTAKGAVDHKLSLESLSYFSIES STKGDVKGSVLSREYSGTASEANT YLNSKSTRSSVKLGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKAHLDIAGSLEG HLRFLKNILPVYDKSLWDFLKLDV TTSIGRRQHRLRVSTAFVYTKPNNGY SFSIPVKVLADKFIIPGLKLNLDNSV LVMPTFHVPFTDLQVPSCKLDFREI QIYKKLRTSSFALNPLTLPEVKFPEV DVLTKYSQPEDSLIPFFEITVPESQLT VSQFTLPKSVSDGIAALDNLNAVANK IADFELPTIIVPEQTIEIPSIKFSVPAGI AIPSFQALTARFEVDSPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAYEEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDDEDDDFSKW NFYYSPPQSSPDKKLTIFKTELVRRES DEETQIKVNWEEEAASGLLTSKDN VPKATGVLYDYVNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGTQYQEWK DKAQNLQYQELLTQEGQASFGGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFRPFQFGPKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPPFELRKHKLIDVISMREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFGPSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNFITSQLSSQVEQFLHRNIQ EYLSILTDPDGKGKEKIAELSATAQ EIIKSQAIAATKKIISDYHQFRYKLO DFSDQLSDYYEK\FIAESKRLNDLSI QM\YHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYHPLIFLKEIFN LFFFSNLNFSHRHRKNCKLPILIKPY SEPALQ
5168	10665	A	5480	2	316	
5169	10666	A	5481	2	401	
5170	10667	A	5482	126	415	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5171	10668	A	5483	3	499	
5172	10669	A	5484	1	241	
5173	10670	A	5485	12	308	
5174	10671	B	5486	394	565	MSAERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK*
5175	10672	B	5487	674	807	MSAERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK*
5176	10673	A	5488	113	339	
5177	10674	A	5490	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVQGAGLELLAPS DPPA
5178	10675	C	5491	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5179	10676	A	5492	768	1081	KGVLFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5180	10677	A	5494	305	477	
5181	10678	A	5495	1	903	
5182	10679	A	5496	111	295	KPATSVPVIVCVCSSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH
5183	10680	A	5497	1	505	
5184	10681	A	5498	3	345	
5185	10682	A	5499	1	1416	
5186	10683	A	5500	618	707	
5187	10684	C	5501	1729	2511	MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQSESGRSL GASRGSSVESLPPTSEGKRMSADMS EIEARIAATTGNGQPRRRSIQDLTVT GTEPGQVSSRSSPSVRMITTSOPTS EKPTRSHPWTPDDSTDNTGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLLQ RKQELVAELDQDEKDQNTSRLVQ EHKLLDENKSLSTYYQCKKQLE VIRSQQKRQGT*
5188	10685	A	5502	1	3489	
5189	10686	A	5503	1	246	
5190	10687	A	5504	40	124	NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC
5191	10688	A	5505	156	1001	GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVLNELARFNRVQPQY KLLD*RGPAHSMFVSQSLGEQT WESEGSSIKKAQQAQVGNKALTESTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; v=possible nucleotide insertion)
						PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNM VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK
5192	10689	A	5506	175	411	
5193	10690	A	5507	198	381	
5194	10691	A	5508	137	346	
5195	10692	A	5510	3	136	
5196	10693	A	5511	2	673	
5197	10694	A	5512	1	257	
5198	10695	A	5513	1	712	PRKT/PPAPH\DGDRKELPRTKLLPP API\STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKDSDLRLVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLD SGHCVP EHS SSGQR LYPEVFYGSAGPSSSQISGGAMDFH LAFSGSQGRHLEKGPPDGQRLGPE GTRSLGCPHAEVPLAPYPRGLYI DYKY/MKGERGGRGGVLGLGPHFP SSPFPWSPVPGAVC
5199	10696	A	5514	2	322	
5200	10697	A	5515	1	6470	MSDRSGPTAKGKD GKKYSSLNLF TYKGKSLEIQKPA\VAPRHGLQSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDG TGWASKQE QSDPK SSDASTAQPPESQPLPASQTPASNQP KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTWRDGGGRGPDELE GPDSKLHHGHDPRGGLQPSGPPQFP PYRGMMPFMYPPYLPFPFPYGPQG PYRYPTPDGSRFPRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEVDYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPPEADGKKGNSEPNSEPTPKTA WAETSRPPETEGPPAPKPLPPGDY PDRGGPPCKPPAPEDEDEAWRQRR KQSSSEISLAVERRRRREEERRM QEERRAACAEKLKRLDEKFGAPDK RLKAEPAPPAAPSTPAPPAVPKE LPAPPAPPASAPTPEPEEPAQAP PAQSTPTGVAAATLVSGGGSTSS TSSGSFEASPVPEQLPSKEGPEPPEE VPPPTTPPVKVEPKGDGIGPTRQPP SQGLGYPKYQKSLPPRFQRQQEQ LLKQQQHQWQQHQQSAPPTVPV PSPQPVTLGAVPAPQAPPPPKALY PGALGRPPPMPPMNFDPRWMMIPP YVDPRLQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEPFDRHAPAMLR ERGTPVDPKLA WVGDVFTATPAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PRPLTSPRLRQAADDDKGMRSCTPP VPPPPPYLASYPGFPENGAGPPISR FPLEEPGPRPLPWPPGSDEVAKIQT PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRRESRTETRWGPRPG SSRRGIPPEEPGAPRRRAGPIKKPPPP TKVEELPPKPLEQGDETPKPPKPDPL KITKGKLGPPKETPPNGNLSPAPRL RRDYSYERVGPTSCRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQRGSET GSETHESDLAPSDKEATPKEGTLT Q/VPLAPPPPGAPP\SP\APARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPQ VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPEEALTTVTVPAPPRAA AKSPDLNQNSDQANEWEWASESS DFTSERRGDKEAPPVLLTPKAVGT PGGGGGGA VPGISAMSRGDLQRA KDLSKRSFSSQRPGMERQNRPPGPG GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWSPKNSRPPPEERPPGLP LPPPPSSSAVFRLDQVIHNPAGIQ QALAQSSRQGSVTAPGGHPRHKP GPPQAPQGSPRPPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSPFPKRRERPPRKPELLQEESLP PPHSSGFLGSKPEGPGQAESRDTG TEALTPHIWNRLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKRPGGSSPLNAVPCGP PGSEPPRRPPAPHDGDRKELPREQP LPPGPIGTERSQRTDRGTEPGPIRPS HRPGPPVQFGTSDKDSLRLVVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLD SGHCVPPESSS GQRLYPEVFYGSAGPSSSQISGGA MDSQLHPNSGG/FRPGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSLQVRQDLPS PSDFYSTPLQPGQSGFLPSGAPAQ QMLLPM/VDSQLPVVNFGLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVLP*LARPPVYF\GRTELHP VNIKPRDF\QKLSSNLGGPGSSRTP PTGRRPSSLSFSGLNSRLQSQRLS NLTSGVFRNQAASTFYQAGLPHPD ALRWIPKPWERTG\RPPR\DGPSRR\A AEEP\GSRGDKEP\GLPPPR
5201	10698	A	5516	2	119	
5202	10699	A	5517	1	325	FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSDSPASASSSFTIHVAPLP

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						QLRHY*IFYDGTSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI
5203	10700	A	5518	228	481	QFFRNTIFF*DRVSLLLPKLECNSAIS AHHNLCLPGSSDSPASASRVAGITG TCHHTRLL\FVFLVETGFYHVSQSG LELLTSGD
5204	10701	A	5519	175	431	LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVCFF*DRVSLLLPRLECN GPISAHRLHLPDSSDSPASAYIKGF VRQLSHEE
5205	10702	A	5520	257	453	TKGGGYTQRTAIQFILFIYLFY*DG VSLLLPRLE*NGAISAHCNHLPGSS DSQKKTCKNFCTQ
5206	10703	A	5521	277	1230	ISFHLSTFGAPSTFFFEFMEFSLLLPR LECNGAISAHRNLRLPGSSDSPASAS PVGWDYRHVHPRSANFVFFFSRDG VSPCWSGLVSNRPQMIPPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCPSWSPCLKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLQPSTPEIKHPPASASQSS WDQRHAPHLANFYFYF*FFETES\ HSVTRLECSGAILAHCNCLPGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSLDLVICLPR PPKVLGLQDVSHHRPAYF
5207	10704	A	5522	1	467	FFFLF*EGVSLLLPRLECSGAISA/HC NLHLPGSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPPE YL VAGFTGMRHHTRLFFFAFLVET GFHPC
5208	10705	A	5523	293	681	QGTILIGLCPFDITPAIVDILLAFWHV RCPRTVSCFCKKVLLV*NFFFFFF FFFETESVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRRHA WPIFVFLVETRFHHVGQAGLELLTS GD
5209	10706	A	5524	274	321	
5210	10707	A	5525	2	733	
5211	10708	A	5527	1	3555	MHYVLNSSSMETFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPIWGCENPAQ MGCPPVGKADRCGLLANSATCEKG MFCHADLVGITPTVFPSPHPRCKTTA SAKLACQQDQVDLDRQSLSSIDKNPS ERGQSQLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAHEMVAAQQDTLDADIHI ETEDQGMKYMSQHLFKLLDCLQ ESHFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQRLLTVCSE ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFAHASMYYPYLCEI

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						MQFDLPELRAVLRKFFLRIGVVYKI WPEEPSQARCRAILPGFECEAERRQ ERVVPATVRGWGSLRFCIPTSSYN KCLLNMYCVPDPIAMELSDANLQT LTEYLKKTLDPDPAIRRP AEKFLESV EGNQNYPLLLLTLEKSQDNVIKVC ASVTFKNIKRNRWIVEDEPNKICE ADRVAIKANIVHMLSSPEQIQKQL SDAISIIGREDFPQKWPDLLTEMVN RFQSGDFHVGVLRTAHS LF KRYR HEFKSNELWTEIKLVDAFALPLTN LFKICDNaALYAQKYDEEFQRYLPR FVTAIWNLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGS DIDTRRRAACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKKHDAAIYLVTSLASK AQTQKHGITQANELVNLTEFFVNHIL LPDLKSANAIMRSFSLQEAIIPIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEEL FLVFTEILQNDV/PSESVDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KK\MFGMVLEKIIPEIQKVS NVEKKICAVGITKLLTECPMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFS QLAFAGK KEHDPVGMVNPNKIHLAQLSHKL STACPGRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPAPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS
5212	10709	A	5528	1	4611	
5213	10710	A	5529	58	3051	CQLRSAAGVPSSVSVPDPIAMEL SDANLQTLTEYLKKTLDPDPAIRRP AEKFLESVEGNQNYPLLLLTLEKS QDNVIKVCASVTFKNIKRNRWIV EDEPNKICEADRV AIKANIVHMLSS SPEQIQKQLSDAISIGREDFPQKWP DLLTEMVNRFQSGDFHVGVLRTAHS LF KRYRHEFKSNELWTEIKLVDAF ALPLTYL F KATIELCSTH ANDASALRILFSSLILISKLFYSLNFQ DLPEFFEDNMETWMNMFHTLLTLD NKLLQTDDEEEAGLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEEYIRRD LEGSDIDTRRRAACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKKHDAAIYLVTSLASKAQTQKH GITQANELVNLTEFFVNHILPDLKSA NVNEFPVLKADGIKYMIFRNQVPK EHLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTA AEIAP FVEILLTNLFKALTLPGSSENEYIMK

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						AIMRSFSLQEAIIPIYPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEELFLVFTEILQ NDVQEFIPYVFQVMSLLLETHKNDI PSSYMALFPHLLQPVLWERTGNIPA LVRLQAFLEGRSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPEVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFNLICYKYGALA LQEIFDGIQPKMFGMVLEKIIPEIQK VSGNVEKKICAVGITNLLTECPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSQLAF AGKKEHDPVGQMVNPNKIHLAQLS HMLSTACPRVPSMVSTSLNAEAL QYLQGYLQAASVTLL
5214	10711	A	5530	1	396	
5215	10712	A	5531	1	1095	
5216	10713	A	5532	1	1077	
5217	10714	A	5533	1	986	
5218	10715	B	5534	214	975	MEVKTARELRDECTSLSSRFQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVKRPNLRVIGVP ESDGENGTKLENTLQDIIQENFPNL ARKANIQIETQRMPPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPINFILKEKNFQPRISYPALKSFIS EGEIKSFTDKQMLRDFVTTTPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG*
5219	10716	A	5535	3	1135	
5220	10717	A	5536	1	1023	
5221	10718	A	5537	2	2747	LHLWGQGTDKQKDSSNLCRLKCPC LTALKRAVVLPARSWRSENGQTAS SKGKLTTRKDIYTENPSVHHHHQRP KVDKTTKMGKKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLFDDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNTEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVSAMEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNILKE KNFQPRISCPALKSFISEGEIKYFTDK QMLRDFVTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKEVEN FEKNLEECITRITNTEKCLKELMELK TKARELREECRLRSRCDQLEERVS AMEDEMNMKREGKFREKRIKRNE QSLQEIWDYVKRPNLRLIGVPESDV ENGTLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATTRNLIV

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						RFTKVEMKEKMLRAAREKGRVTH KGKPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPAEEELLKE ALNMERNNRRTTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFSSA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRICKLTQNCTT TWKLNLLNDYWVQNEMKAEIK MFFENNENKDDTTYQNLWDTFKA VCRGKFIALNAHKRKQKRSKTDTLTS QLKELEKEEKHIQKLAEGKK
5222	10719	A	5538	99	432	
5223	10720	A	5539	100	732	
5224	10721	A	5540	242	1300	NPRRSGHSLEAKLRDSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTNRTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPSNGLSLEADITAKLDSPRVTVAQ LDWDVATVHQLSAFQPDVVIAADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAVTVRNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCAQMHPQQ PLPAHRDTPNPVPVHVGQPVNYRA NKQAST
5225	10722	A	5541	3	167	
5226	10723	A	5542	2	378	
5227	10724	A	5543	3	359	
5228	10725	A	5544	15	347	
5229	10726	B	5545	141	371	DFGYFYGSSYVAAPDSSRTPGLSRS RDGLLVAKLDLNLCCQVNDVWNF KMTGRYEMYARELAEAVKSNYSPT IVKE*
5230	10727	A	5546	1	1154	MAGAEWKSLEECLEKHLPLPDLQE VKRVLYGKELRKLDLPREAFEAAS REDFELQGYAFEAEEQLRRPRIVH VGLVQNRIPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHVP FQTQFGRIAVNICYGRHHPLNWLM YSINGAEIIFNPSATIGALSESLWPIE ARNAAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSRDGLLVAKLDL NLCCQVNDVWKFKITGRYEMYAR ELAEAVKSNYSPTIVKE
5231	10728	A	5547	424	604	
5232	10729	A	5548	52	318	
5233	10730	A	5549	3	148	
5234	10731	A	5550	258	458	

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5235	10732	A	5551	1	217	
5236	10733	A	5552	246	361	
5237	10734	C	5553	69	254	MDHLYNXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXEIQFXXXXERERNKN PFPAGDDIISRGVGGQ*
5238	10735	A	5554	32	169	NPVPPYPLCPALVFFLLIYLLIY*PS PLLMSAPAGKGFLFLSL
5239	10736	A	5555	417	490	
5240	10737	A	5556	2	121	
5241	10738	A	5557	69	398	
5242	10739	A	5558	2	732	GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRRPGAP ESKCSRGCPHSAFSILVTLVVQA INAYFLYH*HGRDLKLTVPQNLQ LENLARMKLPKPPKPVSKMRMATP LLMQALPMGALPQGPQMNAATKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSGLGVTKQDLGPVPM
5243	10740	A	5559	2	359	
5244	10741	A	5560	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5245	10742	A	5561	1724	1941	AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPG\SQSDSPAS ASWVAGITGACHHARHEWNFKC
5246	10743	A	5562	2	362	
5247	10744	A	5563	138	236	
5248	10745	A	5564	1	278	
5249	10746	A	5565	80	591	RGCKREGLSMSSLIRRVISTAKAPG AIGPPTVQAVLVDRTHLHFRDQIG HGPLPSWTSCLPGGVAGRSLNKLL KNMGEIPESLPGCDFTNVVKTTCSS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRAIEIAVAIQ GPLTTAFILSGDPCCVVWDC
5250	10747	A	5566	141	340	
5251	10748	A	5567	209	386	
5252	10749	A	5568	1	346	
5253	10750	A	5569	160	391	
5254	10751	A	5570	101	332	
5255	10752	A	5571	500	752	
5256	10753	A	5572	2	82	
5257	10754	A	5573	3	165	
5258	10755	A	5574	1	219	
5259	10756	A	5575	1	327	
5260	10757	A	5576	2	160	
5261	10758	A	5577	1	189	QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRVSLP LPPKTQGHPhDLDP
5262	10759	A	5578	2	224	
5263	10760	A	5579	1	1392	
5264	10761	A	5580	1	1272	PGCGRPRAFSLNIADIEEKRGTSHF VRQTPSPSPNNL*YLIYRRYRQFHA

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						LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQSG CLWSLSTQSQPSVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPRTRKV*VTPSWAST WPEAAPRAEVTAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRCLKVFKILKDFPEEDDPTNWL CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPLTSPSHGSLSHSKAPSGSQ MSHNAVTSHQRPGWPGPHSPFPH PTLKDLELTR*GAGNGAGELDTLD AEGDLVRLSDEDVALMVRQARGL PSQKRLFPWKLHITQKDNRYVYNT MP
5265	10762	A	5581	437	728	
5266	10763	A	5582	570	1648	TQPGTGWARLSTCSLGPSPPTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGTSHFVFVIEVKTKGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPAKVYVGVKQEIEM RIPALNAYMKSLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRPR TRKVKSVSPQNSVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFPLSFVKILK DFPEEDDPTNWLRCYYYEDTISTIK DIAVEEDLSSTPLLKDLELTRREFQ REDIALNYRDAEGDLVRLSDEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNRYVYNTMP
5267	10764	A	5583	1705	2233	
5268	10765	A	5584	1	354	
5269	10766	A	5585	270	390	
5270	10767	A	5586	3	132	
5271	10768	A	5587	234	362	
5272	10769	A	5588	1	402	
5273	10770	A	5589	2	509	
5274	10771	A	5590	3	1607	SPRPGIPRCFHLVISTEHRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTFSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDNKNTLYLQ MGSRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQTTVTVSSASP TSPKVFPPLSLCSTQPDGNVVIACLP PGLLPPGATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQGCDCAL LPSSLNSTYPISLNSTYPISLMLPPPT VTAPTGPSKDLFLGSKATFTCTLP LARDASGVFTWDALKVGKSAVQG PI*RRDLCC/CYSVASSVLPGCAEAH GTHGEGPSLWHCWYPESKDPA*PP TLFKIRGNTFPGPRFHL\PPPSEGAG PWNELVTL\TCLGIGLSAPRMLLVC

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						WVAGGHRSLLEKYLTLWASRQKP SQGTTTFAVTSILRVAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY
5275	10772	A	5592	2	315	
5276	10773	A	5593	245	455	
5277	10774	A	5594	1	2863	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWDG VSKKAPRHHLSVPCTRPREARQEA DSTSRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPQEQALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFLKTPFMVNSVLA GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGRVMVEQSE KLVGVLEASRLWDNMRKLGECTEE AHQMTDHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPALR\VEPFS\ EDEVNLLYVAVTRAKKRLIMTKS LENILTLAGEYFLQAE\TSNVLKTG VVR\CCVG\QCENNAIPVDVLTMMK L\PIY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF
5278	10775	A	5595	3	613	
5279	10776	A	5596	2	1419	PPHLLSSPFVAAPRARATAGAF TLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGDSDLQLERI NVYYNEATG\GNYVPRAVLV DLEP GTMDSVRSGPFGQIFRPDNFVFGQS GAGNNWAKGHYTEGAELVDVAVLD VVRKEAESCDLQGFQLTHSLGGG TGSGMGTLISKIREFPDRIMNTFS VVPS\PKCQDTVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSATMSGVTTCLRF PGQLNADLRKLAVNMVFPRLHFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MPAFAPLTSRGSQQYRGLTVPELTQ QMFDANKMMAACDPRHGRYLTV AVFRGRMSMKEVDEQMLSVQSKN SSYFVEWIPNNVKTA VCDIPPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGE GMDMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEEEVA
5280	10777	A	5603	1	384	
5281	10778	A	5604	185	700	
5282	10779	A	5605	1	414	
5283	10780	A	5606	3	138	
5284	10781	A	5607	1	433	NNPDFKAGV/MALPTL/LQIQRHDD YLVMLKAIRILVQERLTQDAVAKA NQTK EGLPVALDKHILGFDTGDAV LNEAAQILRLHIEELRELQTKINEA IVAVQAIHFVHWVWVSKCHILGGGS PENWVCSRDLPLLIAFFFNKV
5285	10782	A	5608	1	459	
5286	10783	A	5609	118	375	VAVVQIIFLPVFIAEKYKDLVPD NSK TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLKIA IRILVQERLTQD
5287	10784	A	5610	344	513	
5288	10785	A	5611	3	116	
5289	10786	A	5612	3	869	HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPA GFNCKDETEFRNFIVW LEDQKIRHYKIEDRGWNLRIHSSDW PK\FFEKYLRDVNCPFKIQDRQEAI DWLLGF AVRPEYGDNAEKYKDLV PDNSK\TADNAPKNAEPWINLDVN NPDFK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQE\RLTQDA\VA KAKSNKKRALPVALAQTHILGFD\T GDASSLMKLEILRIACTYEELRELT DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL
5290	10787	A	5613	298	403	
5291	10788	A	5614	3	611	
5292	10789	A	5615	192	340	
5293	10790	A	5616	187	361	
5294	10791	A	5617	187	385	
5295	10792	A	5618	2	340	
5296	10793	A	5619	1	702	EKYIQLVRQRALEGALGNTIYKSQ TAKGTPQETEGTSSGSKSNVRSGKR VPSGRMV/IHSHFPAEVT*E*TRVH WIWQS*COGESWKQVPFLCHSGS* RNALL\CLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLYNKKGRQAVGQVAK QQVASLETNDPNLGIQATNERLFV LTTKNLFLIKVNTEN
5297	10794	A	5620	3	357	
5298	10795	A	5621	1	1926	
5299	10796	A	5622	1	362	LQTSDEETGFSCLEFYVCAATSFVL VCIINNWSCKAD*DTRWTFRIKIGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						T/SVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHFP
5300	10797	A	5623	247	533	KSFPGWQTYFSCGWVGCGLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSGWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRRR
5301	10798	A	5624	128	667	
5302	10799	A	5625	12	3756	VPRLSRPSPSQSSPTPTTARGSETRP RRRRQQQLQHHLHPPAMEDLDQSPL VSSSDSPRPQPAFKYQFVREPEDEE EEEEEEEEDEDEDLEELEVLERKPA AGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPPPASVSPQAEPVWTP PAPAPAAPPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAASFKEHEYLGNLSTVLPT GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIIVKNKDEEEKLVSNNI LHNQQELPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDKKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFLLGDPSTSE NKTDEKKIEEKKQIVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLT KV TEEVVANMPEGLTPDLVQEACESEL NEVTGTKIAYETKMDLVQTSEVMQ ESLYPAAQLCPSFESEATPSPVLPD IVMEAPLNSAVPSAGASVIQSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKPENINAALQET EAPYISIACDLIKETKLSAEPAPDFSD YSEMAKVEQVPDPHSELVEDSSPDS EPVDLFSDDSIQVDPQKQDETVMLV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSDDSSPIIIDEF PTLISSKTDSFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSKNGSATSKV LLLPPDVSALATQAEIESIVKPKVLV KEAEKKLPDTEKEDRSPSAIFSAEL SKTSVVDLLYWRD/KKT/GVVFGA/ SAVFLLSLTVF/SIVSVTAYIALAL LSVTISFRIYKGVIAIQKSDEGHFP FRAISGNL/ESCLYLRELGSGRYSNS/ ALGSMWNCTVKGNFRAPSFSSWM DLVDSL/RSFAVLMWVFTYVVGCLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQUDHYLGLANKNVKDAMA KIQAKIPGLKRKAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5303	10800	A	5626	2	436	RRQFEERQQEMEHVYELLENKMQ LQESRLAKNEAARMAALVEAEKE CNLESEKLGVTKNWEDVPGDQV KPDQYTEALAQDK*VPSVLFLRL SFAHSQGIQQLSCSLRT/RQ*ELHY F*DFMGPQPKTFFSGLNFQWYPL
5304	10801	A	5627	3	309	
5305	10802	B	5628	454	645	MTCKKENFSLKLLIYFLEERMQQK YEASREDIYKRNTTELKVEVESLKRE LQDKKQPSGLKPWA*
5306	10803	A	5629	1	294	
5307	10804	A	5630	14	228	
5308	10805	A	5631	201	350	
5309	10806	A	5632	262	626	PSARPHCFGLEAMHARSLPCWNC SRLLILAFS/WGSE/CCTRKPRIIDV VYNASNNELVRTKTLVKNCIVLIDS TPYR\QWYESH\YALPLGRKKGAKL TPEEEILNKKRSKKIQKKYDERKE NAKISSLEEQFQQGKLLACIASRPK QCGRADGYVLEGKELEFYLRK\IK RKRQINPCFVFTHGNGRVYCFVPTF MLPEYMTVFS AIFPCPAKLIWGGGL QPLALTSASYCPETGSPHC
5310	10807	A	5633	3	452	
5311	10808	A	5634	26	477	NSTDSETHHGARLLPDKTNVKA WGKVGAGAHAGYGAELERMFLSF PTTKTYFPFDLASHG\SAQVKG/HT GKKVADALTNAVAN\DDMPNAL SALSDLHAHKLRLVDPVNFKLLSHCL AGGPWAAHLPRPSSTPGGATPSLEQ SSWASC
5312	10809	A	5635	1	147	
5313	10810	A	5636	1	503	AAAAARAAGTAGPWRSAARLPALP ASSLGAAAMAASAKRKQEEKHLK MLRDMTGLPHNRKCFDCDQRGPT VNMTVGSFVCTSCSGSLRG*NPPHR VKSISMTTFTQGEIEFLQKHGNEVC PPEQAKVVASVHASISGSSASTSS TPEVRPLKSLLGDSAPTLHLN
5314	10811	A	5637	272	360	
5315	10812	A	5638	1	1934	WRRRRRLSRLCRLVWPVSPRTTAP GPRRAQYSQAAAAGSGAGGARRR RAAAAAARAAGTAGPRRSAARLPA LPASSLGAAAMAASAKRKQEEKHL KMLRDMTGLPHNRKCFDCDQRGPT YVNMTVGSFVCTSCSGSLRGLNPPH K/VGKSISMTTFTQGEIEFLQKHGNE VCKQIWLGLFDDRSSAIPDFRDPQK VKEFLQEKYEKKRWYVPPEQAKVV ASVHASISGSSASSTSTPEVKPLKS LLGDSAPTLHLNKGTPSQSPVVGSR QGQQQEKKQFDLLSDLGSDIFAAPA PQSTATANFANFAHFNHAAQNSA NADFANFDAFGQSSGSSNFGGFPTA SHSPFPQPTTGGAASVNFANFAHFD NFPKSSADFGTFNTSQSHQTASAV SKVSTNKAGLQTADKYAALANLDN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IFSAGQGGDQGSFGTTGKAPVGSV VSVPSQSSASSDKYAALAE LDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSVPAPFGRTPTSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQAAPQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTGGQFTGSSSTN PFL
5316	10813	A	5639	1	307	
5317	10814	A	5640	957	3132	GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHA EKQAR *PLGPWCSRRKKKGAE EEPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPYYSR LAIPAAQLVLPYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQQLQYVERYG KRLKAKNLMYKQILYLLEKFVAV LGGNIKQNPNTQSLSQTGTELKTIN DFLFQSQIDNINLFKVCVPSAPQMK HGHCR LNPKLVTOISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTEALAAP ADESQASTLRPASPLMHIQGF LAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLACAGVEAERVVE FSCGHVIPPDNILPLVICSGISNQPLE FTFQKREL PQMMDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGR LAARKKIFQEPKSAHQV EQVLLAYSRCIQACGQERGQVTGA LLSVVGGMSEGINFSDNLGR CV VMVGMPFPNIRSAELQEKMAYLDQ TLPRAPGQAPPGKALVENLCMKAV NQSIGRAIRHQKDFASVLLDQRYA RPPVLAKLP AWIRARVEVKATFGPA IAAVQKFLQVYGTSLPLNHL SKLQD TFYPNTSNYAKGR
5318	10815	A	5641	1	1668	
5319	10816	A	5642	947	2782	GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHA EKQAR\ KKKGAE EEPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYYSRLAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQQLQYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSQTGTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQP RTTEALAAPADESQASTLRPASPLM HIQGF LAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGTMQPVSDFRQQLACAG

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						VEAER\VVEF/SCGHVIPPDNILPLVI CSGISNQPLEFTFQKRELPMIFQEP KSAHQVEQVLLAYSRCIQACGQER GQVTGALLSVVGGKMSEGINFSD NLGRCVVMVGMPPFNIRSAELQEK MAYLDQTLPRAPGQAPPKALVEN LCMKAVNQSIGRAIRHQKDFASVV LLDQRYARPPVLAKLPWIRARVE VKATFGPAIAAVQKFHREKSASS
5320	10817	A	5643	1143	3233	GEEPLWQGCAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAEKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYRSRLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGS\ LCQAHSQQLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIQ NPNTQSLSQGTGTELKTINDFLFQSQI DNINLFKVQRYCEKSMISRKLFQFT ERYGAVFSSREQPKLAGFQQFLQSL QPRTEALAAPADESQASVPQPASP LMHIEGFLAALTANQDGRVILSRQ GSLSQSTLKFLLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLAC AGVEAERVVEFSCVFGPSLALTGH VIPPDNILPLVICSGISNQPLEFTFQK RELPMMDDEVGRILCNLCGVVPGG VVCFFPSYEYLRQVHAHWEKGGLL GRLAARKKIFQEPKSAHQVEQVLL AYSRCIQACGQERGQVTGALLSV VGGKMSEGINFSDNLGRCVVMVG MPPFNIRSAELQEKMAYLDQTLPR PGQAPPKALVENLCMKAVNQSIG RAIRHQKDFASIVLLDQRYARPPVL AKLPWIRARVEVKATFGPAIAAV QKVSPTFFFLRASPPRDHISHCLLSA QFHREKSASS
5321	10818	A	5644	3	744	
5322	10819	A	5645	40	126	
5323	10820	C	5646	187	366	MDERDSHCPYLLSSETTAKGTGLAE SAGKEDPVELDSSLEARVRRRRPST SMPLTSAPC*
5324	10821	A	5647	1	382	TADCAKPVPLAVVSLDSRYGQWES RSSIHA\VTN*ASSSSSSSSSS\FSR\V YPRFIEFIHFDIQSTGQ/RITSR*HPPR/ DLRDALF*LNSLIPLVRTSSKSAARR RP\GEAPRGTA VPGADPAGGTRPR
5325	10822	A	5648	3	684	QGPRAALGALFPCWAPGKYVHGV RAKHPRATARAPRGSP/LPPHRVSE KTIRVVVFHRRPAGPADPAPGPSRG HRGGAG/EPPTYSTPLMSLHRARLE SSSTGSSFPADSAKPVPLAVVSLDSR *GQWESRSSIHA\VTN*ASSSSSSSS SS\FSR\VYPRFIEFLHFDIQSTGQ/RIT SRQHPPR/DLRDALF*LNSRIPLVRTS SKSAARRRP\GEAPRGTAAPGADPA GGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5326	10823	A	5649	2	331	
5327	10824	A	5650	3	340	
5328	10825	A	5651	1	94	
5329	10826	A	5652	2	496	ASMGCSPLLSLLVGAWLKLG H*TAGHAGGAGKGDGALRPGGREG EAPLPASGMRLQPPAGEVALGAQG ASPPCAFNFLWNLSIQQLRRVRG QGCSWRWLVLAQAIEELLGDPALV PTRRQPVGRAAPAASSLCCADPA GREVTQVVVVQVVVNSSS
5330	10827	A	5653	3	997	
5331	10828	A	5654	3	131	
5332	10829	A	5655	112	289	
5333	10830	A	5656	35	5228	LDPLGRMVMGIFANCIFCLKVKYLP QQQKKKLQTDIKENGKFSFSLNPQ CTHILDNADVLSQYQLNSIQKNHV HIANPDFIWKSIREKRLLDVKNYDP YKPLDITPPPDQKASSEVKTEGLCP DSATEEEDTVELTEFGMQNVEIPHL PQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLDD GMETRRQFAIKKTSSEDASEYFENYI EELKKQGFLREHFTPEATQLASEQ LQALLLEEVMNSSTLSQEVSDLVE MIWAEALGHLEHMLLKPVNRISLN DVSKAEGILLVKAALKNGETAEQ LQKMMTEFYRLIPHKGTMPKEVNL GLLAKKADLCQLIRDMVNV CETNL SKPNPPSLAKYRALRCKIEHVEQNT EEFLVRKEVLQNHHSKSPVDVLQI FRVGRVNETTEFLSKLGNVRPLLHG SPVQNVGILCRGLLPKVVEDRGV QRTDVGNLGSIGYFSDSLSTSIKYSH PGETDGTLLICDVALGKCMDLH EKDFSLTEAPPGYDSVHGVSQTASV TTDFEDDEFVYKTNQVKMKYIHKF SMPGDQIKDFHPSDHTLEEYRPEF SNFSKVEDYQLPDAKTSSSTKAGLQ DASGNLVPLEDVHIKGRIDTVAQVI VFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHIVGEIKEKEEAQ QEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITEL SILG TVGVFFMPATVAPWQQDKALNEN LQDTVEKICIKEIGTKQSFSLTMSIE MPYVIEFIFSDTHELKQKRTDCKAVI STMEGSSLDSSGFSLHIGLSAAYLPR MWVEKHPEKESEACMLVFQPDLD VDLPDLANESEVIICLDCSSMEGVT FLQAKEIALHALSLVGEKQKVNIIQF GTGYKELFSYPKHITSNTAAEFIM SATPTMGNTDFWKTLYLSLLYPA RGSRNILLVSDGHLQDESLTLQLVK RSRPHTRLFACGIGSTANRHVLRIL SQCGAGVFEYFNAKSKHSWRKQIE DQMTRLCSPSCHSVSVK WQQLNPD APEALQAPAVPSLFRNDRLLVYGF IPHCTQATLCALIQEKEFCTMVSTTE

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						LQKTTGTMIHKLAARALIRDYEDGI LHENETSHMKKQTLKSLIKLSKE NSLITQFTSFVA VEKRDENESPPDI PKVSELIAKEDVDFLPYMSWQGE QEAVRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLP AFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPPRQFDASQF SQGPVPGTCADWIPQSASCPTGPPQ NPPSAPYCGIVFSGSSLSSAQSAPLQ HPGGFTTRPSAGTFPELDSPLHFSL PTDPDPIRGFGSYHPSAYSPFHQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGRCPVFAF QSSDTESEDELSEVLQDSCFLQKCDT KDDSI PCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEDGFWKLTPELG LILNLNTNGLHSFLKQKGIQSLGVK GRECLLDLIATMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNPWAFEAI KQASEWVRRTGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPHRLV HYSQG
5334	10831	A	5657	10	82	
5335	10832	C	5658	189	396	MVHPAGPLASQXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXELWLHHLSSSS *
5336	10833	C	5659	54	485	MXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXRPEDFATYYCQ QNYISPLTFGGGKVEIXRTVAAPS VFIFPPSX*
5337	10834	A	5660	5	417	
5338	10835	A	5661	3	398	
5339	10836	C	5662	12	451	MXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXFFSYYCQ QSYSVPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQ*
5340	10837	A	5663	3	679	AWWNSETPAQLFLLLLWLPYTS EIVLTQAPGTLSPGERATLSCRAS QTIGSTYLA WYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSS SSSSSSSSSQYYTSPLTFGGGKTV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLN NFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYLSST LTLKADYEKHKVYA\CEVTHQG
5341	10838	B	5664	94	321	XDRVITTCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RSGTHFTFTISSLQPEDATYYCQQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YX*
5342	10839	A	5665	3	764	AWLESISPTMRVPAQLLGLLLWIP GSVADIMMTQTPLSLVSPGQSASIS CKSSQSLHSDGKTHVYWYLQKPG QSPQLLIYEVSSRFSGVPDRFSGSGS GTDFTLKITRVEAEDVG VYYCQQY NSYLLFTFGPGTKVDIKRTVAAPSV FIFPPASDEQLKSGVTASVVCLLNNFL FPARRAKVQWEGGINALQSGNSQEC VTE\QDSKGSTYSL\SSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGEC
5343	10840	A	5666	1	534	RRPRREPWKQRSFSSSCYS/ELPDT TGEIVLTQSPGTLSPGERATLSCR ASQSVSNYYLA WYQQKPGQAPRLL IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVYYCQQYGGSPPMY TFGGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW
5344	10841	A	5667	184	621	LHECISVLFPSIDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNYYLA WYQQKPGQPPRLIYDASNRTGIP ARFSGSGSGTEFTFHSAACSLKDF CSLFTVQQLINWASDSPLGQGTSL GD/IKRTVAAPSVFIFPPSDE
5345	10842	A	5668	156	364	
5346	10843	A	5669	2	2143	SSDGSWWTGFQWREWQAGRSVN SWDNPKEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPLVIHRQTGSGEDLQQ TPTDLQLRVLTIRKTNKQKGHPHQ NPISRRQEITKIRAEKKIETQKPFK KINESRSWFEKINKIDRLARLIKK KIEKNQIDAIKNDKGNITTNPTIQT TIREYYKHL YANKLEHLEEMDKFL DIYTLPRLNQEEVESVNRPTGSEIE AIINSLPTKKSPGPDRFTAEL YQRYK EELVPFLKLFQSIEKEGILPNSFYEA SIILISKPGRDTTKKNFRPISLMNID AKILNKILANQIQQHIKKLIHHQV GFIPGMQGWFNILKSINVHHINRTK DKNHMIISIEAEKAFDKIQPFMLKT LNKLIDGTLYLTYLKIIRAIYDKPTA NIILNGQKLEAFPFTGTGRQGCPLSP LLFNIVLEALARAIRQEKEIKGIQLG KEDVKLSLFADDMIVYLENPVISAQ NLLKLISNFSEVSGYKINVQKSQAF YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNI PCSWIGRINIVKMAIL PKTLNQKFSYWFRVKNHYIHQRTFP LKETEFNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDREEGVSWCP GGP
5347	10844	A	5670	1	2781	
5348	10845	A	5671	1	2988	

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5349	10846	A	5672	1	3516	
5350	10847	A	5673	1	2850	
5351	10848	A	5674	1	2850	
5352	10849	A	5675	1	3087	
5353	10850	A	5676	1	3111	
5354	10851	A	5677	1	2742	
5355	10852	A	5678	1	3474	
5356	10853	B	5679	1	3264	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALLSKC KRTEITNCLSDHSAIKLELRIKNLTQ NRSTTWKLNQLNDYWAHNEMK AEIKMFFETNENKDTTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTSHSKASRRQEIT KIRAELEKETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITDPTTEIQNTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPIITGPEIVAIINSLPTKK SPGPDGFTAKFYQRYKEELVPFLLK LFQSIEKEGILPNSFYEASIIIPKPGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHHMISID AEKAFDKIQPFMLKTLNKLIDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAIPIK LPMFTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYQYQNRDIDQWNRTEPSEIT PHIYNLYLFDKPEKNKQWGKDSLLN KWCWENWLAICRKLKLDPLTPYT KINSRWIKDLNVRPKTIKTEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIREMQIK TTRYHLTPVRMAIHKSGNNRTW EYNILCSLVPLLCSSLWLHLDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSCAPRRI QGHLCVGSDDLTFMDDVAVILIDVS PF*
5357	10854	A	5680	1	3780	
5358	10855	A	5681	1	3290	MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEITNYLSDHSAIKLELRIKNLTQN RSTTWKLNLLNDYWIHNEMKAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IKMFFETNENKDDTYQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIATNPTEIQTITIREYYKHLN KLENLEEMDKFLDTYTLPRLNQEE VESLNRPTGAEIVAIINSLPTKKSPG PDGFTAESYQRYKEELVPFLKLQ SIEKEGILPNSFYEASIIIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQGWFI RKSINVIQHINRAKDKNHMISIDAE KAFDKIQQPFMLKTLNKLIGDGYF KIIRAIYDKPTANIIENGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLARAI QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNI PCSW VGRISIVKMAILPKVIYRFSAPIKLP MTFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSL NKWCWENWLAICRKLKLDPFLTPY TKINSRWIKDLNIRPKTIKLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAACKHMKKCSSSLAIRQMQIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLLSHHSALSATHNPTCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT
5359	10856	A	5682	1	3780	
5360	10857	A	5683	1	2877	
5361	10858	A	5684	1	3126	
5362	10859	A	5685	3	3244	
5363	10860	A	5686	1540	3288	SSSLHPWDARLVQYTQINKCNPAY KQSQRQKPHYQLEAFPLKTGT QPFMLKT/LYSIVLEVLARAIQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTKNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNI PCSW VGRISIVKMAILPKVIYRFSAPIKLP MTFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSL NKWCWENWLAICRKLKLDPFLTPY TKINSRWIKDLNIRPKTIKLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAACKHMKKCSSSLAIRQMQIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLLSHHSALSATHNPTCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT

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						IGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTT WEKIFTTYSDDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKHKMKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDCKLVLQPLWKS VWRFLRDLELEIPFDPAIPLLGIPND YKSCCYKDTCT
5364	10861	A	5687	1182	3406	YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFI P GMQGWFNIRKSINVTQHINRAKDK NHMIISIDAFAFDKIQQPFMLKTLN KLGIDGTIFYKIIRAIYDNPTANIILN G QKLEAFPLKTGTROGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSQYKINVQKSQAFLYTNNR QTESQIMSPLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSGVEGRINIVKMAILP/KELE KTTLKFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNQWQKDSLFNKWCWEN WLAICRKLKLDPFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLSFCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHKMKCSSSLAIREMQIKTTMRY HLTPVRMAIHKSGNNRCWRGCGE TGTLHCWWDCKLQPLWKS VWRFLRDLELEIPFDPAIPLLGIPNDYKS CCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMYYAAIK NDEFVSFVGTWMKLEIILSKLSQEQ KTTHRIFSLIGGN
5365	10862	A	5688	1	7578	
5366	10863	A	5689	16775	19999	KMIKGISPPIPQKYKTTIREYYKHL Y ANKLENLEEMDKFLDTYTLPRLNQ EEVESLNRSITGSEIEAIINSLPTK KSP GPDGFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYESSILIPKGRDT TKKENFRPISPISLMNIDAKILNKILA KRIQQHIKKLMHHDQVGFI P GMQGWFNIRKSINVIQHINRAKDKNH MIIS IDAEKAFDKIQQPFMLKTLNKL GID GTIFYKIIRAIYDKPTANIILNGQ KLE AFPLKTGTROGCPLSPLLFNIVLE VL ARAIRQEKEIKGIQLGKEEVKLSL FA DDMIVYVENPIVSAQNLLKLISNFS KVSQYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINTVKMAILPKVIYRF NAIPIKLPMPFFTELEKTTLKF IWNQ

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						KRARIASILRQKNKAGGITLPDFK LYYKATVTKTAWYQNRDIDQW NRTEPSEITPHIYNLIFHKPEKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKDKIDKWDLIKLSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYKAKKTNNPIKKWA RDMNRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLTPVRMAII KKSGNNRSWYFEKINKIDRLRLARLI KKKREKNQIDAINDKGDITTDPTET QTTTREYYKHLYANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAINSLPTKKSPGPDGFTAIFYHR YKEELVPLLLKLFQSIEKEVILPNSF YEASIIIPKPDRTAKKENFRPISLM NIDAKILNKILANRIQQHIKKLIHHD QVGFIQGMQGWFNIRKSVNVIQHIN RTKDKNHMII SIDAESFDKIQQHF MLKTLNKL GIDGSYLKIIRATYDKP TANILNGQKLEAFPLKTGTRHGCP LSPLLFNIVLEV LARAIRQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ
5367	10864	A	5690	78	308	
5368	10865	A	5691	1	611	GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQTWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLES LGQSELASRLTLNCQ NSYVEPHKIRDIPVTIMDVFDQSAL STEAKEEMVQA\YPNARRAHLKTG GNFPYLCRSAEGNLMVQIHLQFH GTKYAAIDPSMVSAEELEVQKGS GISQEEQ
5369	10866	A	5692	3	301	
5370	10867	A	5693	75	361	
5371	10868	A	5694	3	356	
5372	10869	A	5695	1	583	SPLAAKSPPSLHLE/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERNV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLPSPTESRHSSSIPPVSSP PEQKVGLYRRQTELQDKSEFSDVD KLAFKDNEEFESSFECVDQKQIEEQ KEEEKIREQQVKERRQR
5373	10870	A	5696	306	4412	RLMMAQSNMFTVADVLSQDELRLK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPRISIVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFPPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGFLMHFLKEL AEYHQAKESCNMETQTSSTFNDRDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQLRAEMCQKLF FKDTEIAKIKMEAKKKYEKELTMF

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						QNDFEKACQAKSEALVLEKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAELKQORVEAFELNQLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELLNFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLEPKGQL VTAGKGK*NCENVPFGIANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFVSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKAVHLQEELIATNSKKEELNQS VN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLLESRNENLRLLNRLAQ APELAVFQKELRKAIEAIVVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKSLTTQVADLKLQKQT QTALENEVYCNPKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQAERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLAEAFKNITSSSPERHIFGEDRVV SEQPQVGTLEERNDVVEALTGSE ASRLRGGTSSRRLSSTPLPAKARS\ ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHSLSIPPVSSPPEQKVGLY RRQTELDQKSEFSDVDKLA FKDNE EFESSFEFNSFNENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMPRQLEMGGSLSPAGDMSH VDAAAAAVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIIQQEQDQESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSKKMVQEGSLVD TLQSSDKVERHCIDPLWRTQQGGTI LEAETGSPDIEPASAFDLRLPSL
5374	10871	A	5697	3	721	
5375	10872	A	5698	3	265	
5376	10873	A	5699	2	216	
5377	10874	A	5700	3	268	
5378	10875	A	5701	2	465	
5379	10876	A	5702	1	196	
5380	10877	A	5703	2	213	
5381	10878	A	5704	1	438	LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESRFENLGV SSLGERKKLLSYIQRVLVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPF SHMFDG RFIPLARPEVKWTVCIHTVNSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5382	10879	A	5705	2	1925	
5383	10880	A	5706	330	590	
5384	10881	A	5707	3	139	
5385	10882	A	5708	2	126	
5386	10883	A	5709	1	157	
5387	10884	A	5710	85	489	EKPLRWDSHLSCMLCWQAGFEAEQ KVSGSSRKLAISSHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMPVAPHMG GPPMMPMMGPPPPGMPVGPAPG MRPPMGGHMPMPGPPVTRPPARP MMVPTRPGMTRPDR
5388	10885	A	5711	235	874	VVRRSGFLFCLFVFLSSMNSASVD GHLGCRFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYYQK\WMEK\QSQSL\DKTTAA FQQGKIPPTPFSAPPPAGA\MIPPPPK /SFGPPSPLV*MPKHPHMGPPFPW MPPMMPGSFLLGDGWPVG\PASGEL RPMPMG\GHYCQLIAWGPPMDVGPS CPFH*WCPLGPGMTRPDR
5389	10886	A	5712	2	406	FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLE\FELEA YSLSHNDYDGIKKLLQQLFLKAPVN TAELTNFLIQNHIGSVIKHTDVS*D SIDDMDDEDAFGFISLLNLPDRKGT QCGEQIQE
5390	10887	A	5713	3	379	AVERGVPHFPDSPVQRDEEEEKEVD TEDDDDDSDQEKDDDNALDEEV NIEF\EAYSLSYNDYDGIKKLLPQLFI AAPVNTAKLPDLLIQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN
5391	10888	B	5714	65	188	MWGFRIPADALIQRDEEEEKEVLNE DEDDDDSDKEKDEEDRX*
5392	10889	A	5715	3	365	
5393	10890	A	5716	3	356	
5394	10891	A	5717	1	168	
5395	10892	A	5718	281	422	
5396	10893	A	5719	1	107	
5397	10894	A	5720	3	291	
5398	10895	A	5721	1	1260	WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLNLGSYS SIQPEEYSSVVCEVVLQDLLAYVSS KHSYLRDLPPRQPQRVNSIDFVEL\ EHLQPDVLVHGSKELLDFITLLEG S/VYSYRGQKQKKVMLTVDAQAG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFOKS APSFVKISDLATHLEDKCSGVVLIK AQISELAFPITASQKIALNAHSSLKSI FSSLPNIVYTGCAKCGLELETDENRI YKQCFSCLPFTMKKIYYRPAIMTAI DGRHDVCIRVESKLIKILLNISADC LNRVIVPSSEITYGMVVADLFHSL AVSAEPCVLKIQSLFVLDENSYP LQ QDFSLLDFYPDIVKHGANARL
5399	10896	A	5722	122	390	TFCVRSGLLDFAFPEPWRWGEKWK

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						NWPESLEVWVLVLA VPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSASSPG
5400	10897	A	5723	605	902	
5401	10898	A	5724	116	470	
5402	10899	A	5725	1	9786	
5403	10900	A	5726	10996	13825	MLTLRTRRS DGKMKSGFILGLSRAR SSFPMTKKRATPGHCRDPLEGLHRF LKNILPVYDKSLWDFLKLDVTTSIG RRQHRLRVSTAFVYTKNPNNGYSFSIP VKVLADKFITPGLKLNLDLNSVLVM PTFHVPFTDLQVPSCKLD FREIQIYK KLRTSSFALNPLTLP EVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF TLPKSVSDGIAALDLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFS AEYEEDGKFEGLEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTSA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKL TIFKTEL RVRESDE ETQIKVNWEEEAASGLLTSKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEVWYQGAIRQ IDDIDVRFQKAASGTTGT YQEWKD KAQNL YQELLTQEGQAS FQGLKDN VFDGLVRVTQKFHMKVKHLIDSLID FLNFRPFQFP GKPGIY TREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISM YREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDPSIVGWT VKY YELEEKIVSLIKNLLVALKDFHSEYI VSASNFTSQLSSQVEQFLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIATKKIISDYHQQFRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMPYMK LAPGELTIIL
5404	10901	A	5727	3	182	
5405	10902	A	5728	2	221	
5406	10903	A	5729	577	722	
5407	10904	A	5730	3	176	
5408	10905	A	5731	1	496	LLGVAPSR AFQEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKT FIPGQ GNNAYVFP GVALGVIAGGIRHIPDEI FLLTAEQIAQEVFEQHL SQGRLYPP LSTIRDVSLRIAKVLDYA YKHNLD S YTPWKEAMNVQTV
5409	10906	A	5732	228	448	
5410	10907	A	5733	3	1877	EGEDRGLPRTMGAALGTGTRLAPW

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						PGRACGALPRWTPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDEKFMPIVYT PTVGLACQHYGLTFRPRGLFITIHD KGHLATMLNSWPEDNIKAVVVTDG ERILGLGDLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTTNEEL LRDPLYIGLKHQRVHGKAYDDLDD EFMQAVTDKFGINCLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAAALRITNNKLSNHVVFQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQDHPESNSLDEVVRLVK PTAIIGVAAIAEA\FTEQILRNMAF\ RRAPIIFALSNPPRKAECTAEKCYR VTEGPRGFFASG\SPF*GVLIWEMGK TFIPGGRGNNA\YVFPG\ VATG\ VIA\ GGIRHIP\DEIFLLDSRAKL PQEVSEQ HLASQGRLYPPLSTIRDVSLRIAIVL DYAYKHNLVSYYPEPKDEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV
5411	10908	A	5734	14	304	
5412	10909	A	5735	3	413	
5413	10910	A	5736	2	328	
5414	10911	A	5737	3	472	VTEFAKTCVADESAENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPPLRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDEL RD EGKASSAKQRLKASLQKFGERA F KA\VARLSQRFP
5415	10912	A	5738	1	2975	MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKL CATYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKLVNEV TEFAKTCVADESA*/ENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPPLRLVRP EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIAPELLFFAKRYKAFT\ ECCQAADKAACL\LPKLDEL\RD EG KASSAKQRLKASLQKFGKSF SK HGAVARLSQEVFPKLEFCQEV SQV *WTGL*PKFPHGNC\CHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TGRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVFPGACFLY

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						\DYARRAS*FTLFVPAEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCLEFEQLGEYKFQN A\LLVRYTKKVPQVSTPTLVEVSRN LGKVGSKCKHPEAKRMPCAEDYL SVVLNHLCLVHEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCKKADDKETCFAEEGKK LVAASQAALGLTPLGPASSLPQSFL LKCLEQVRKIQGDGAALQEKLCAT YKLCHPEELVLLGHSLGIPWAPLSS CPSQALQLAGCLSQLHSGFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTIWQQMEELGMAPALQPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRHLAQP
5416	10913	A	5739	132	918	
5417	10914	A	5740	59	335	
5418	10915	A	5741	219	642	KGWFLGAFHKLKTMKHLLLTGMG C/VF*VKSQGVNDN\EEGFFSARGHR PLDDKKREEAP\SLRPAPPISGRWAI RASSQPKQLATSKGK*ERKSPWIAG KVVFSRLDPDLG\VVCCSLQGCSVC QGGFFLTTRGKGPFQELVV
5419	10916	A	5742	1	359	
5420	10917	A	5743	1	322	
5421	10918	A	5744	2	862	FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNV\RFCLEGMEE SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGGKKPCITYGLRGICYFFI EVECSNLDLHSGVYGGSVHEAMTD LILLMEEHKL\YDDIDFIEEFAKDV GAQILLHSHKSHLHLDLLPVVVRLL GQALFHTAHFPDNPSSSKDILMHR WRYPSSLHGIEGAFSGSGAKTVIP RKVVGKFSIRLVPNMTPEVVGEQA CGAGTRESMSSLGYPSRAEDDSGLS ALPSQPQPFIYAT
5422	10919	A	5745	455	601	SLAICGSCPF\KTFTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK
5423	10920	A	5746	25	458	
5424	10921	A	5747	3	396	
5425	10922	A	5748	2	797	AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNKAYFKRYQVKFRRR\R KGKTDYYARKRLVIQDKNKYNTPT KYRMIVRV\TNRDIICQIAYARIEGD MIVCAA*CTPNLPKYGVKVG\LTNY AAA\YCT\GLLLAARLL\LNRF\GMDN \YEGQV\EVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TT\TGKNVFG\ ALKGM\LMGGLSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFNAEVRRKHI MGQKFADDLHCLIEEDENASKK
5426	10923	A	5749	172	333	
5427	10924	A	5750	2	282	SLSREVQRQMHLVFFSKNKLKAGY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADINAACKF VS/GQKSMAAGGNLGHPTLVDEL
5428	10925	A	5751	813	998	
5429	10926	A	5752	1	1418	MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTHLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAITVEC LRGDVDILMEFLNVTTAPEFRRWE VADLQPOLKIDKAVAFQNPQTHVIE NLHAAAYQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSLVAHAFV AESAVAGSAEANAFSVLQHGRVRL GHHVKSQGGQPPAHLHQ\AVAKA\T QQP\FDVSAFNASYSDS\GLFGI\YTIS QGHQLAGDCIK\AA\YNQVKTIA\QG NLSNTD\VQAAQEPS*KAGIP*WSV ESSE\CFLEEVVRVPRALVAGSYMPP VHSSFQOI\DSPKRGWGGAKMPDII NGGKRSFVSGPEVQWAASLENLGT LHLFV
5430	10927	A	5753	150	355	
5431	10928	A	5754	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGOASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5432	10929	C	5755	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5433	10930	A	5756	764	1079	KGVLFFFKTES\HSVAQAGV\QW CTLGSLQPP\PSRGSSDSPASARVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5434	10931	A	5757	213	383	
5435	10932	A	5758	1	981	
5436	10933	A	5759	124	354	
5437	10934	A	5760	2	646	CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRGTG PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGPLS QAFEYILYNKGIMGEDTYPYQGKD GYCK\FQP\GKAIGFVKDVANITIYD EEAMVEAVALYNPVSFAFEVTQDF MMYRTGIYSSTSCHKTPDK
5438	10935	A	5761	1	218	
5439	10936	A	5762	272	364	
5440	10937	A	5763	1	1956	
5441	10938	A	5764	105	533	
5442	10939	A	5765	292	568	
5443	10940	A	5766	1	279	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5444	10941	A	5767	3	352	
5445	10942	A	5768	375	485	TPGLK*FSLDLLNCWDYRCETVH LAEIAQVSEKQI
5446	10943	A	5769	3	221	
5447	10944	A	5770	793	1039	SFSFTFKMLSGRRRETFFFGGRFFWF VVVFFFLAGRGSFALVAQAGVQ WRDLRSLQPPPRGFRFFCLSLPGA CGPRYLGG
5448	10945	C	5771	33	334	MSDSGKSSPVAHSILWIWGRSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V*
5449	10946	A	5772	194	593	
5450	10947	A	5773	1	877	
5451	10948	A	5774	2	352	
5452	10949	A	5775	3	726	EQEVDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLS\VVNLQCLV\H/EK TPVSDRVTKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLSRGPEPVMCVA
5453	10950	A	5776	4274	5255	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFQHKDDNPNLPR LVRPEVDMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNILPKFNHLCCTHTHTHTLTLFST YLNDRDKTIMCKLSLIG*LÆSLEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
5454	10951	A	5777	15	218	
5455	10952	A	5778	141	318	
5456	10953	A	5779	1	290	TMSLNRLQEFGTSLVTLDAIPHILPE GDELLENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHQKPPRLQPPQHSVCQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5457	10954	A	5780	2	643	GTRLFEQLGEYKFQNALLIRYTKKV PQVSTPTLVEVSRNLGKVGSKCK HPESKKECPVQEDYLSRGSWNQLL CVCIE\KTPVKLTESPK\CTESLG*T GRPLLFSA LGKFDWKHYGFPKRSF NCLKTFHLSMAGFMAHFFEEGRRT NSRKTNWHLFELVETQGPRQKQKQ LKA\VMGGFAAFVEKCKKADDKET CFAEEGKKLVAASQAALGL
5458	10955	A	5781	1	135	
5459	10956	A	5782	1	330	
5460	10957	A	5783	247	434	
5461	10958	A	5784	140	2569	SGSPVLDPSEPQPLAAMHVIKRDGR QERVMFDKITSRIQKLCYGLNMDF VDPAQITMKVIQGLYSGVTTVELDT LAAETAATLTTKHPDYAILAARIA\V SNLHKETKKVFSDVMEDLYNYINP HNGKHSPMVAKSTL\DIVLANKDRL NSAIIYDRDFS\YNYFGFKTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNLLSERWFTHASPTLFN AGTNRPLSSCFLLSMKDDSIIEGY DTLKQCALISKSAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMLRVYNN TARYVDQGGNKRPGAFIAYLEPWH LDIFEFLDLKNTGKEEQARDLFF ALWIPDLFMKRVETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQNLGTIKCSN LCTEIVEYTSKDEVAVCNLASLALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAEQQLN KQIFETIYYGALEASCDLAKEGGPY ETYEGSPVSKGILQYDMWNVTPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNEIEPYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPDDLKQL YKTVWEISQKTVLKMAAERGAFID QSQSLNIHIAEPNYGKLTSMHFYGW KQGLKTGMYYLRTTPAANPIQFTL NKEKLKDKEKVSKEEEKERNTAA MVCSLENRDECLMCGS
5462	10959	A	5785	1	161	
5463	10960	A	5786	2	170	
5464	10961	C	5787	219	398	MSQESVILFYSVGMSLFLFLFRVVT NFTFFPLAVICIRASHLLACPLPSLS LPHQPTH*
5465	10962	A	5788	2	472	
5466	10963	A	5789	3720	5308	PLL PFLSPPHLTEVEGQGRMVGTEE TWSNCSGAFKPKCSPQPQICLVLP TRELAQQVQQVADDYGKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRLIDFLESGKTNLSRCTYLVLDET DKMLDMGSEPQIL*IGDPIRPDRQTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MWSATWPKEVRQLAEDFLRDYTOI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIFVETK RRCDDLTRRMRRDGPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSED YVHRJGRTARSTNKGTA YFTFTPGN LKQARELIKVLEENQAINPKLMQL VDHRGGGGGGGGKGGRSRYRTSSA NNPNLMYQDECRRRLRGVKDGG RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQGTGAAA YGTSSYTAQEYAGTYGASSTTSTG RSSQSSSQFSGIGRSGQQPQPLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK
5467	10964	A	5790	1	307	
5468	10965	A	5791	2821	5781	
5469	10966	A	5792	1	981	
5470	10967	A	5793	99	1023	NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDSL FNKWC WENWLAICRKLKLD PFLTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIKAKIDKW DLIKLSFCTEKEKTIRVNRQPTWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA KKT*KNAHHHMKKCSSPAIREIQI KTTMRYHLIPRMVIAKKSGNKGW RGCGEIGTVLH
5471	10968	A	5794	3	1218	
5472	10969	B	5795	1	1098	MIDKGDITDPSEIQTIREYYNYLY TNKLENLEEMDKFLDTYTL PRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVS KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWKSI PCSWV GRINIMKMAILPKVIYRFNAIPNKLP MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES*
5473	10970	A	5796	1	1245	
5474	10971	A	5797	1	969	MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKKWKNI PCS WVGRINIVKIALPKVIYRFAIPKLP PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTLEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKDWL/LRFCTAK*TTIRV
5475	10972	B	5798	1	1383	MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEITNCLSDHSAIKLELRIKKLTQ NRSTTWKLNLLNLDYVWHNEMK AEIKMFFETNENKDTTYQNLRTLK AVCRGKFVALNAHQKQKISKIDTL TSQLEKEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINDSRSWAIR QEKEIKGIQLGKEEVQLSLFADDMI VHLENPIVSAQNLLKLIGNFSKVS YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAISIK LPMTFFTELGKPTLKLWNQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYWYQNRDIDQWNRTEP SEIMPHITTI*
5476	10973	A	5799	1	1272	MIISMDAEKAFDKIQQCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPSPLLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSGYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSL FNKWCWENWLAK CRKLKLHPFLTPYTKINSRWIKDLH VRPKTIKTLEENLGITQDKGMGKD FMSKTPEALATKANIDKSDLIKLS SCK\ETTIRVNRQPTWEKIFAIYSS
5477	10974	A	5800	1	1398	
5478	10975	A	5801	564	2444	LTNQKKSRTRWIHSRILPEVQGGAV LEVLARAIRQE\EVKGIQLGKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSGYKINVQKSQAFLYTNN RETESQIMSELPFTTASRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIAILPKVICI FNAIPIKLPMTFFTELEKTTLKFIRNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYWYQNRDIDQW NRTEPSEIILHIYNHLIFDTPDKNKK WGKDSL FNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK TLEENLGNTIQDIGIGKDFMTKTQK AMATNAEIHKWDLIKLFHCTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIYKRKTNNPINKWAKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIIKK SGNNRCWRGCGENHSQQTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLVVFFGLCQNAFNLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPSSSTS S
5479	10976	A	5802	1	2430	
5480	10977	A	5803	2022	4573	
5481	10978	A	5804	1169	3077	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSGYKINVQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNILFDK PDKNKKWKGDSL FNK WFWENCL AICRKLKLDPFLATNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIKLSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK K\TNNPIKKWAKDTNRHFSKEDIYA ANRHMRCSSSLVIREMQIKTTMR YHLTPVRTAIKKSGDNRCWRGCGE IGTLLHCWWDCKLVQPLWKS VWR FLRDLELEIPFDPAPLLGIYPKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKMWHIYTMYYAAI KNDEFVSFVG TWKLEIILSKLSQE QKTKHCIFSLIGGN
5482	10979	A	5806	133	358	
5483	10980	A	5807	3	164	
5484	10981	A	5808	1573	1720	
5485	10982	A	5809	1573	1720	
5486	10983	A	5810	1	4860	
5487	10984	A	5811	2	2887	VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLPP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIKLLNKLKQQQQQQQ QHSENKRENSDPEESWENLVSD DFSALSLESANVEDLEPVRNLFRL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRVVVAVGETGSGKSTQV PHFLLEDLLLNEWEASKCNIVCTQP RRISAVSLANRVCDLGCENGPG\G RNSLCGYQIRMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EVHER/SVQSDFLIILKEILQKRS LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIIEETGFVLEK

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						DSEYCQKFLEEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFYQKY SSRTQHAILYMNPBKINLDLILELLA YLDKSPQFRNIEGAVLIFLPLAHIQ QLYDLLSNDRRFYSEYKVIALLHSI LSTQDQAAAFLLPPGVRKIVLATNI AETGITPDVVFVIDTGRTKENKYHE SSQMSSLVETFSKASALQRQGRA GRVRDGFRCFRMYTRERFEGFMDYS VPEILRVLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQHLAALPVNVKI GKMLIFGAIFGCLDPVATLAAMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRNRLNRTSLLTLEDVKQELI KLVKAAGFSSSTSTSWEGNRASQT LSFQEIALLKAVLVAGLYDNVKGII YTKSVDVTEKLACIVETAQKKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRRETTLITPPFVLLFGGDIEVQH RERLLSIDGWYFQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QITELIKTENN
5488	10985	A	5812	1	132	
5489	10986	A	5813	383	667	
5490	10987	A	5814	2444	2755	DYYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5491	10988	A	5815	1724	1941	AHLLYEWIFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPG\SQSDSPAS ASWVAGITGACHHARHEWNFKC
5492	10989	A	5817	37	2496	
5493	10990	A	5818	2	1814	
5494	10991	A	5819	1	394	
5495	10992	A	5820	2	1785	QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTTFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSSTANSCSSSASNTPGAP ETHPSSSPTPTSSNTQEEAQSSVSD LSPMSMPFASNSEPAPLTLSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATIHQDPQSIFVT NPVTLTTPQGPAAVQLSSAVNIMN GSQMHNIPANKSLPPTFGPATLFNH FSSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQRVSTSPVGLP SIDPSG\SSPSSSSAPL\ASFSGIPGNQ GFFLQGPVAPVGGLSFNRQHF/SFP HPWTSASNSCDSPIPSVSSGSSSPLS ATSAPPTLG\QPKGSQCQSRIRKGY LPIGTERLARILQGGVAQAPAGT SFVAPVGHSGVWSFGVNAVSEGLAS GWSQSVMG\NHMAFNFFSGPKAH FSQHQPIMERDDSGMVAPSNIFHQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MASGFVDFSKGLPISMYGGTIIPSHP QLADVPGGPLFNGLHNPDPAWNPM IKVIQNSTECTDAQQVKA
5496	10993	A	5821	3	125	
5497	10994	A	5822	3448	3831	KNRFCSGVSSNSKSNNSCVYVYIDR DIDTHTYIHIHTNICIHLFFFFFETES HALSPRLECNGVISAHCNLHPPGASS DSPASAARVAGVTGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR*S TPLGFPKC*DYRR/AAIVPGIFLLH*I R*KVPTLLTDMRNASEYDCDFSTN KIDKEETF*S*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 25 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-5497.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with
 - 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the
 - 15 sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
 - 25
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so
5 that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from
10 the group consisting of a polynucleotide sequence of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-5497, under conditions sufficient to express the polypeptide in said cell; and

15 b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5498-10994, the mature protein portion thereof, or the active domain thereof.

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21 The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-5497.

25 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

30 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.